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Enhanced Cellular Automata with Autonomous Agents for Covid-19 Pandemic Modeling

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Abstract. The paper presents several experiments realized with an original model, the enhanced cellular automata with autonomous agents, in order to simulate the evolution of disease spreading. The simulations presented in the paper contain specific details of the actual Covid-19 infection: the atypicality of evolution of cases, the proximity required for infection, the long gestation time. The simulations show that the combination of cellular automata with autonomous agents can be used to model the evolution of a disease, due to its sensitivity to parameters associated to processes of infection and healing. The ability of the modeling system to find critical situations is also discussed. The details of the model include the topography of the space (contextual cellular automata), the timer associated with each autonomous agent to model the change of state (and the testing strategies), a FIFO memory that models the treatment facilities and the global control loop that introduces the central control of the system associated to the law enforcement and authorities.

1. Introduction

This paper presents a model for epidemics evolution, which is a topic of maximum interest in the context of the global Covid-19 pandemic. Scientific tools that could help the design of best strategies of crisis management and realistic forecast are requested in such situations. Some studies show that the Covid-19 pandemic will lead to social unrest in countries with poorly developed health systems [1], while other studies are optimistic and predict that the pandemic will be stopped by restrictive measures [2].

The dynamics of the epidemic spreading phenomena in large populations can be controlled and even stopped efficiently if appropriate measures are taken and especially if those measures

are tailored to the specificity of each population. A model including factors that influence the dynamics of the epidemic and the dynamics of the population, could be of much help for authorities and scientists in this context.

The next section presents the state of the art in epidemic modelling. The next section introduces the model of combined cellular automata with autonomous agents and presents four improvements we propose for the cellular automata in order to deal more accurately with the problems raised by modelling epidemics. The main part of the article presents several experiments with the enhanced model. The model takes into consideration specific details of the actual Covid-19 infection: the atypicality of evolution of cases, the proximity required for infection, the long gestation time.

The aim of this paper is to show that the combined model of cellular automata with autonomous agents can be used to model the evolution of a disease. The sensitivity of the model to the various parameters of the system will be emphasized. The ability of the modeling system to find critical situations is proved. The last section presents some concluding remarks and future development of this work.

2. Overview of Scientific Literature

Most of the simulators for modeling epidemics are based on one of these three computing models: the agent-based model, the large-scale spatial model and the dynamic system-based model [3, 4].

Simulators using the agent-based model involve the behavioral description of individuals and the mechanisms of epidemic spread in a particular spatial topography [5]. These simulators require a lot of input data and high computing power. They are used for restricted geographical topographies in which accurate forecasts of the spread of the epidemic are desired [6–8]. In [6] several strategies for stopping the smallpox epidemic were analyzed. The dynamic bipartite graphs were used to model the physical contact patterns resulting from the movements of individuals between certain locations. The studies from [7] shows that border restrictions and/or internal travel restrictions are unlikely to delay spread by more than 2-3 weeks. A stochastic influenza simulation model for rural Southeast Asia was used to investigate the effectiveness of targeted antiviral prophylaxis quarantine [8]. Simulators from this category use real data about the population distribution in a precise topographic space (city GeoMAP) and intend to offer an efficient identification of the best measures to stop the epidemic [5]. In [5] spatial and temporal patterns of disease diffusion among zero-intelligent agents were compared to those produced by a population of intelligent agents.

Large-scale spatial model simulators involve dividing the population into groups by regions, describing the connections between groups, and the behavioral patterns within each group that also determine a certain infection rate [9–11]. In [9] was highlighted the role of the time frame for setting up interventions, where and at what administrative levels in order to control the spread of epidemic. In [11] are presented the results of simulations of an SEIR epidemic model coupled with air transportation data for 52 global cities. The second category simulators use statistical data. They are used to model epidemics on large geo- graphical areas (countries, continents) and provide general forecasts based on a large number of simulations runs [3].

The model based on dynamic systems uses differential equations, stock and flow diagrams for graphical representation of the three states of the individuals: Susceptible- Infected-Recovered

[12, 13]. A simulator based on differential equations for the infectious disease Varicella is presented in [12].

