Multi agent Simulation: A Unified Framework for the analysis of viral infections within a bovine population

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Abstract

Multi-agent systems [1] is an approach which allows to study population dynamics from a qualitative point of view by defining the attributes and the behaviors for the interacting individuals of the system . So, multi agent systems allow the design and the implementation of the individual models proposed for the study of population dynamics which have major advantages compared to the aggregate models. The present paper presents a multi agent based framework for the simulation of the impact of viral infections on a population of cows which may be modern (only females) or mixed. This simulation creates an artificial life [2] [3] which will make it possible to the user to feel in a virtual laboratory and will facilitate to him the forecasts of the impact of viral infections on the evolution of the targeted population..

Keywords: *multi agent systems, viral infection, modeling and simulation, population dynamics, artificial life.*

1 – Introduction

The dairy production estimated to two Billion liters per year covers only the 2/3 of the Algerian citizens needs. The remainder is a billion liters of milk, imported in the form of dried milk and represents an invoice exceeding a Billion of Dollars. This involves enormous economic losses and does not allow Algeria to have its food independence as regards dairy production. To cure in this irrefutable fact, Algeria tries to develop the bovine breeding, by importing of cows with high genetic potential. Unfortunately these an imals, too selected for the dairy production, became too sensitive to various pathologies, in particular the viral diseases. These last are often underhand and with fast trans mission, so that when the veterinary surgeons decide for a decision making, it is often too late. The ideal would be to have tools able to envisage the evolution of these diseases, and which make it possible to anticipate the fatal consequences of these viral diseases by fast and suitable decision making. The discounted objective of this work is the creation of thi s kind of tools. It is a question of proposing a unified framework allowing the study of the evolution of the viral infections within a population of dairy cows. The dynamics of the interactions between the indivi duals (cows) is a nonlinear dynamics (nonlinear evolution in time), which will encourage us to call upon the individual models of the dynamics of the pop ulations “the individual is the handled basic entity” [4]. In this tool each individual will be represented by an agent to which we assign a set of attributes and behaviors allowing us to follow its evolution [5]. The agents carry out their procedures simultaneously and are distinguished from/to each other; the addition or the withdrawal of an agent or a set of agents is easy [6], which will enable us to be closer to reality.

The proposed tool is able to study all the viral diseases within a high bovine population in a modern way or on a mixed population. The first type of population is only made up of females since the males are sold after 3 months as of their birth and then stockbreeders use artificial insemination for the reproduction of these cows. The second type of population is made up of males and females with various ages. To carry out simulations, the user of this tool will limit himself to introduce the parameters of the disease on which he wants to make a study and the characteristics of the studied populati on (for example: the number of patients at the time of the declaration of the disease and the number of males in the population).

2. Related work

In the first work [7], the authors used the Multi agent system approach to model the impact of the Virus of the Human Immunodeficiency (HIV) on a population made up of cells intervening during the infection. In order to show the effectiveness of the individual model compared to the aggregate model based on mathematics. In this work the objective consists in creating a virtual environment in which the various agents evolve and interact between them. It is an environment with three dimensions corresponding to 1 mm^3 of blood. Three classes of agents were conceived simulating cells which are: The agents cells CD4, the agents infected cells CD4, the agents virus VIH besides another agent representing body THYMUS responsible for the production of cells CD4. The results obtained show the benefits of the Multi agent system approach making it possible to bring us closer to the reality.
The second work [8] aiming to study the impact of the practices of breeding and measurements of control on the dynamics of CIRCOVIRUS type-2 infection within a porcine population. In this work, a stochastic mathematical model in discrete time describing the dynamics of population in a porcine breeding of the standard borne -fattener, was developed. The results of this study show in particular the effect of the preventive measures, such as vaccination on the attenuation of the epidemic propagation.

The first work uses an individual model and implements it by a multi agent system but takes into account only one type of infection. In the second work, besides its taking into account of only one type of infection, rests on a discrete and stochastic model of the epidemic thus supposes automatically that the individuals have similar behaviors but each individual is primarily influenced by the behavior of the individuals of its entourage.

