Affinity Classification Problem by Stochastic Cellular Automata

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This paper introduces the affinity classification problem, which is a generalization of the density classification problem. To solve this problem, we introduce temporally stochastic cellular automata where two rules are stochastically applied in each step on all cells of the automata. Our model is defined on a two-dimensional grid having affection capability. We show that this model can be used in several applications, such as modeling self-healing systems.

Keywords: Cellular Automata (CAs); Stochastic CA; Affinity Classification; Affection; Density Classification; Self-Healing

1. Introduction

The density classification problem is a well-known problem in cellular automata (CAs). Given an initial configuration, the goal is to find a binary cellular automaton (CA) that converges to an all-0 (resp. all-1) configuration, a fixed point, if the number of 0s (resp. 1s) in the initial configuration is higher than the number of 1s (resp. 0s). That is, the CA reaches an all-1 configuration if it has an affinity toward 1 in its initial configuration with respect to the density of 1s in it and reaches an all-0 configuration otherwise. However, sometimes the requirement of many applications is that this density itself is to be treated as a variable—still, a binary CA is required that can converge to the all-1 (resp. all-0) configuration. In this paper, we introduce this problem as a generalization of the density classification problem. Formally, the problem can be stated as:

Given an initial configuration, find a binary CA that converges to an all-1 configuration if the density of 1s is more than ρ . Otherwise, it converges to an all-0 configuration.

Here, ρ is calculated as the density of 1s in the initial configuration and all-0 and all-1 are the only fixed points of the CA. We call this the *affinity classification* problem, as the CA has an affection toward the all-1 configuration. When $\rho = 0.5$, the problem is reduced to the classical density classification problem.

Several attempts have been made in the literature to solve the density classification problem. However, in [1] it is proved that it is impossible to solve this problem with 100% accuracy using classical CAs. Because of this, research efforts have been shifted toward finding the nonclassical CAs that can solve the problem "almost" perfectly. In [2], the density classification task is shown to be solvable by running in sequence the trivial combination of elementary rules 184 and 232. In [3] this solution is extended for two dimensions using a stochastic component in the two rules 184 and 232. In [4], a stochastic CA is used to solve the problem with arbitrary precision. In this solution, the cells of one-dimensional CAs stochastically choose a rule in each step from a set of rules to evolve. These nonclassical CAs can be called *spatially* stochastic CAs. Another approach has been to tackle this problem with nonuniform CAs where the cells can use different rules to evolve. A nonuniform CA that performs the best on the density classification task is identified in [5]. However, neither (spatial) stochastic CAs nor nonuniform CAs can perfectly solve the density classification problem, whereas the nonclassical CA of [2], which may be called a *temporally* nonuniform CA, can do it perfectly.

As the affinity classification problem is an extension of the density classification problem, it is most likely to be unsolvable using classical CAs. We may need nonclassical CAs with temporal nonuniformity and stochastic components for this. Hence, to solve this problem, in this paper, we introduce *temporally stochastic* CAs. We define our problem over two-dimensional binary CAs and use two different CA rules uniformly over the grid. The default rule is deterministic, whereas another rule is stochastic whose application at each time step is dependent on some probability. Section 2 describes the proposed model. The simulation and convergence to the solution for different densities is shown in Section 3. It is shown that our model is not blind, as it intelligently decides and converges to its point of attraction. Finally, Section 4 shows that this model has several applications, including a model for self-healing systems.

2. The Model

The proposed CA is defined over a two-dimensional square grid that uses a periodic boundary condition. The CA is binary and considers

the Moore neighborhood dependency; that is, a cell takes any of the two states 0 or 1 and depends on itself and its eight nearest neighbors. At time step t, a cell can be updated using one of the two rules f and g. Here, f is deterministic and the default rule for the grid, whereas g is stochastic and is applied with some probability. As the CA is defined over a Moore neighborhood, both f and g have the same domain and range:

$$f: \{0, 1\}^9 \to \{0, 1\} \text{ and } g: \{0, 1\}^9 \to \{0, 1\}.$$

We now discuss the default rule f. This rule is spatially deterministic—at any time, it is applied over all cells uniformly. At each time step t+1, this rule updates the state of cell (i, j) depending on the present states of its neighboring cells:

$$(i-1, j)$$
, $(i-1, j-1)$, $(i, j-1)$, $(i+1, j-1)$, $(i+1, j)$, $(i+1, j+1)$, $(i, j+1)$, $(i-1, j+1)$.

