

A PREDATOR-PREY MODEL BASED ON THE FULLY PARALLEL CELLULAR AUTOMATA

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We presented a predator-prey lattice model containing moveable wolves and sheep, which are characterized by Penna double bit strings. Sexual reproduction and child-care strategies are considered. To implement this model in an efficient way, we build a fully parallel Cellular Automata based on a new definition of the neighborhood. We show the roles played by the initial densities of the populations, the mutation rate and the linear size of the lattice in the evolution of this model.

Keywords: Evolution; Parallel; Cellular automata; Predator-prey model.

1. Introduction

The problem of dynamical relations between two or more interacting populations already has a long history. It started with the classic papers by Volterra¹ and Lotka² describing the fluctuations in the fish catch in the Adriatic. Since then various models have been introduced in order to consider different aspects of natural life, including motion, birth and death processes, evolution and extinction^{3,4,7}. But the unrealistic unlimited growth of a population has been found in the classic Lotka-Volterra models. In order to include the effect of food and space restrictions and to keep the population within the carrying capacity the population can sustain, Verhulst factor is imposed in models of^{5,6,16}.

Recently, there are some lattice models discussed this problem via computer simulation to try to bring the models more realistic⁷⁻¹¹. They all used the standard square two-dimensional lattice on which predators and prey move and reproduce

following a set of rules. The lattice models are dynamic computational systems that are discrete in space, time and state and whose behavior is specified by rules governing local relationships. They also have a benefit in being visually informative of the progress of dynamic events. Especially, Verhulst factor can be replaced in a natural way.²⁴

The Monte Carlo (MC) method is used to simulate the predator-prey system.^{7–11} In one Monte Carlo step, a random sequence of discrete events is generated. Although MC simulations provide tractable rules for the predator-prey model, they are not suitable for efficient parallelization due to the random selection of lattice cells. However, there is another important approach to simulate discrete events of predator-prey system on lattice, the Cellular Automata (CA). This approach is fully parallel in the sense that all the lattice cells can be updated simultaneously. This has the advantages that fewer random numbers are required, and the global updating is easier to implement in a parallel code²¹. A kinematic, asynchronous, stochastic cellular automata was proposed to model water and solution phenomena encountered in complex biological systems.¹² A stochastic cellular automata is built to test sensitivity of model response under different spatial and temporal sequences of events.¹⁹ A probabilistic cellular automata method was adopted to model a lattice system.²⁰ It may be viewed as an automata network with a mixed transition rule, at each time step the evolution results from the application of the synchronous subrule followed by the sequential one.

In this paper we presented a parallel cellular automata model containing moveable wolves and sheep. For the implementation of the parallel updating, we describe in detail a new definition of neighborhood. The population is composed of individuals characterized by their genetic strings and ages by applying the Penna model¹³ with sexual reproduction.

The paper is organized as follows: in the next section we present the model, section 3 contains the simulation method, section 4 contains the results and discussion, and the conclusions are in the final section.

2. The predator-prey model with sexual reproduction

We consider a cellular automata model composed of wolves, sheep and grass on a square lattice of linear size L (L is a common multiple of 4), with periodic boundary conditions. The time was considered as a discrete variable ($t = 1, 2, 3, \dots$) as suited for implementation on computers.

On a cell it is occupied by one independently moveable animal at most, or it maybe empty, i.e., an independently moveable wolf, an independently moveable sheep, a mother wolf or a mother sheep with her child who can not move independently, or grass only. It is forbidden for two or more independently moveable animals to occupy the same cell at the same time. Grass, which grows on each cell, can be eaten up by a sheep in one time step, and grow again after certain time steps. The grass in our model is not always available, which has not been considered in

previous papers.

Each individual has a reserve of food, in our model it is represented by a counter containing its "food rations". The counter is increased to the maximum value after each "meal" (eating grass by a sheep or eating sheep by a wolf) and decreased by one after completing one simulation step. The animal dies when its counter reads zero.