In addition to these three major categories, hybrid simulators that combine two models were built, such as the GLEAM (Global Epidemic and Mobility project) simulator: a hybrid stochastic simulator that relies on the structured meta-population GLEAM model worldwide, while at the same time using a high-resolution agent-based model (ABM) in selected countries [14].

Cellular automata model is included into the first category of models and being massively parallel systems are ideal for modelling self-organized criticality and chaos theory phenomena that characterize pandemics [4, 15]. Cellular automatons are thus used for artificial society simulators, in which complex phenomena that occur in large populations of individuals are studied, most commonly known as John Conway's Game of Life [16]. In artificial societies simulators, the phenomena generated by a pandemic are studied both at the individual level (Healthy, Carrier, Infected, Recovered or Dead) and at the population level (the decrease of the standard of living, social, economic and political implications) [18, 20].

3. Enhanced Model of Cellular Automata with Autonomous Agents

Cellular automata consist of a network of interconnected cells that evolve synchronously based on evolution local rules. They are completely defined by their topology, the cell functionality [21] and by the boundary conditions in case of non-ring (linear, planar) topologies [22–24]. One of the main models of massive parallelism, cellular automata provide efficient tools for com- plex systems modelling [25]. The model was also used to study criticality phenomena: systems with an evolution that changes abruptly due to the action of a combination of factors at a critical time.

Cellular automata models allow the identification of those critical moments in the evolution of a phenomenon that causes its general state to jump out of the predicted path and inevitably produce a catastrophe. Within the evolution of an epidemic there are critical moments of time in which the dynamics of the epidemic can change radically, and if we act before those critical moments of time with certain effective measures the epidemic can be stopped. In order for intervention measures to be very effective, they must be applied at certain key points in the area where the population of individuals lives. If the dynamics of an epidemic are studied from this point of view, then it will be possible to identify in advance those critical moments in which the local rules of evolution that are applied to cells must be changed so that the evolution of the general condition does not lead irreversibly to a catastrophe. In studying the phenomena that characterize the spread of an epidemic, it is important to identify not only those factors that accelerate the dynamics of these phenomena but also those that slow it down.

The basic model of cellular automata may be combined with that of the autonomous agents that evolve in the cellular space. An agent-based model cellular automaton is a tool for simulating a group of autonomous agents with the purpose of analyzing how the system as a whole evolves. In an agent-based model each agent follows a specific set of rules. As an observer, we can see how these rules impact the overall behavior of the system. Such a model was already used in the so-called "artificial societies" [17–19] for simulation of simple collective phenomena associated to the social behavior of a population distributed over a cellular space. The dynamic of a population is determined by both micro and macro factors:

- micro factors (level of individuals): the behavior of individuals, interaction between individuals, interaction of individuals with the environment;

- macro factors (level of population): the topography of the locality, the total number of people, the distribution of the population by categories of vulnerability, the standard of living and the specificity of the economic activities of the population, the political and social priorities of the population, the number of health institutions and the existence of medical personnel, the existence of law enforcement for the implementation of restrictive measures, etc.

A simulator in which these factors are ignored will not be able to model the real dynamic of an epidemic spread in that population, and will not be able to identify those measures that will stop the epidemic.

In order to increase the accuracy of modelling an epidemic, we propose additional features to the hybrid model of cellular automata, as follows:

1. elements of a restrictive context are included in the cellular space where the actors evolve. The experimental space in not uniform, and can be adjusted to the specificity of a building, in our model.

2. a timer for each actor is defined. It is used by each actor internally, to decide its states evolution.

3. an associated FIFO (first-in-first out) memory is added to the model. The actors can be temporary moved from the simulation space, into the FIFO memory, in order to change their state.

4. a global loop is closed over the cellular automaton [26, 27]. This acts as a control mechanism, as it changes the values of some parameters according to the evolution.

All the components of the enhanced model will be explained in the following section.