Let $s_{i,j}^t$ be the present state of cell (i, j) and $C_{(i,j)}^d$ represents the number of neighbors for the cell (i, j) with $s_{i,j}^t = d$ where $d \in \{0, 1\}$. Then f works in the following way:

$$s_{i,j}^{t+1} = f(s_{i-1,j}^t, s_{i-1,j-1}^t, s_{i,j-1}^t, s_{i,j}^t, s_{i+1,j-1}^t, s_{i+1,j+1}^t, s_{i+1,j+1}^t, s_{i-1,j+1}^t)$$

$$= \begin{cases} 0 & \text{if } s_{i,j}^t = 1 \text{ and } \sum_{\substack{i-1 \le l \le i+1 \\ j-1 \le m \le j+1}} C_{(l,m)}^0 > K \end{cases}$$

$$= \begin{cases} 1 & \text{if } s_{i,j}^t = 0 \text{ and } \sum_{\substack{i-1 \le l \le i+1, \\ j-1 \le m \le j+1}} C_{(l,m)}^1 = 8 - K \end{cases}$$

$$s_{i,j}^t \text{ otherwise}$$

where K is a constant and $0 \le K \le 8$. That means, if a cell is in state 1 and it has more than K neighbors with state 0, it changes to state 0 in the next step, whereas a cell of state 0 with 8 - K or more neighbors with state 1 becomes state 1 in the next step. This number K of neighbors required for state transition is the first parameter of the model.

The most significant characteristic of our model comes from the second rule g. As already mentioned, g is a stochastic rule; that is, it is applied to each cell with some probabilities. Moreover, at which time step this rule is to be applied is also stochastically decided. Hence, we call the CA a temporally stochastic CA. However, when selected, this rule is also applied uniformly over all cells. Here is the rule definition:

$$s_{i,j}^{t+1} = g(s_{i-1,j}^t, s_{i-1,j-1}^t, s_{i,j-1}^t, s_{i,j}^t, s_{i+1,j-1}^t, s_{i+1,j}^t, s_{i+1,j+1}^t, s_{i,j+1}^t, s_{i-1,j+1}^t)$$

$$= \begin{cases} 0 \text{ with probability } \phi(x) & \text{if } s_{i,j}^t = 1 \text{ and } \sum_{\substack{i-1 \le l \le i+1, \\ j-1 \le m \le j+1}} C_{(l,m)}^0 = x \end{cases}$$

$$= \begin{cases} 1 \text{ with probability } \psi(x) & \text{if } s_{i,j}^t = 0 \text{ and } \sum_{\substack{i-1 \le l \le i+1, \\ j-1 \le m \le j+1}} C_{(l,m)}^1 = x \end{cases}$$

$$s_{i,j}^t & \text{otherwise.}$$

Here, $\phi(x)$, $\psi(x): \{0, 1, ..., K\} \rightarrow [0, 1]$ are two probability distribution functions. We call x the number of *supporting neighbors* or simply *support*.

This rule implies if a cell is at state 1 and it has x number of neighbors with state 0, it updates its value to state 0 with some probability $\phi(x)$. Similarly, if a cell is at state 0 and it has x number of neighbors with state 1, it updates its value to state 1 with some probability $\psi(x)$. We call $\phi(x)$ the *affection probability* and $\psi(x)$ the *repulsion probability* function. These two probability distribution functions are the second and third parameters of our model.