Another feature characterizing an individual is its genotype that is a double bit string (of 32 positions) of 0's and 1's. It could have the form

$$\begin{cases} 0010110\dots \\ 0101101\dots \end{cases}$$

They are defined at birth, kept unchanged during the individual lifetime and read in parallel.

From the genotype the phenotype of the individual is constructed, as a single string of the same length, according to the following rule.

All the sites are sorted as recessive and dominant sites, each of which take up 50% of the total sites. On the dominant sites, if a "1" appears, i.e., (0,1), (1,0) or (1,1), a 1 is put at the corresponding place of the phenotype, otherwise a 0. While on the recessive sites, if a "0" appears, i.e., (0,0), (0,1) or (1,0), a 0 is put at the corresponding place of the phenotype, otherwise a 1. For details see Table 1.

Table 1. The phenotype determined by the genotype.

Type of sites	Genotype	Phenotype
Dominant	(0,0)	0
	(0,1) (1,0) and (1,1)	1
Recessive	(1,1)	1
	(0,0) (0,1) and (1,0)	0

The bit on the i th site of the phenotype gives the information if the individual will suffer from the effects of a genetic disease in its i th year of life. Diseases are represented by 1. In each time step, the total amount of diseases until the individual's current age is compared with a threshold T , when it overloads this limit, the individual dies. Here we assumed a predation rule that only when the number of the genetic diseases a wolf suffered is less than that of a sheep, the predation can be successful.

Each offspring receives its genotype constructed through recombination and formation of two gametes from each parent (genetic shuffling). The process may be described as follows. The two strings of a parent's genotype are cut at a random place. The resulting four pieces are glued across, forming two gametes. The same is done for the second parent. From each parent one gamete is chosen randomly and modified by M random mutations, thus forming two strings for the genotype of the offspring. Similar ideas of the formation of the genotype of the offspring have been considered.^{17,18,23} Here we consider both deleterious and helpful mutations.

If an animal has one neighbor of the same species with opposite sex, the pair reproduce one offspring. In order to breed, apart from finding a partner in its neighborhood, the animal must be strong enough, i.e., it must have at least r_{min} food rations and at least reach the minimum reproduction age A_r . We call these reproduction terms. The sex of the newborn offspring is randomly selected, and its food ration is equal to its mother's.

Considering the strategy of child-care²², we defined a period during which if there is no empty site in the neighborhood the child could stay with its mother and move together. In this period, if there is an empty site in the neighborhood, the child leaves its mother and moves into it. The child will die, if there is still not any empty site in the neighborhood, after having overloaded the period C_c . Thus fewer children survive because of lack of space. This procedure takes care of the unrealistic unlimited growth of a population found in the classic Lotka-Volterra models and replaces naturally the phenomenological Verhulst factor.

3. Cellular automata simulation method

A cellular automaton (CA) is a regular array of cells. Each cell can be in one of a set of possible states. The CA evolves in time in discrete steps by changing the states of all cells simultaneously. The next state which a cell will take is based on its previous state and the states of the neighboring cells. The behavior of CA is specified by rules governing local relationships, the set of states, the neighbors, and the transition rules. They are an attempt to simplify the often numerically intractable dynamic simulations into a set of simple rules that are easy to compute. As an approach to the modeling of properties of complex systems they have a great benefit in being visually informative of the progress of dynamic events. From their early development by von Neumann¹³, a variety of biological applications have been reported.^{14–16}

In our model containing moveable wolves and sheep, in order to obey the CA laws in von Neumann neighborhood (Fig. 1(a)), it is necessary disobey the common sense because a wolf may be participant in several hunts, which is unreasonable.

To solve this problem, we present a new definition of neighborhood. A sub-lattice is considered as an elementary component of the whole lattice. Then there are two schemes for the definition of the neighborhood as shown in Fig. 1(b), 1(c) and 1(d). In this way the sub-lattice is divided into eight neighbor pairs. Only neighbor sites belonging to the same neighbor pair can react, so all the neighbor pairs can be accessed in parallel.