4. Experiments with Enhanced CA Models

The basic model in our experiments consists of the cellular space plus autonomous agents, that model the humans moving in a certain space. Each agent is in one of three states, that are associated with health, sickness, and immunity. The representation of the agents is directional (i.e, each actor has a “face”) is order to model the face-to-face contact of persons. The agents can move into unoccupied neighboring cells in the main directions (up, down, left, right). The disease is transmitted by proximity between sick and healthy people, when two agents are facing each other.

The main parameters considered are the population dimension, the distribution of states (healthy, sick, immune) and the probabilities of movements for each agent. Additional parameters will be added when the proposed elements of the model are introduced, as shown in the examples in this section.

All programs are written in ***Processing***, a flexible language for learning how to code within the context of the visual arts.

4.1. Contextual Cellular Automaton

In contrast to the uniform cellular automaton, we define the *Contextual Cellular Automaton*, CCA, by adding elements of the context in order to simulate the interaction between people in various delimited spaces. Thus, instead of a rectangular space, we introduce an organized space. The "walls" restrict the movement of the agents; they are represented by cells that cannot be occupied by agents and therefore cannot be crossed.

Example 1. *A simple example of CCA is represented in Figure 1, where on the surface of a squared cellular automaton are figured walls (black cells). The three subspaces created correspond to rooms in a building and are populated with agents. The color of the agents corresponds to their state: healthy, or not infected (the green triangles), immune (blue triangles) and infected or sick (red triangles). Each agent is looking in the direction indicated by the top of the triangle.*

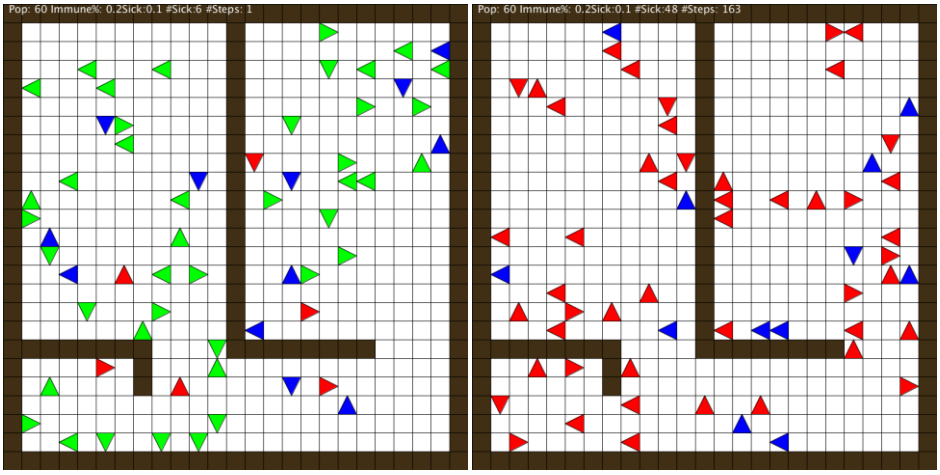

Fig. 1. Example of Contextual Cellular Automaton (CAA). The frame consists of two rooms, a corridor and a bathroom populated with 60 people out of which 10% are infected, and 20% are immune. The moving rules are: $p_f = p_l = p_r = p_b = p_s = 0.2$. **a.** The initial state. **b.** The state after 163 cycles when all non-immune people are infected.

The initialization of the simulation consists in the following actions:

- define the architecture of the space (in our example two rooms, a corridor and a bathroom)
- specify the population by setting:
  - the initial number of people: $N(0)$
  - the initial percentage of sick people: $S(0)$
  - the initial percentage of immune people: $I(0)$
- distribute the people randomly in the four subspaces

The moving rules, for this preliminary example, are defined by the following parameters:

- the probability to move straight: p_f
- the probability to move left: p_l
- the probability to move right: p_r
- the probability to move back: p_b
- the probability to stay: p_s

with the condition: $p_f + p_l + p_r + p_b \leq 1$ because the actors can chose not to move.