However, this stochastic rule g does not act in each step. When it is to be applied is decided by another probability p, which we call the *upgrade probability*. This p is the fourth and final parameter of our model. Hence, the parameters required by the model are:

- K, the number of neighbors required to change from one state to another
- $\phi(x)$, the affection probability function
- $\psi(x)$, the repulsion probability function
- p, the upgrade probability

Observe that in our model, the role of g is to give the cells an extra chance to change their status. During evolution of the CA by f, if some cells are left out that are eager to update their states but cannot do so because of the surrounding neighbors (hostile environment), they get a booster to upgrade their current status through g. This g helps them achieve their desired status even if they have a smaller number of neighboring cells as support (as $x \le K$). But whether the cell will be updated or not is dependent on the probability value. Both cells with state 0 and state 1 get this advantage uniformly in terms of the two probability distribution functions $\phi(x)$ and $\psi(x)$. As g gives precedence toward some cells, it is to be applied with caution—so there is the upgrade probability value p, which works as a

controlling measure. Therefore, when K = 4, f works as a simple majority rule and depending on g, the system can be inclined toward a specific state.

Note that the parameters give us flexibility to design the model according to the needs of an application. For example, for the model to have an affection to converge to all-0 as a fixed point, we can set $\phi(x)$ and $\psi(x)$ accordingly. Similarly, we can change the value of our parameter(s) to get different versions of the model, which can be used for a specific purpose. In fact, we may also consider that in our model rule, g is applied with probability p, whereas the rule f is applied with probability (1-p), with p being any probability value. This way of looking at these rules makes both of them temporally stochastic. The next section shows some simulation results solving the affinity classification problem with specific parameter values.

3. Solving Affinity Classification Problem: A Simulation

We now simulate our proposed model to understand its efficacy in solving the affinity classification problem. As mentioned before, the model is a two-dimensional finite CA that uses periodic boundary conditions. For the purposes of the simulation, we consider a grid size of $10^3 \times 10^3$; that is a total of 10^6 cells. Further, our model is characterized by four parameters: K, $\phi(x)$, $\psi(x)$ and p. In our simulation, we set the following values for the parameters:

$$K = 4$$

$$\phi(x) = \begin{cases} 0 & \text{if } x \le 1 \\ \log_K(x) & 2 \le x \le K \end{cases}$$

$$\psi(x) = \begin{cases} 0 & \text{if } x = 0 \\ e^{x-K} & 1 \le x \le K \end{cases}$$

$$p = 0.2.$$

As our model uses a Moore neighborhood dependency on a twodimensional grid, K is very small: $0 \le K \le 8$. In this small range of K, logarithmic functions grow faster than exponential functions. Therefore, since we want to observe the affinity of the model toward an all-0 configuration, we take $\phi(x)$ as a logarithmic function and $\psi(x)$ as an exponential function. As per our model, we use x = 0, 1, ..., K to get the probability values for $\phi(x)$ and $\psi(x)$. We have plotted $\phi(x)$ and $\psi(x)$ for different x to see their behavior at K = 4 (see Figures 1(b) and 2(b), respectively). At K = 4 we can observe that $\phi(1) = 0.0$, $\phi(2) = 0.5$, $\phi(3) = 0.79248$, $\phi(4) = 1.0$, whereas $\psi(1) = 0.0497$, $\psi(2) = 0.1353$, $\psi(3) = 0.3679$, $\psi(4) = 1.0$. We observe that if the number of supporting neighbors x is increased, then the probability of changing from state 1 to state 0 is also increased (Figure 1(b)); however, if x is decreased, then the probability of changing from state 0 to state 1 is increased, with the growth of the first function being faster than the latter (Figure 2(b)).

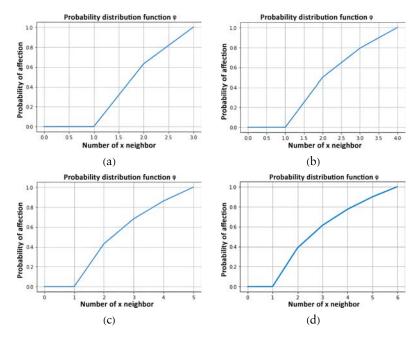


Figure 1. Graph of $\phi(x)$ for different K: (a) K=3; (b) K=4; (c) K=5; (d) K=6.