Applying this rule to the (L is a common multiple of 4) lattice, we build up a tiled mask over the whole lattice, considering periodic boundary conditions. For any lattice, which size is ($L = 4k$), it can be proved that there are only sixteen possible partitions. Take a lattice for instance (Fig. 2), cells of the same gray scale belong to the same elementary component.

The dynamics is not confined to big blocks (elementary components), because

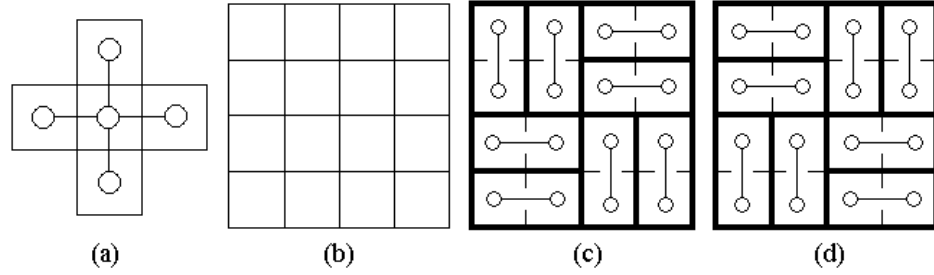


Fig. 1. We show the traditional neighborhood and the new defined one. (a) von Neumann neighborhood, (b) a sub-lattice is considered as an elementary component, (c) scheme 1 for the definition of the neighborhood, (d) scheme 2 for the definition of the neighborhood.

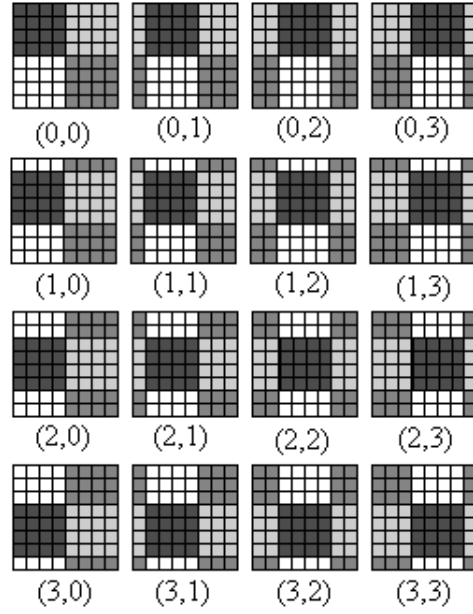


Fig. 2. The sixteen possible partitions of elementary components in a lattice. Cells of the same gray scale belong to one elementary component.

the boundary between blocks is changing from one time step to the next. In this way, the implementation of this model is more tractable than the asynchronous Cellular Automata and more efficient than Monte Carlo simulation.

The evolution runs along the following steps: 1. Choose randomly one of the sixteen possible partitions as shown in Fig. 2. Inside each elementary component specify the neighbor pairs by selecting one of the two schemes randomly. 2. Sweep over all the neighbor pairs and inside each neighbor pair do the reaction. 3. Increase the time by one time step. 4. Return to step 1. We applied this simulation method to this predator-prey model. The states of the sites are denoted as a set of symbols, (Table 2), and the reaction rules inside the neighbor pairs are shown in Table 3.

Table 2. The Symbol set according to the resident in the sites.

The resident in the sites	Genotype
A wolf	W
A male wolf	W_m
A female wolf	W_f
A female wolf with her child under the care	W_f^*
A sheep	S
A male sheep	S_m
A female sheep	S_f
A mother sheep with her child under the care	S_f^*
Grass only(empty site)	G

The parameters of the model are as follows: linear size of the lattice L , which is a common multiple of 4; initial densities of both species: prey (sheep) $C_s(0)$ and predator (wolves) $C_w(0)$; the number of time steps needed for the grass to grow again g ; the maximum food ration k ; the amount of food r_{min} needed to be fit for breeding; the minimum reproduction age A_r ; the mutation rate M ; the limit number of genetic disease T ; the period C_c for the new born animal under child-care. For simplicity, we assume the same value of k , r_{min} , A_r , M , T and C_c and for predators and prey. To make the model tractable, we fixed some of the parameters at the following reasonable values: $g = 4, k = 3, r_{min} = 2, A_r = 8, T = 3, C_c = 3$.