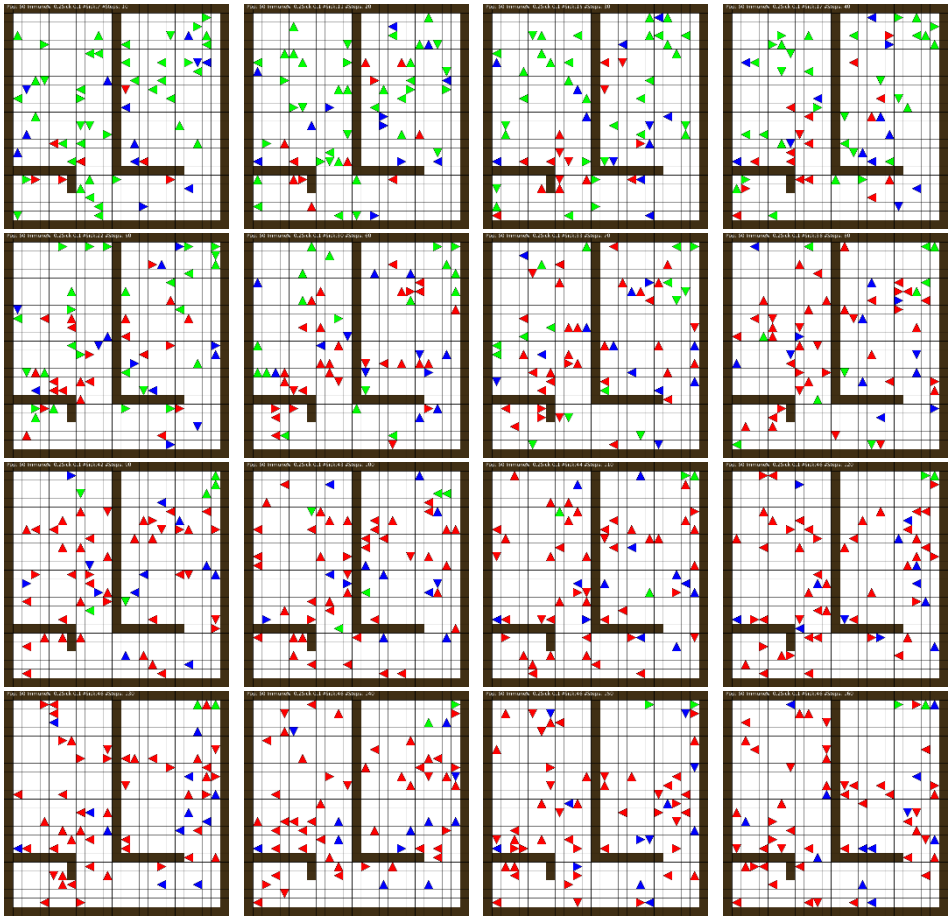

Fig. 2. The 16 intermediate states, from 10 to 10 cycles, out of the 163 of the cellular automaton exemplified in Figure 1.

The state of the CCA switches in three steps:

- randomly, according the established probabilities, each agent decides the move

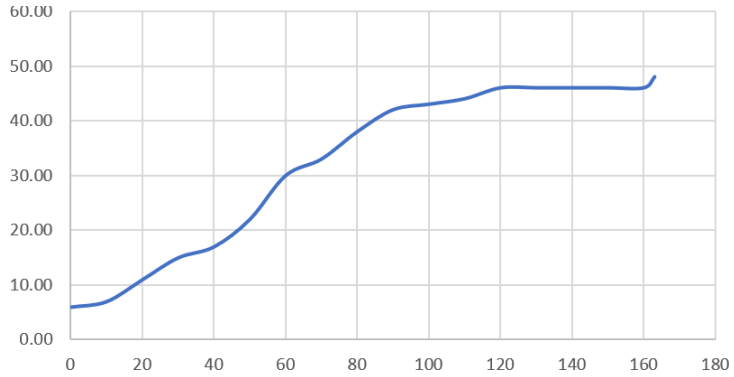

Fig. 3. The evolution in time (expressed in number of simulation cycles) of the number of infected people from the initial stage until all are infected. The graph corresponds to the evolution presented in the previous two images.