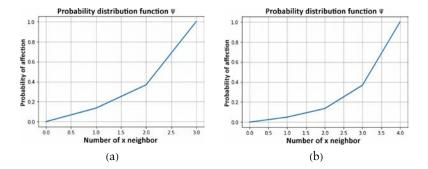


Figure 2. (continues)

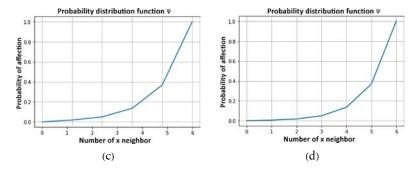


Figure 2. Graph of $\psi(x)$ for different K: (a) K=3; (b) K=4; (c) K=5; (d) K=6.

■ 3.1 Random Initial Configuration

We have used our model with a large number of random initial configurations with various values of ρ where

$$\rho = \frac{\text{number of 1}}{\text{total number of cells}}.$$

Following are some sample results from our experiment when K=4. Here, 0 is represented in yellow and 1 is represented in red. Figure 3 shows that at $\rho=0.475$, for a random initial configuration, all the cells become yellow after 150 iterations; that means the model converges to its point of attraction (all-0). We have experimented with a large number of random initial configurations and seen that when the initial configuration has $\rho \le 0.675$, the model converges to all-0; otherwise, it converges to all-1.

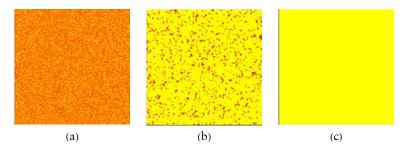


Figure 3. For K=4 and $\rho=0.475$, the model converges after 150 iterations: (a) initial configuration, (b) an intermediate configuration, (c) final configuration (all-0).

Figure 4 shows another sample random initial configuration with an arbitrary $\rho > 0.675$ (here $\rho = 0.6989$). Here, the model converges to all-1 after 137 iterations.

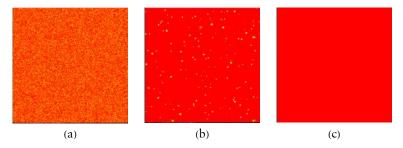


Figure 4. For K=4 and $\rho=0.6989$, the model converges to all-1 after 137 iterations: (a) initial configuration, (b) an intermediate configuration, (c) final configuration (all-1).

Naturally, the question arises, Can we increase the affection probability so that even if we take a lot of 1s in the initial configuration the model still converges to all-0? To search for this answer, we have again done a large number of experiments by varying the value of K. In our experiments, we have observed that when we decrease the value of K, the model converges to all-0 even though $\rho > 0.68$. For example, for the initial configuration of Figure 5, if K = 3, then although $\rho \le 0.96$, the model converges to all-0. By further experimentation, we observe that if the value of K is decreased to two, then ρ can be as high as 0.99, but the model may still converge to all-0. Similarly, when we increase the value of K, then the value of ρ is to be decreased for converging to all-0.

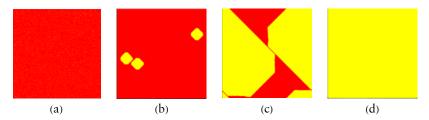


Figure 5. For K = 3 and $\rho = 0.969852$, after 3132 iterations, the model converges to all-0: (a) initial configuration, (b) an intermediate configuration, (c) another intermediate configuration, (d) final configuration (all-0).

Figures 1 and 2 show the variation of the probability distribution functions for different K values. If K is changed, then the growth of the probability distribution functions $\phi(x)$ and $\psi(x)$ is also changed with respect to K. Table 1 gives some of our experimental results. In each of the subtables of this table, columns 1 and 2 describe the initial configurations in the form of K and ρ , whereas columns 3 and 4 show experimental outcomes.

