Applications of Multilevel Cellular Automata in Epidemiology

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Abstract: This paper presents a multilevel simulator for a hierarchical cellular automata with applications in epidemiology, describing some particular experiments and general capacities of the model. In the particular example of the spreading of an infectious disease between children, various realistic features can be modeled with this tool. Taking into account the recent outspreading of various dangerous epidemics, the tool proposed here can be very useful for development of health strategies in fighting these epidemics, mainly because it can be easily configured for different landscapes and for the configuration of a particular city.

Key-Words: Cellular automata, virtual environment, epidemiology

1 Introduction

Recently it became obvious that in spite of remarkable progress achieved in medicine and pharmacy (industry and research) development, humanity is confronted with new diseases, new viruses and different major epidemics which threat cannot longer be ignored. Many issues in this domain are not yet clearly understood, including the origin of the new viruses, the infection processes, the efficiency of the vaccination etc. Epidemiology is a science that becomes more and more important as major issues emerge in health policy. Scientific tools to model the facts and different aspects of an epidemic, including spatial (landscape) spreading could be a tremendous help for understanding, predicting and fighting a specific epidemic. New tools and simulators are wellcome in order to elaborate health policies and strategies to defend epidemics from their very beginning.

Major challenges for epidemic models could be verification of the new hypothesis regarding infection processes, including chemtrails. One of the many concerns of researchers in the field of epidemiology is the emergence of new viruses, that require fast development of antidotes, i.e. vaccines. The problem is that the omologation process of any medicine requires lot of tests and long-time studies, that are lately easily skipped, because of the imminence of threats of new epidemics. Is this policy a good bet for the future of the humankind?

The main subject of this paper is an application of the cellular automata in epidemiology. Could this amazingly simple and elegant model sustain such complex issues as those rised by the specific domain of epidemiology? It seems that, with elementary adjustments and adequate setting of parameters, cellular automata offer an attractive tool for exploration of various conditions and aspects of epidemics, vaccination and related topics.

Modern medicine, as modern pharmacology, cannot be concived without the presence of different complex electronic systems and without computers, starting with databases, visualisation of results of medical investigations, modelling of different aspects and simulation of various processes. The spreading of infectious diseases is such a domain where new modelling tools are generally wellcomed, because of the many factors that affect trasmission and spread, the complex interactions between those, the incidence of various stochastic processes and uncertainties and also because of the difficulty to see the “big picture” starting from particular events. A computer model can give the possibility to make virtual experiments and also to understand the dynamics of the processes.

The models can be classified in four great categories:

- Decision Analytic Models
- Compartment Models
- Discrete Event Simulation
- Agent-Based Models
The simplest version of the agent-based models is the cellular automata model.

2 Cellular automata: simple and effective

Although the model was theoretically described by John von Neumann in 1950, cellular automata made a dramatic entry in the computer science world only in the 70s, with the popular Game of Life invented by John Conway. The elegant model of the Game of Life is still considered to be the origin of the artificial life research domain. In the context of our subject, it is the most appropriate example to introduce the model of cellular automata.

Consider a regular landscape of elementary cells, each of them having two possible states: 1 or 0. The logic states can be associated with the presence (or, respectively, absence), of a living cell – meaning simply that the cell is “alive” or “dead”. The landscape thus become a population of cells that evolves by elementary timesteps, forming generations and patterns that reveal a fascinating variety, in spite of the very simple rule hidden behind. The rule first proposed by Conway can be stated as simple as that: if a living cell has 2 or 3 living neighbours, it will continue to live, if not, it will die either of loneliness (if it has less neighbours), or of overcrowding (if it has more). A “dead” cell can be brought to life by the presence of exactly 3 living neighbours.

Different variations of the model were afterwards discovered and studied. Still, the basic cellular automata computer model is defined by to elements:
- a regular grid, or network, or landscape, consisting of elementary cells locally interconnected
- a set of local rules that describe the evolution of each cell, thus meaning that each cell evolve depending on the specific state of its neighbourhood.

The main characteristic of cellular automata is the apparent complex global evolution, based on simple local rules and simple local interconnection patterns. The huge variety of possible evolutions make cellular automata an interesting choice for various modelling and simulation applications, but one should take into account the important restriction of difficult and empiric synthesis process. By now, in spite of various interesting and valuable studies, there is still no clear method to develop applications of cellular automata, i.e. to obtain the local rules that will lead to a specific global behaviour.

Theoretical results are very promising, stating doubtlesly that cellular automata is an universal computation model. Everything that can be computed with a Turing machine can also be computed with cellular automata, even if there is no algorithm to discover the solution.

Researchers in the field of cellular automata underline their efficiency in modelling applications, where the synthesis process is significantly eased by similarities with the physical, chemical, ecological, sociological etc. processed to be modelled. Very difficult tasks, as turbulent flow or concrete solidification can be realisticaly modelled with cellular automata. There are certain domains where the model is definitelly the best choice, as for instance turbulent flow, forest fire, traffic simulation etc.

In epidemiology, cellular automata can find another area of applications, since many researchers reported good results in particular modelling and simulation tasks. Such interesting results are:
- landscape epidemiology: study of spreading of different diseases;
- a case study of avian influenza in Indonesia (Java and Sumatra), the epidemic in the beginning of 2004;
- interesting studies are also those that discuss the efficiency of the vaccination, proposing different strategies of vaccinations, etc.