3. The Adopted approach

Contrary to similar work, our approach tries to propose a general framework of multi agent simulation taking into account a large range of viral infections within a population of cows. The discounted goal is to provide a powerful tool for simulation to be used by veterinary surgeons and epidemiologists enabling them to envisage the evolution of these diseases on a modern or mixed population and to prevent the consequences of these last by adequate decision making at the convenient period. We tried to approach to the maximum of reality by taking into account of two types of modern and traditional breeding, the consideration of the horizontal/vertical transmission of the diseases. Also, and by preoccupation with extensibility, the various parameters of the viruses are modifiable by the user because these factors can vary during the duration of study, for example increase in the virulence of the virus. Before describing our multi agent based approach, we will make a panorama on the domain

of discourse.

3.1 Description of the domain of discourse

The cows produce, in general a calf a year, they give their first calf when they are three years old. Their average lifetime is 15 years, during which, they can produce 10 calves. They live in certain promiscuity and have an average space of 10 m^2 by cow. The exploitation is only made up of females (dairy cows and heifers of replacement), the males are sold as of their birth. The stockbreeder uses artificial insemination for the reproduction of his cows. According to the objectives of the stockbreeders, we can find two types of populations: population only made up of females (dairy cows and heifers of replacement), the males are sold as of their birth. The stockbreeder uses artificial insemination for the reproduction of his cows (modern breeding). The second type of population is called “mixed”, i.e. composed of males and females at various ages.
During their diseases the animals can transmit microbes to other animals. This transmission of disease is called “contagion” and its rate varies according to the nature of disease. The sick animals can cure if they develop antibodies which confer immunity to them. The time necessary to obtain an immunity (lasted of immunity) depends on the type of the disease. The chances so that a sick animal acquires immunity depend on its conditions of breeding (food, hygiene, and parasitism). Indeed weak animals are unable to resist, they are more sensitive to the disease, and can die throughout installation

of immunity (mortality rate during the acute phase). The more resistant animals, can resist the disease and develop immu nity (chance of survival), some among can, nevertheless to die, but mortality rate in this case is weaker. Besides these parameters, it is necessary to take into account the fact that certain diseases are transmis sible from mothers to calves during their birth.

3.2 Agents of our system and their interactions

Each agent is characterized by a set of attributes and of behaviors. The attributes selected are: Age, Disease_ Counter, Number_ of _ Children, sex (M/F), Immunized (O/N), Patient (O/N). The agents are distinguished by behaviors common to all the individuals: (Ageing, Displacement), behaviors common to animals of female sex (Reproduction) and behaviors of the sick animals: (Infected,Recovered). The interactions between the agents are expressed by the transfer of the disease (contagion) which is concretized in the behaviors Infected and Displacement. Fi gures 1 and 2 illustrate these interactions.

4. Implementation and results of simu lation

We used Netlogo platform [9] which is a multi-agent programming language and an environment for the simulation of natural and social phenomena. It is particularly well adapted for the simulation of complex systems evolving through time.