- the possibility of the decided move is tested, and only the moves allowed by the current state are performed (depending on the positions of the other agents and the topography of CCA)
- in the new position if a red agent is face to face with a green agent, the green agent gets infected (becomes red)

In the example illustrated in Figure 1 the number of cells is established considering that each cell corresponds to the space occupied by a person: $0.25m^2$. Thus, the rooms's are of $45m^2$, a realistic size for a space populated with 25 persons. The result of the simulation are presented in Figures 1, 2, 3.

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The model is fully parameterized allowing the run of various scenarios. For example:

- the dimension of the initial population (N) is related to the social distance; if N is large, then the so called social distance is small.
- if the initial value of S (sick people) is small, then there are a small number of outbreaks of infection
- if the initial I (number of immune agents) is large, then the spread out of the infection is slowed down because many agents are immune
- if $p_f + p_l + p_r + p_b$ is small (the people move a little), then the spread out of the infection is slowed down

All these parameters can be changed in order to test the global effect on the pandemic process. The model is designed so that additional parameters can be added, such as, for example, the probability of the infection, pi, when a red triangle is face to face with a green one. Note that the model does not include (yet) a mechanism related to therapy as the change from healthy to

sick is irreversible. Therefore, obviously all non-immune agents are going to be contaminated sooner or later and the final state is corresponding to a no-green population, with only immune or infected agents.

Simulation 1. *Let us use the CCA presented in Example 1 to simulate various scenarios. In Table 1 are shown the initial conditions for each experiment and, in the last column, the average time, expressed in cycles, until all the healthy agents (green triangles) are infected. The actors are randomly distributed initially on the surface of the cellular automaton. Each of the 20 experiments are repeated until the mean square deviation becomes stable.*

The results prove that our model is sensitive to the variation of the parameters associated to the CCA defined in Example 1. We list a few comments on the content of Table 1:

#	N(0)	S(0)	I(0)	p_f	p_b	p_r	p_l	p_s	Average time to no-green
1	60	10%	20%	0.25	0.25	0.25	0.25	0.00	229 cycles
2	60	10%	20%	0.20	0.20	0.20	0.20	0.20	273 cycles
3	60	10%	20%	0.10	0.10	0.10	0.10	0.60	531 cycles
4	60	10%	50%	0.10	0.10	0.10	0.10	0.60	798 cycles
5	60	5%	20%	0.25	0.25	0.25	0.25	0.00	325 cycles
6	60	5%	20%	0.20	0.20	0.20	0.20	0.20	330 cycles
7	60	5%	20%	0.10	0.10	0.10	0.10	0.60	647 cycles
8	60	5%	50%	0.10	0.10	0.10	0.10	0.60	1559 cycles
9	60	2%	20%	0.25	0.25	0.25	0.25	0.00	568 cycles
10	60	2%	20%	0.20	0.20	0.20	0.20	0.20	665 cycles
11	60	2%	20%	0.10	0.10	0.10	0.10	0.60	1561 cycles
12	60	2%	50%	0.10	0.10	0.10	0.10	0.60	1583 cycles
13	30	10%	20%	0.25	0.25	0.25	0.25	0.00	472 cycles
14	30	10%	20%	0.20	0.20	0.20	0.20	0.20	447 cycles
15	30	10%	20%	0.10	0.10	0.10	0.10	0.60	1044 cycles
16	30	10%	50%	0.10	0.10	0.10	0.10	0.60	1081 cycles
17	30	5%	20%	0.25	0.25	0.25	0.25	0.00	993 cycles
18	30	5%	20%	0.20	0.20	0.20	0.20	0.20	1090 cycles
19	30	5%	20%	0.10	0.10	0.10	0.10	0.60	2439 cycles
20	30	5%	50%	0.10	0.10	0.10	0.10	0.60	3239 cycles

Table 1. Synthetic table for simulations performed on the CCA defined in Example 1.