3. Multilayered (multilevel or hierachical) cellular automata as modeling and simulation tool

Multilayered cellular automata, a slightly variation of the basic concept of cellular automata, offer a wide variety of new computing possibilities and, most of all, synthesis methods. The idea is simple: the cellular automata is defined as such at least at two levels. Each cell of the main (top) level of the cellular automata is in its turn a cellular automata, defining the internal behaviour of one structural element from the top level. The phenomena can thus be modelled both at macroscopic and microscopic level, offering a huge variety of new computing possibilities. In order to
understand the impact of this structural and conceptual innovation, one should take into account the fact that cellular automata model implies a set of simple processing elements named cells (that are usualy finite automata) connected in a simple, regular network (that may be unidimensional, bidimensional or multidimensional) that evolve according to simple local evolution rules (that are digital functions). The evolution rules are “local” because their variables are the states of the neighbourhood of each cell.

The concept of multilayered cellular automata does not mean the addition of a new dimension for the array of processing elements, but simply adding internal rules of evolution for each cell, offering the possibility to explore the correlation between the phenomena that take place at microscopic and macroscopic level.

When applying this model to design a modelling and simulation tool, the following features can model different aspects of the phenomena:
- the topology of the connection network
- the dimension of the array of processing elements
- the topology of the neighbourhood and the number of cells in the neighbourhood
- the number of states of the finite automata (the cells) and their significance
- the local function
- all parameters mentioned above, for the second hierarchical level.

The parameters that affect drastically the complexity of the computation are the number of variables of the digital functions, related with the dimension of the neighbourhood and mostly the number of state bits of each finite automata.

The simulator was developed for much more complex sociologic applications, so the version presented here is simplified for particular issues in epidemiologic applications. Taking into account the specificity of the model, best appropriate applications stick to geographical representations (the direct correlation between the two-dimensional array of cells and the geographical area where the epidemics take place). Any other type of applications would be less explicit and effective.

Figure 1 Captures from the main window of the simulator, with menus and functions
Main applications of this model in epidemiology are: the analysis of the evolution of the infection area in case of an epidemics (and correct estimation of infection sources and spreading phenomena) and the study of the impact of profilaxy strategies, in order to develop most efficient emergency plans that should stop or minimize the damages (number of infected persons and number of casualties).

The majority of existing epidemic models, based of differential equations, do not take into account many spatial factors, as for instance population dynamics and density. These models, such as those using Markov chains, assume populations are closed and “well mixed”; implying high (and constant) rate of mobility, in terms of host numbers and possibility to travel anywhere. More realistic models should incorporate spatial parameters to reflect the heterogeneous real environment.

4. Experimental results

This experiment is inspired by the recent epidemics that took place in Romania. Several political decisions where made in order to limit their spreading, and some of this decisions refer to the education system (closing schools, vaccination campaigns). The experiment applies the multilayered cellular automata model to study the spreading of an infectious disease between children, who are most vulnerable in such cases mainly because they are daily exposed to possible contamination in large colectivities such as schools.

Assume the cellular automata network reproduce the simplified map of a town divided in 25 districts. At the first hierarchical level the model consists of a lattice of 5x5 cells, with the central zone distinctly designed. Each district itself is modelled as a cellular automata with a lattice of 100x100 cells, having 3 schools each and 10 playgrounds (in the central zone there are only 5 playgrounds). In this experiment the location of these is determined randomly, but it can be easily ajusted to real conditions.

Let’s assume that:
- the population of children is uniform in each district, but with different values – for instance, in the central zone it is lower;
- most children go to school at the closest school in their district, but a number of kids will go to better schools that located in the central zone;
- the capacity is equal for all schools, but can be set at different values;
- all children play in the playground closest to their home, excepting the central zones where not all of them are allowed to go out to the playground;
- some of the children travel by public transportation system, but some of them travel with their family cars.

Hence, the child is exposed to contact to other persons and contaminations appear most probably in schools, in public transportation system or at the playground. Main parameters of the simulations are the probability to get infected in each of these 3 cases, toghether with the mobility of the population of the children in their own neighbourhood or between their home and the central zone and the rate of children that move around in the public transportation system.
The second level cellular automata consist of a lattice of 100x100 cells. The “landscape” contains: 3 schools, 5 playgrounds, circulation zones (comercial zones and streets) and private zones (buildings) for living. In each such zones there is a probability of infection. The mobility of the population of children is generally considered to be low, since they don’t walk around too much except for going to school or playing in the playground, also the risk of infection in commercial zones is considered to be lower mainly because children spend less time there.

The different conditions of a particular agent can be: healthy, infected (during the incubation period), ill, immune having different symbols in the simulations (visible only at the lowest level as for instance in figure 3.

Figure 3. Detail of local state during simulation

In figure 3 the population of agents move around a school (hexagon) and a playground (circle). The grey cells correspond to infected children and the diagonal cross to immune (vaccinated) children. The spreading of the disease can be visualised as the evolution of the population of “gray cells”.

Figure 4 illustrates the spreading of a disease in one district, starting from one infection spot in one public school, at various timesteps (the initial state is reproduced in figure 2).
5. Conclusions

The experiment confirms that the greatest danger of contamination appears in schools, because of the large number of kids that interact and because their living places are distributed in a much larger space, where they interfere (for instance at the playground) with children going to different schools. Taking into account the specificity of each epidemics, including the period of latency and recovery, this type of simulations can suggest most effective health policy that should be applied in each case, including quarantine and vaccination.

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