The initial populations are random, i.e. , they have random genotypes, ages and food rations. The spatial distribution is random, too, with the given initial concentrations.

4. Results and discussion

As could be expected, we have found three possible states: the coexisting one with prey and predators, the absorbing one with prey only, and the empty one where no animal survived, Fig. 3(a), 3(b) and 3(c), The fate of the two species mainly depends on their initial densities. The first typical stationary state is shown in Fig. 3(a) (which is the most usual state for the system to achieve in the model), which

Table 3. Reaction rules inside the neighbor pairs. (R_p : both of the male and female animals satisfy the reproduction terms. S_p : the number of the genetic diseases the wolf suffered is less than that of the sheep)

Current states of a neighbor pair	States of a neighbor pair in the next time step	Interpretation
$S + G$	$G + S$	A sheep move into an empty site.
$S_f^* + G$	$S_f + S$	A baby sheep leave its mother and move into an empty site.
$W + G$	$G + W$	A wolf moves into an empty site.
$W_f^* + G$	$W_f + W$	A baby wolf leaves its mother and moves into an empty site.
$S_m + S_f$	$S_m + S_f^*$	A pair of male and female sheep reproduce an offspring when they satisfy the R_p term.
$W + S$	$W + G$	A wolf eats up a sheep when they satisfy the S_p term.
$S + W_f^*$	$W + W_f$	A mother wolf eats up a sheep, then the baby wolf left mother.
$W_m + W_f$	$W_m + W_f^*$	A pair of male and female wolves reproduce an offspring when they satisfy the R_p term.
$G + G$ $S_m + S_m$ $S_f + S_f$ $S_f^* + S_f^*$ $W_m + W_m$ $W_f + W_f$ $W_f^* + W_f^*$ $S_m + S_f^*$ $S_f + S_f^*$ $W_m + W_f^*$ $W_f + W_f^*$	—	Under these cases, keep unchanged.

the oscillatory coexistence of the system is shown out. The three curves represent the densities of the predators, the prey and the grass respectively. The oscillations about the densities of the wolves, the sheep and the grass are not damped away and persist with big amplitude.

The second typical stationary state is shown in Fig. 3(b). The wolves die out rapidly, leaving the sheep and the grass. There are many factors resulting in the extinction of the wolves. The critical one is that the initial density of the sheep is too low while the one of the wolf is too high. After capturing most of the sheep, the wolves starve to death because of lack of food. The survived sheep spread rapidly after the wolf's extinction. In this case the sheep and the grass reach an asymptotical stationary state. Compared with Penna models without lattice^{5,13}, the oscillation of the density of sheep in this model are not damped away even after 2000 time steps.

The third typical stationary state is shown in Fig. 3(c). The initial density of the wolves is so high that they eat up all the sheep and subsequently starve to death. Finally it leads to the extinction of both of the species.

Then we investigated the effect of the mutation on the evolution of the two species. In Fig. 4(a), 4(b) and 4(c), $C_s(0) = 0.3$, $C_w(0) = 0.3$, $L = 256$, $M = 1, 2$ and 4 respectively. N_{bg} is the average number of "1" in the phenotype of the species. One can see that the N_{bg} drops with time step. What is the reason? There are mainly two factors. First, the mutation ensures the genetic diversity, including deleterious and helpful mutations. And then, the predation rule we assumed in this model plays the role of natural selection, that is, only the animals with better genotype are able to survive and reproduce. From the comparison of the three figures, one can see increasing the mutation rate leads to the faster evolution.

Now we discuss the role played by the linear size of the lattice on the type of the steady state reached by the system. The possible range of the initial concentrations is defined as $A = (x_1, x_2) | (x_1 + x_2 < 1, 0 < x_1 < 1, 0 < x_2 < 1)$. The interval from 0 to 1 can be divided evenly into N points. The position of each point represents the possible initial densities of the wolves and the sheep, and its color represents the steady state led by the initial densities. The $N * N/2$ points are sorted according to the final states they reach after 3000 simulation steps (Fig. 5(a), 5(b) and 5(c)) (2000 simulation steps is enough by plenty of experiments). From the three figures with different value of L , we concluded that the bigger the linear size of the lattice L is, the larger the proportion of the coexistence area will be.