Г		Number of				Number of	
K	ρ	Iterations	Converge to	K	ρ	Iterations	Converge to
1	0.000002	1	all-0	4	0.61	3074	all-0
1	0.0002	2	all-0	4	0.65	7019	all-0
1	0.0051	2	all-0	4	0.67	12385	all-0
1	0.3	3	all-0	4	0.675	16186	all-0
1	0.55	4	all-0	4	0.6864	261	all-1
1	0.67	6	all-0	4	0.7	159	all-1
1	0.6864	8	all-0	4	0.74	69	all-1
1	0.943	21	all-0	4	0.8	8	all-1
1	0.991	76	all-0	4	0.943	4	all-1
1	0.997	170	all-0	4	0.965	4	all-1
1	0.9995	489	all-0	4	0.991	2	all-1
2	0.1	3	all-0	5	0.06	8	all-0
2	0.3	4	all-0	5	0.08	14	all-0
2	0.4	5	all-0	5	0.09512	8	all-0
2	0.61	7	all-0	5	0.1	14	all-0
2	0.74	14	all-0	5	0.3	304	all-1
2	0.8	16	all-0	5	0.4	91	all-1
2	0.9536	90	all-0	5	0.55	12	all-1
2	0.965	151	all-0	5	0.61	10	all-1
2	0.982	323	all-0	5	0.686	6	all-1
2	0.993	759	all-0	6	0.001	2	all-0
2	0.995	3	all-1	6	0.0051	3	all-0
2	0.9995	2	all-1	6	0.00994	8	all-0
3	0.1	3	all-0	6	0.03	638	all-1
3	0.3	6	all-0	6	0.0629	230	all-1
3	0.4	9	all-0	6	0.076	194	all-1
3	0.55	20	all-0	6	0.08	98	all-1
3	0.61	22	all-0	6	0.1	58	all-1
3	0.6864	44	all-0	7	0.000002	2	all-0
3	0.8	109	all-0	7	0.0002	2	all-0
3	0.943	518	all-0	7	0.0004	2	all-0
3	0.953	2042	all-0	7	0.0005	976	all-1
3	0.96	2372	all-0	7	0.0009	375	all-1
3	0.965	3220	all-0	7	0.001	417	all-1
3	0.982	3	all-1	7	0.00499	136	all-1
3	0.991	3	all-1	7	0.00994	83	all-1
3	0.995	2	all-1	7	0.0676	25	all-1
4	0.1	4	all-0	7	0.1	12	all-1
4	0.4	66	all-0	7	0.55	4	all-1
4	0.55	805	all-0	7	0.95	2	all-1

Table 1. Relationship between the values of K and ρ where the model converges to all-0 or all-1.

3.2 Initial Configuration with a Block of 0s and 1s

The previous subsection shows the results when 0 and 1 are randomly distributed in the initial configuration. Now, we experiment with initial configurations where a block of cells is set to have the same value. Tables 2 and 3 depict our sample results. In Table 2, we consider initial configurations with a small number of consecutive cells in state 0 and the remaining cells in state 1. For every value of K ($1 \le K \le 7$), column 2 shows the number of consecutive cells having the same value in our experiments, so that the model converges to all-0. For instance, when K = 4, then an initial configuration having a block of 100 consecutive 0s, the model converges to all-0. These consecutive 0s form a cluster that grows in size until the model converges to all-0. Figure 6 shows a random initial configuration with 10⁶ cells, where only 25 consecutive cells are in state 0 and K = 3. We can observe that although the number of 0s is very small, the model still converges to all-0 after 4093 iterations (see Figure 6). Therefore, our model has an affinity to converge to all-0 even if the number of 0s in the initial configuration is very small in comparison to the grid size.

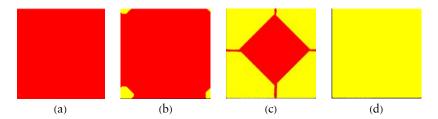


Figure 6. K = 3 and the block of 25 0s; the model converges to all 0s after 4093 iterations: (a) initial configuration, (b) intermediate configuration, (c) another intermediate configuration, (d) final configuration converges to all-0.

However, the model does not always converge to the desired fixed point. For example, at K=3, for a random initial configuration having a block of 81 0s, the model converges to all-1 (Table 2). Table 3 depicts some sample results from our experiment where we take a small number of 1s organized in sequential order; that is, they make a cluster. Here, we can see that after taking K>4, sometimes the model converges to all-1 even if the number of 1s is very small. Therefore, even if the model has an affection to converge to all-0, the value of K may take a major role and cause the model to converge in a direction (all-0 or all-1).