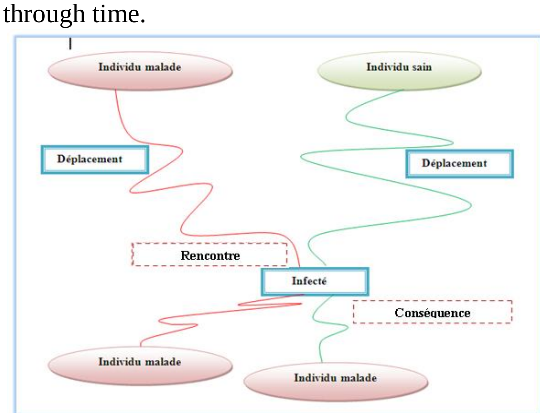


Fig. 1 Interaction between agents

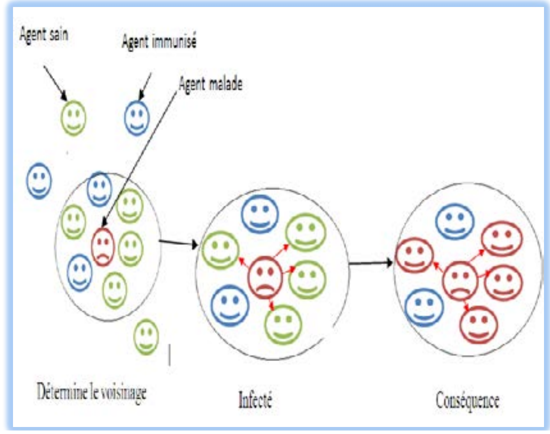


Fig. 2 Another representation of the Interaction between agents

Modelers can allot instructions to hundreds or thousands o f the independent agents in order to make operations simultaneously. This is why, one can explore connections between small degree be haviors of agents and the great degree ones which emergent after their interactions. The world of Netlogo consists of re active and mobile agents which can carry out behaviors in a simultaneous way. Three types of agents exist under Netlogo: *Patches*, *Turtles* and *Observer*. Turtles represent agents. The patch represents the environment of the agents . The evolution of simulation is managed by the Observer agent. Figure 3 and figure 4 show part of the developed code. With an aim of illustrating the interest of our application, we will take as example certain typical viral diseases (See Table 1). We will base ourselves on the specific parameters which characterize ea ch disease namely: rates of contagion, of mortality in acute phase, duration of immunity acquisition of and the chance of survival and we will establish a forecast of the impact of these diseases on the e volution of the population namely: patient, healthy, immun ized (Figures 5,6; Figures 7,8; Figures 9,10; Figures 11 ,12).

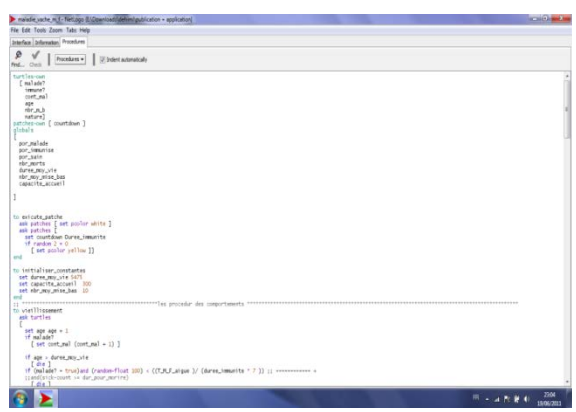


Fig. 3 A part of the developed code

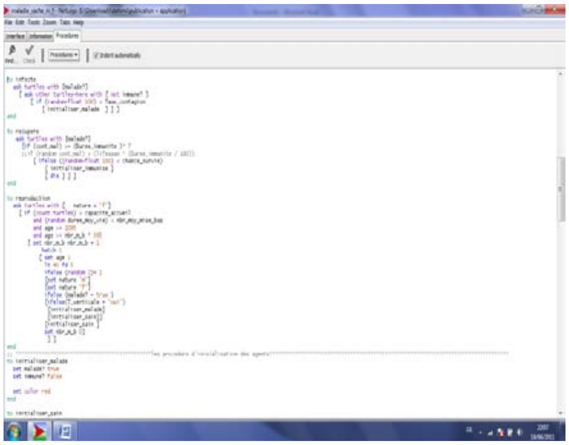
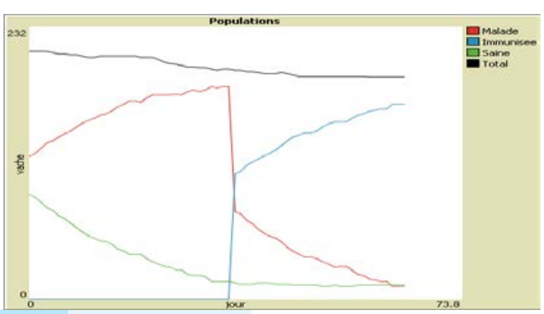