Snapshots are given to show the spatial evolution of this predator-prey system, Fig. 6(a), 6(b) and 6(c). The initial random distribution of the wolves and sheep ($C_s = 0.3, C_w = 0.3, M = 2, L = 256$) is shown in Fig. 6(a). After 100 and 200 time steps, spatial self-organization can be observed in Fig. 6(b) and Fig. 6(c)

5. Conclusions

We have presented a lattice model of prey and predators that characterized by

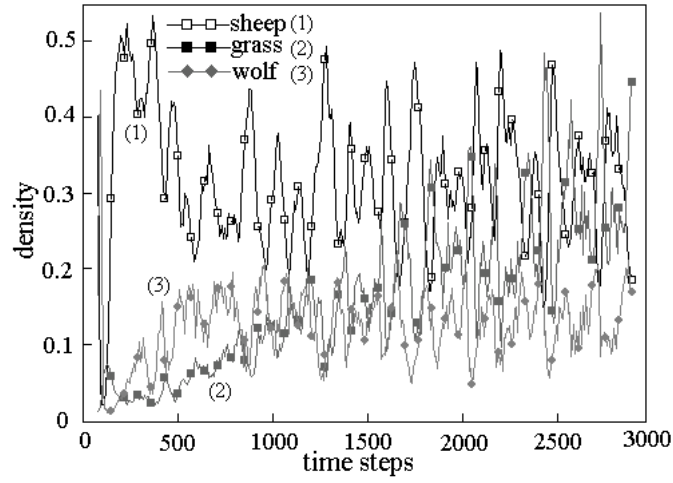
Penna bit-string. To survive, each animal has to eat at least certain time steps. A pair of male and female animals in adjacent cells can reproduce an offspring, if they have enough food reserves and over the minimum reproduction age. The child-care strategy allows the offspring to stay and move together with its mother within a certain period, if there is no empty cell in the neighborhood. Most of the predator-prey lattice models are simulated via Monte Carlo method. In our model containing moveable wolves and sheep, in order to obey the CA laws in von Neumann neighborhood, it is necessary disobey the common sense because a wolf may be participant in several hunts, which is unreasonable. To solve this problem, we present a new definition of neighborhood and built a fully parallel cellular automata simulation method, which is more tractable than the asynchronous Cellular Automata and more efficient than Monte Carlo simulation. As could be expected, we have found three possible states: the coexisting one with prey and predators, the absorbing one with prey only, and the empty one where no animal survive. In addition, we discussed the final states attained by the population with certain initial densities, the effect of the mutation on the evolution of the two species and the role played by the linear size of the lattice on the type of the steady state reached by the system.

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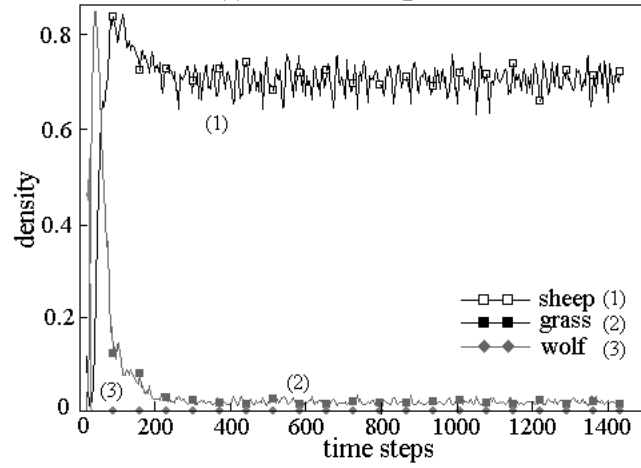
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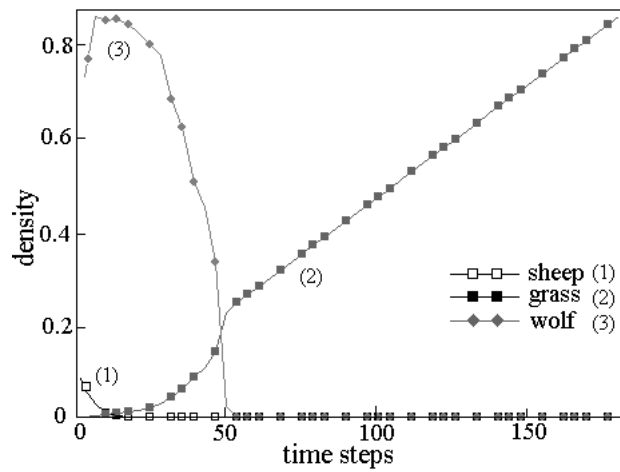
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(a) The coexisting one