K	Number of 0s	Iterations (Time Steps)	Converges to
1	1	1	all-1
1	2	998	all-0
2	2	1	all-1
2	3	1152	all-0
2	4	1148	all-0
3	3	1	all-1
3	4	3874	all-0
3	25	4093	all-0
4	49	64	all-1
4	64	92	all-1
4	70	492	all-1
4	81	576	all-1
4	100	15915	all-0
4	144	16138	all-0

Table 2. Relationship between the values of *K* and the block of 0s where the model converges to all-0 or all-1 when the numbers of 0s are placed sequentially in the grid.

K	Number of 1s	Iterations (Time Steps)	Attractor
5	25	24	all-0
5	225	212	all-0
5	256	483	all-0
5	324	12148	all-1
5	400	11870	all-1
6	2	1	all-0
6	4	13	all-0
6	5	1519	all-1
6	6	1510	all-1
6	8	1507	all-1
6	9	1493	all-1
7	1	1	all-0
7	2	979	all-1

Table 3. Relationship between the values of K and the block of 0s where the model converges to all-0 or all-1 when the numbers of 1s are placed sequentially in the grid.

4. Applications

As discussed in Section 2, the parameters give us flexibility to design our model according to the need of the solution to a particular problem. There are several possible applications of our model. Here we discuss some of them.

■ 4.1 Modeling Self-Healing Systems

Living systems are assumed to be more intelligent than a nonliving system. Therefore, to be intelligent, a machine (nonliving system) has to emulate the properties of living systems. Among the properties, self-healing is a basic and important biological property that is a sign of life. Self-healing is the ability for a system to reorganize and heal itself. If a machine has self-healing ability, it is likely to mimic other properties of living elements like self-replication. Hence, it will be more intelligent, just like a living system. We can show that our proposed CA can be used to model any self-healing system, where parameters of our abstract model can be interpreted as the characteristics of the self-healing system.

Let us interpret our model as the following. Let a grid of cells embody a collection of living elements (they can be cells, humans, animals, anything), where state 0 means the cell is healthy and 1 means it is sick. We want to model how much infection the cells can endure and still heal. By default, the living system is healthy; that is, all cells are in state 0. Now, suppose, because of some environmental change, a number of cells get infected and update their states to 1 (become sick). This is the initial configuration from which we start to observe the system dynamics. Let us consider that in our model, the system's immunity is the immunity of individual cells, and as a whole, the system's health is the health condition of the majority of the individual cells. So, at the initial configuration, if we ask the system, Are you sick?, it can answer yes or no depending on the density of 1s (ρ) . If the system can heal itself using this model, that is, come back to all-0, then we can call it a model for self-healing systems. At that time, the answer to Are you sick? will always be no. Therefore, our target is that the grid converges to all-0 so that we can say there is no infection and the model is not sick. However, if the model converges to all-1, then we have to declare that the model is sick.

Now, any living body has some built-in immunity status. This immunity is represented by the first parameter K. Just like immunity is different for different elements, K itself is a variable. When K = 4, the system can be interpreted as the situation of natural immunity having no prevailing sickness. The deterministic rule f plays the role of natural healing process based on immunity K. Results from Section 3 show that if the converging point is set to all-0 and $K \le 4$, then there

is a tendency to converge toward all-0 even if in the initial configuration the number of 1s is greater than the number of 0s. This indicates, like any living body, our model also wants to become not sick.

However, even in this condition, if the number of infected cells becomes too large (ρ is high), then, according to our rule, the system is sick. So, inherent immunity is not enough to restore its health. For example, if we take a random initial configuration with some infected cells (cell state 1) where $\rho = 0.632275$ (ρ is the density of 1s) and K = 4, then at this stage the model is sick (see Figure 7(a)). At this point, the cells are given some booster to improve their immunity in terms of g. Here, g may be considered as a vaccine for the infection, as if it can bypass the natural justice process giving the cells a second chance to live. But whether the vaccine will be effective for a cell is not deterministic (so g is stochastic). Further, when this vaccine is to be applied to the system is also not pre-determined (temporally stochastic CA with probability p).