Fig. 4 Another part of the developed code

Table 1: parameters of certain typical Viral diseases

Disease	incubation	Contagion rate	Mortality rate	cause	Chance of survival	Installation of immunity	Contagion mode	transmission vertical
Foot-and-mouth disease	2 - 7 days	80%	5%	virus	99%	21 days	contact	no
Plague of the ruminants	3 – 10 days	90%	80%	virus	90%	10 days	contact	no
Infectious Rhinotracheine (I.B.R)	2 - 4 days	80%	15%	Virus	98%	35 days	contact	yes
Virus of the bovine viral diarrhea (B.V.D)	07 days	85%	50%	virus	90%	15 days	contact	no

I.B. R



Plague of the ruminants

Fig. 5 Appearance of immunized individuals

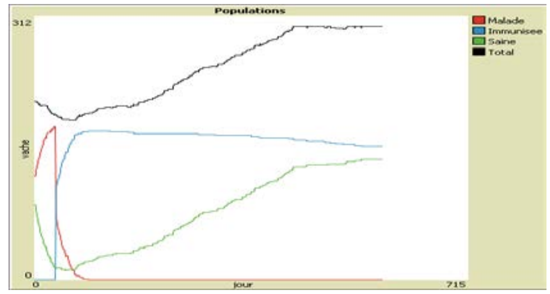


Fig. 6 Stabilization

B.V.D

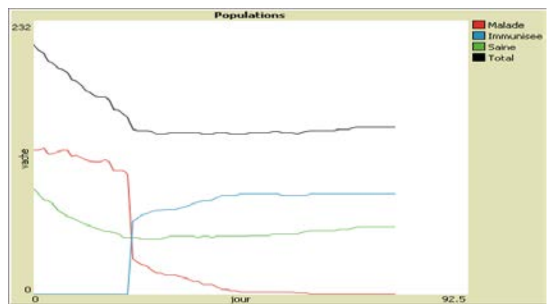


Fig. 7 Appearance of immunized individuals

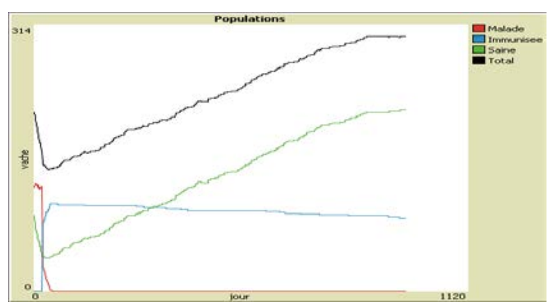


Fig. 8 Stabilization

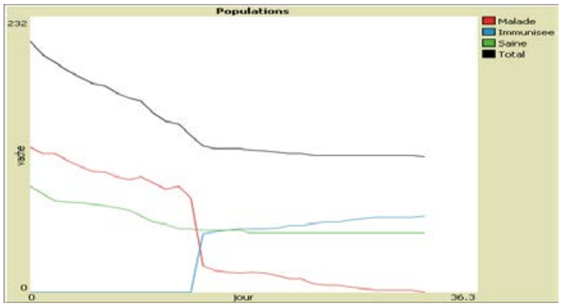


Fig. 9 Appearance of immunized individuals

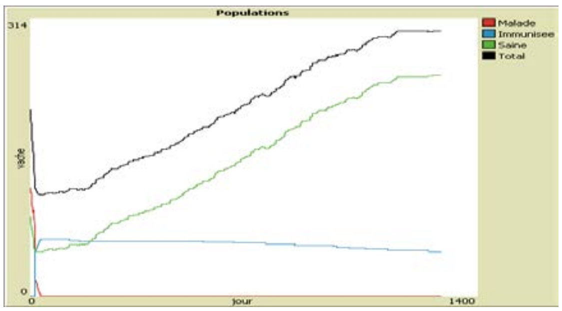


Fig. 10 Stabilization

Foot-and-mouth disease

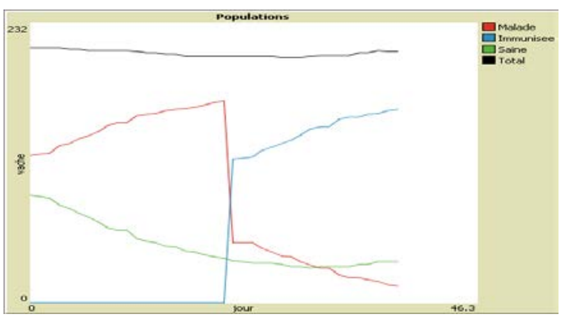


Fig. 11 Appearance of immunized individuals

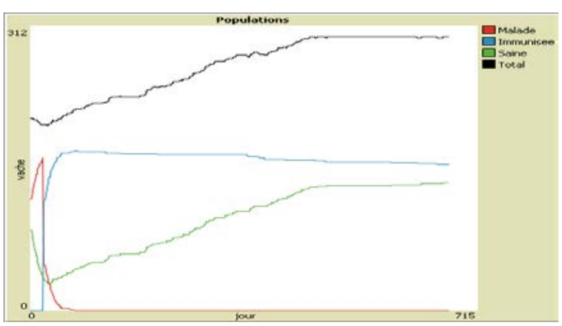


Fig. 12 Stabilization

5. Conclusion

Population dynamics behaves as a complex system with an unforeseeable evolution in time, the study of this kind of systems must be done using the individual directed model which justified our choice for the use of agent based modeling and simulation approach. Indeed, the use of the a gent paradigm enabled us to represent the individuals as agents, distinguished from each other, each one being able to move, reproduce and transmit the disease. Also, it enabled us to produce a tool able to envisage the impact of the viral diseases in a reliable and perennial way, very useful for the epidemiologists, offering a practical complement to them t o their biological theories in the fight against the underhan d and unforeseeable effects of the viral diseases. The only disadvantage would be the fact that the simulation of the typical cases takes much time but on the other hand gives better results. Nevertheless, our work remains open to other improvemen ts namely:

- Generalizing our tool so that it will be able to deal with any type of population.