- simulations #1 and #2 shows that it is no big difference if staying is considered or not
- the simulation #3, compared with the simulations #1 and #2, shows that if the moving of the actors is diminished, then the infection of the entire population is delayed significantly. The same result is obtained for all simulations with different N, S, I, changing the probability to move/stay
- the simulations #4, #8, #12, #16, #20 show that if the population contains a lot of immune people, the contamination is slowing down

- if the initial weight of the infected people is smaller, then the time for infecting the entire population increases (simulations #5-#8 compared to #1-#4))
- the same tendency is manifests when, in the simulations #9 to #12 the initial number of infected actors is reduced to 2%
- when the density of population is halved, the average time to total infection increases significantly (simulations #13-#20 compared to previous ones)
- for a dense, intensely moving population, the speed of the infection process is with more than one magnitude order faster than the for the rare population moving minimally.

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The main limitation of the previous model is the lack of the healing mechanism, corresponding either to a natural healing or an efficient therapy. This is why the system evolves fatally to the state when all non-immune actors become infected. In the following we will introduce mechanisms able to model some more optimistic evolutions, starting with the detection and isolation of infected agents.

4.2. Internal Timer of the Actors

In order to model the possible evolution of the infected agents, an internal timer is defined for each red triangle. When a triangle becomes red, the timer starts counting. After a certain time, the infected actor is extracted from the system because it is considered ill. Thus, the source of infection is diminished.

The parameter associated with the timer is the number of cycles before deciding if the actor is infected or not: T_i. This parameter is related to the testing rate if the community affected by the disease. If the infected people are not detected as infected, they remain in community and infect other people. If the testing rate is high, the time T_i is set small and an infected actor infects a smaller number of healthy agents.

Example 2. *We consider the CCA defined in Example 1 and we add the parameter T_i, the time the infected actor stays in community*.

Simulation 2. *We consider the condition of the experiment* #4 *from Example 1. For each T_i, from 5 to 120 we take the average number of infected people. The results are represented in Table 2. The table presents the percentage of the population that gets sick after the end of simulation, when all infected people are extracted from the community*.

If the life time in community of an infected agent is short, then the number of agents who get infected by the sick ones is small until all the infected actors are extracted from community. If the life time in community of an infected agent is long, then it infects more agents. There is a ***critical point***, around 100 cycles, for which the infected people succeed to infect all non-immune people. Nobody escapes if the infected agents are not early detected as infected.

#	T_i time each infected stays in community	I_{final} average number of infected people
1	3 cycles	1.125 = 2.67% of healthy people
2	5 cycles	1.500 = 3.57% of healthy people
3	10 cycles	3.875 = 9.22% of healthy people
4	20 cycles	8.000 = 19.05% of healthy people
5	40 cycles	23.625 = 56.25% of healthy people
6	80 cycles	36.125 = 86.01% of healthy people
7	100 cycles	39.125 = 93.15% of healthy people
8	120 cycles	39.571 = 94.21% of healthy people

Table 2. Synthetic table for simulations in Example 2.

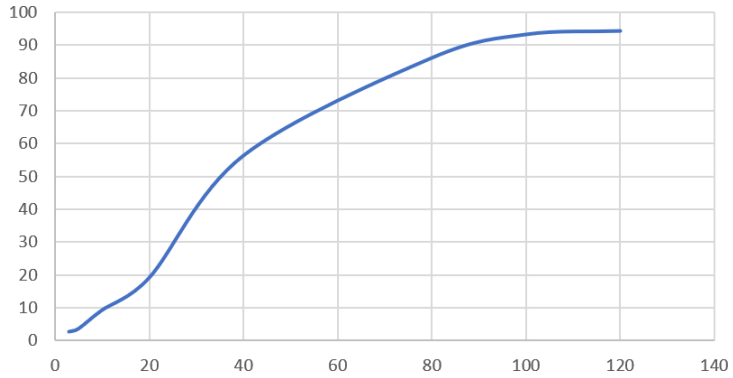

Fig. 4. The percentage of infected people depending on the time (expressed in simulation cycles) spent in community (Example 2).

4.3. "Hospital" Extended CCA

The pandemic model could be enhanced adding a constant size queue (FIFO) to simulate the hospital. This also implies the healing possibility, and therefore offers a more realistic approach than the basic model. When an actor from CCA is detected as ill, it is extracted from its environment and is stored in FIFO, if it is not full, else the actor remains in its environment to be extracted when the queue becomes not-full.