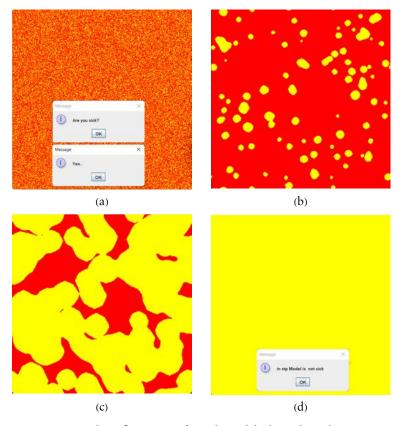


Figure 7. (a) Initial configuration of a sick model; (b) and (c) show two intermediate configurations during evaluation; (d) the model is healed.

Nevertheless, for every cell, the vaccine will not react similarly. A large number of sick cells with a favorable environment may become healthy (represented by $\phi(x)$), whereas some healthy cells with an unhealthy environment can become sick (represented by $\psi(x)$). But if we take $\phi(x)$ as logarithmic and $\psi(x)$ as exponential as defined in Section 3, by choosing K and x, we can see that after some iterations the model converges to all-0 (see Table 1). Then we can say the model is not sick (Figure 7(d)).

However, if we further increase the value of ρ (say, from 0.675 to 0.68 or more), then for the same K and x, the model may converge to all-1 (see Table 1) and become sick. Therefore, the role of K and x is very important to model self-healing systems. If we want our system to have a larger tendency to heal, then we need to choose the parameters of our model wisely. Moreover, if the affection probability $\phi(x)$ is large, then the system has more tendency to heal. This probability indicates the ability to repair or heal oneself automatically and evolve oneself according to the demands of the environment.

This is how self-healing is modeled by our CA. It also shows that our abstract model can be a good interpretation of the role of vaccination in a living population. Also, observe that our proposed model takes the global decision democratically, where every single cell makes its own decision and the system comes to a consensus. Because of these properties, we claim that our proposed model is intelligent.

■ 4.2 Modeling Transformation Process

In the natural and chemical world, we get glimpses of several transformation processes: water evaporates into vapor; a drop of color in a glass of liquid dissolves giving the whole glass of liquid a lighter shade of that color. All these processes happen to conserve the law of mass and energy. This section shows that our CA can be used to model such transformation processes.

During the process of transformation, the particles are divided into smaller-sized particles and dissolve until the system comes to an equilibrium. In our model, if we set K=3 (and other parameters the same as Section 3), then for some special initial configurations, the evolution of the CA looks like transformation processes—the configuration is divided into two or more smaller configurations. It goes on dividing and dissolving until the system converges to a fixed point, which signifies the equilibrium state. For example, in Figure 8, an initial configuration is shown, which, after some iterations, is divided into more than three configurations. It keeps on getting smaller until it converges to the fixed point all-0 when the system has reached its equilibrium. Hence, we can say that by varying the parameters of our model, we can simulate the transformation process from one system to another by our CA.

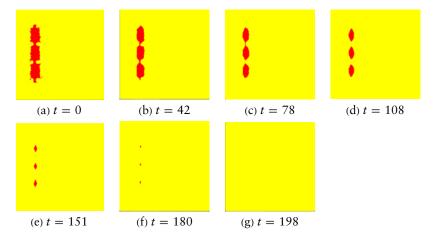


Figure 8. Simulation of a transformation process.

4.3 Density Classification Problem

The density classification problem can also be addressed by our model. According to the definition of the affinity classification problem, this problem reduces to the former if we take the density of 1s as $\rho=0.5$. However, here, instead of taking ρ as exactly 0.5, we take it as a variable and see how close we can get to solving this classical problem using our model.

Previous papers have established that the density classification problem is not solvable by spatially stochastic CAs (uniform or nonuniform) but can be solved by using temporally nonuniform CAs [2, 3]. So we also take our CA as temporally nonuniform with a stochastic component g, which perfectly fits our model. However, a property of this problem is that there is no affinity toward any state at any time. Hence, to make the system unbiased, we take the number of neighbors K required to change from one state to another as 4. Also, we choose both the probability distribution functions $\phi(x)$ and $\psi(x)$ to be the same. That is, if a cell is at state 1 and it has x number of neighbors with state 0, it updates its value to 0 with the same probability distribution function as in the case of the cell being at state 0 with x number of neighbors with state 1 and getting updated to state 1. Further, we consider the upgrade probability value p = 0.1 such that the stochastic component g is applied with very low probability.