- Introducing fuzzy parameters enabling us to create classes of cases of simulation thus facilitating decisi on making for the users of this tool.

References

[1] J. Ferber, Multi-Agent Systems: An Introduction to Distributed Artificial Intelligence. Addison-Wesley Longman Publishing Co., Inc., 1999.

[2] D. Floreano and S. Nolfi , “Adaptive behavior in competing co-evolving species”, In the Proceedings of the 4th European Conference on Artificial Life , 1997, Edited by Husbands P., Harvey I., MIT Press, Cambridge, p.378–387.

[3] J. Ventrella., “Emergent morphology and locomotion without a fitness function”, In the Proceedings of the 4th International Conference on Simulation of Adaptive Behavior, 1996, Edited by Maes P., Mataric M.J., Meyer J.A. PollackJ., Wilson S.W., MIT

Press, p.484–495.

[4] A. Lomnicki, “Population ecology from the individual perspective". In Individual-based models and approaches in ecology, 1999, Edited by de Angelis D. and Gross L. J. Chapman and Hall, New York, p.3–17.

[5] M. Bouzid,. “Contribution à la modélisation de l’interaction Agent/Environnement, modélisation stochastique et simulation parallèle », Thèse de doctorat de l’université Henri Poincaré, Laboratoire Lorrain de recherche en informatique et ses applications, Nancy, France, 2001.

[6] P. Ballet, “Intérêts Mutuels des Systèmes Multi-agents et de l’Immunologie. Applications à l’immunologie, l’hématologie et au traitement d’image“, Thèse de doctorat Université De Bretagne Occidentale, France, 2000.

[7] L. Toufik, and T. Bornia. “Modélisation en dynamique des populations, intérêt de l’approche Multi-Agents“ , in Proceedings of MajecSTIC, 2009, Avignon, France, 16- 18 Novembre 2009.

[8] A. Mathieu, G. Béatrice, A. J, François, and R. Nicolas, “Étude de l’impact des pratiques d’élevage et de mesures de maîtrise sur la dynamique d’infection par le Circovirus porcin de type 2: une approche par modélisation“, Bulletin Epidémiologique N° 33, 2009, pp : 7-10
http://www.afssa.fr/bulletin-epidemiologique/Documents/BEP-mg-BE33.pdf

[9] NetLogo Uri Wilensky. NetLogo 4.0.2 User Manual. http://ccl.northwestern.edu/netlogo/docs/NetLogoUser Manual.pdf

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