An agent leaves the hospital recovered or dead. This is modeled by the FIFO, from which an agent is extracted with a parameterized rate, if the FIFO is not empty. The recovered actors are inserted back as blue triangles (immune agents) in CCA, while the dead actors are added to the list of victims.

Example 3. *The parameters associated with the queue are:*

- *the size of the queue (the number of patients the hospital is able to treat):* $H << N$
- *the average time an actor is treated in hospital (expressed in number of cycles):* T_h

- *the rate of agents recovered when leave the hospital:* $R \in (0,1)$

Simulation 3. *We consider the case #1 from Simulation 1: the mobility of people is high. Table 3, gives the parameter R, H,* T_i, T_h *and the result of the simulation:*

- *I: the average number of immune people at the end of simulation when all the people have left the hospital immune or dead and no infected people are present in community*
- *D: the average number of dead people at the end of the simulation*
- *time: the average time of simulation expressed in cycles*

#	R	H	T_i	T_h	I	D	time
1	0.6	2	14	10	13.6	5.80	120 cycles
2	0.6	2	14	5	11.4	4.45	67 cycles
3	0.6	2	5	10	7.75	3.75	72 cycles
4	0.6	2	5	5	7.40	3.50	39 cycles

Table 3. Synthetic table for simulations with people which move maximally ($p_f = p_b = p_r = p_l = 0.25$)

From the first two experiments we learn that if Th is large, then the epidemic is longer, i.e., the number of people going through hospital is higher and the immune people at the end of epidemic is higher at the price of increasing of the dead people.

If T_i is smaller, then the number of people infected and going through hospital is reduced. The best situation is when both T_i and T_h are minimized. In this case, the time of the epidemic is shorter.

The result of this simulations shows us that an early detection of the illness and a fast treatment in hospital minimize the effect of the epidemic. High testing rate and well-equipped hospitals it the key solution.

4.4. CCA with Global Loop

The evolution of the CCA depends only on the local rules defined for a finite neighborhood. In simulation of a pandemic process the global control performed by a global authority is mandatory. Introducing a global loop over a CA means to use certain global parameters to modulate the parameters used in defining the local rules [27]. For example, at the moment t of simulation the population is $N(t)$ and is distributed according to $S(t)$ and $I(t)$. These figures can be used to change the parameters involved in defining the local rules. Thus, a tendency in the evolution of the disease can be modified. If the "global authority" decide in the right moment t to change the local rules, then the evolution of the disease can be curved downwards.

Example 4. *In the configuration from case #3 in Simulation 1 we consider* $T_i = 40$, $H = 5$, $R = 0.6$, $T_h = 2$. *The loop takes into consideration the evolution of the number of infected people sent to the hospital. When the threshold* $0.15N$ *is reached (the number of hospitalized people becomes to big), the value of* T_i *is switched to 5 (this corresponds to an increase of the testing).*

Simulation 4. *The results of simulations are presented in Table 4. When the global loop is applied all the number of infected agents goes down to* 68.75%. *Similarly, the number of dead agents and the duration of epidemic go down*

#	I	D	time
1: open loop	32	12	136 cycles
2: closed loop	22	9	81 cycles

Table 4.

5. Concluding Remarks

Cellular automata enhanced models offer an experimental tool to study the evolution of epidemics, and also to study the possible effects of different factors/measures depending on the moment when they are applied to a population of individuals. The same factors/measures produce different effects if applied at different intervals from the outbreak of an epidemic. In the context of the global Covid-19 pandemic, several approaches and strategies were adopted in different countries.

The experiments presented in the paper emphasize the utility of adding new features to the model of cellular automata. The simulations we have done have only the role to prove the sensitivity of our enhanced model of cellular automata combined with autonomous agents. The main improvement is the global loop used to model the authority in charge with the struggle with the epidemics.

The future work will use the featured cellular automaton model for modelling real epidemics in real context with real data. The main purpose of the research is to provide a tool able to identify critical values for the main parameters involved in defining an epidemic. Another direction of interest is the analysis of possible strategies of pandemics control.

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