Here we show simulation results for two different probability distribution functions—linear and exponential. For the first case, the values of the parameters for the model are:

$$K = 4$$

$$\phi(x) = \left\{ \frac{x}{K} \text{ for } 0 \le x \le K \right.$$

$$\psi(x) = \left\{ \frac{x}{K} \text{ for } 0 \le x \le K \right.$$

$$p = 0.1.$$

We have performed a large number of experiments with random initial configurations over a 200×200 grid based on this model. Some sample simulation results are shown in Table 4. Here, the first column indicates some ρ values, whereas the third and fourth columns represent for each of these ρ , out of 100 experiments how many converge to all-0 and all-1, respectively. In our experiments, we observe that with random initial configurations and $\rho \leq 0.4647$ or $\rho \geq 0.54$, our model converges to its fixed point (all-0 and all-1, respectively).

	Number of	Converge to	Converge to	
ρ (Number of 1s)	Experiments	All-0	All-1	
≤ 0.4647	100	100	0	
0.4779710	100	96	4	
0.49112875	100	73	27	
0.5036035	100	37	63	
0.51548925	100	9	91	
0.52758225	100	5	95	
0.5394037	100	1	99	
≥ 0.54	100	0	100	

Table 4. Taking a 200×200 two-dimensional square grid and both ϕ and ψ as linear functions.

For the second case, we take both ϕ and ψ as exponential functions with K=4 and p=0.1. Hence, the changed parameters of the model are:

$$\phi(x) = \begin{cases} 0 & \text{if } x = 0 \\ e^{x-K} & \text{for } 1 \le x \le K \end{cases}$$

$$\psi(x) = \begin{cases} 0 & \text{if } x = 0 \\ e^{x-K} & \text{for } 1 \le x \le K. \end{cases}$$

We repeat our experiments with a large set of random initial configurations over a 100×100 grid. Table 5 shows some sample results of this experiment. Here also we observe that when the initial configuration is random, then for $\rho \le 0.4679$ or ≥ 0.520 , the model reaches its

desired fixed point (all-0 or all-1). However, when the configurations are a block of 0s or 1s forming a cluster, then it fails to reach the desired fixed point. Figure 9(a) shows examples of two such patterns where the model cannot reach its fixed point (see Section 3.2 for more details).

	Number of	Converge to	Converge to
ρ (Number of 1s)	Experiments	All-0	All-1
≤ 0.4679	100	100	0
0.47837	100	96	4
0.513014	100	30	70
0.5181367	100	0	100
≥ 0.520	100	0	100

Table 5. Taking a 100×100 two-dimensional square grid and both ϕ and ψ as exponential functions.

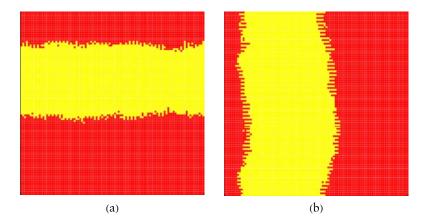


Figure 9. Some unsolvable configurations for the density classification problem in a two-dimensional square grid.

5. Conclusion and Future Scope

There are several properties in living systems that make them intelligent—affection is one of them. In this paper, we propose a new problem, called the affinity classification problem. We develop a devoted machine that is embedded in a two-dimensional cellular automaton (CA) having a Moore neighborhood dependency and

periodic boundary conditions. Our model has affection capabilities to a converging point, all-1 or all-0 and can be characterized by four parameters K, $\phi(x)$, $\psi(x)$ and p. Using this model, we can develop a self-healing system. We know that because of self-healing any species can survive in the environment. As our model has this feature and it makes decisions democratically, we can say that the model is acting like a natural living system to some extent and we can conclude that the model is intelligent.

However, there are some other properties of life that an intelligent machine needs to possess; we have to see if our model possesses them. Similarly, here we have considered only the Moore neighborhood; what kind of behavior might arise if we change the neighborhood dependency for the rules is still not seen. Different other behaviors might emerge by varying the parameters of our model. And, apart from self-healing systems, our model may be useful for several other areas of application. Answers to these questions remain work for the future.

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