(b) The absorbing one



(c) The empty one

Fig. 3. Density versus time step, $M = 2, L = 256$

- (a) the final state is the prey only one, $C_s(0) = 0.3, C_w(0) = 0.3$;
 (b) the final state is the empty one, $C_s(0) = 0.1, C_w(0) = 0.8$;
 (c) the final state is the empty one, $C_s(0) = 0.1, C_w(0) = 0.8$.

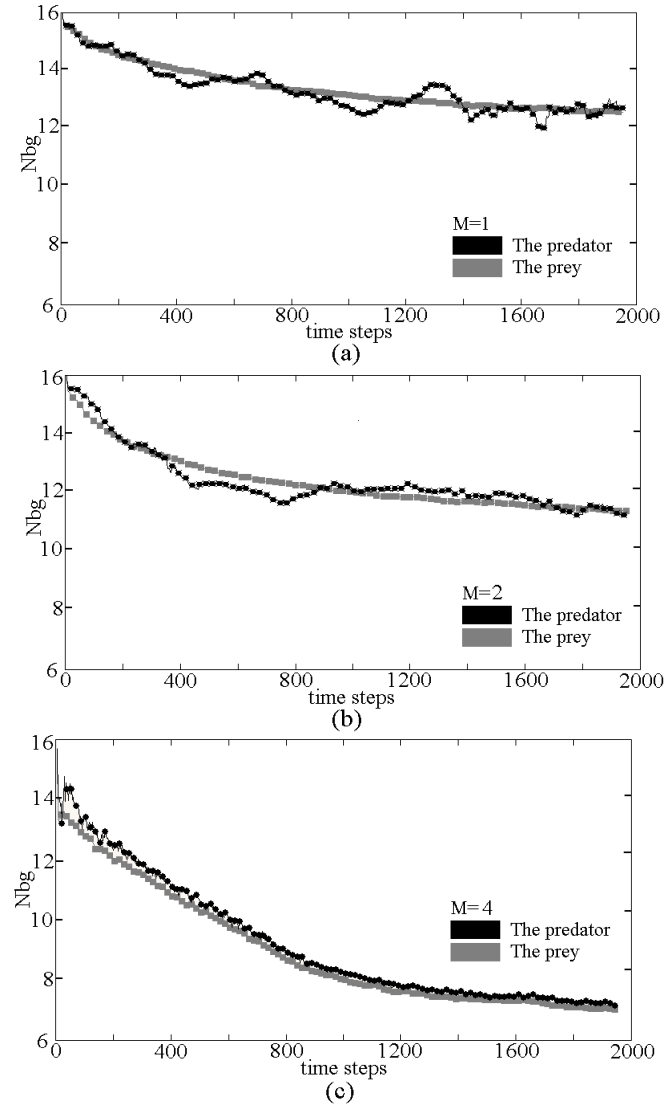


Fig. 4. Time dependence of the N_{bg} of the predators and prey, $C_w(0) = 0.3$, $C_s(0) = 0.3$, $L = 256$, (a) $M = 1$, (b) $M = 2$, (c) $M = 4$.

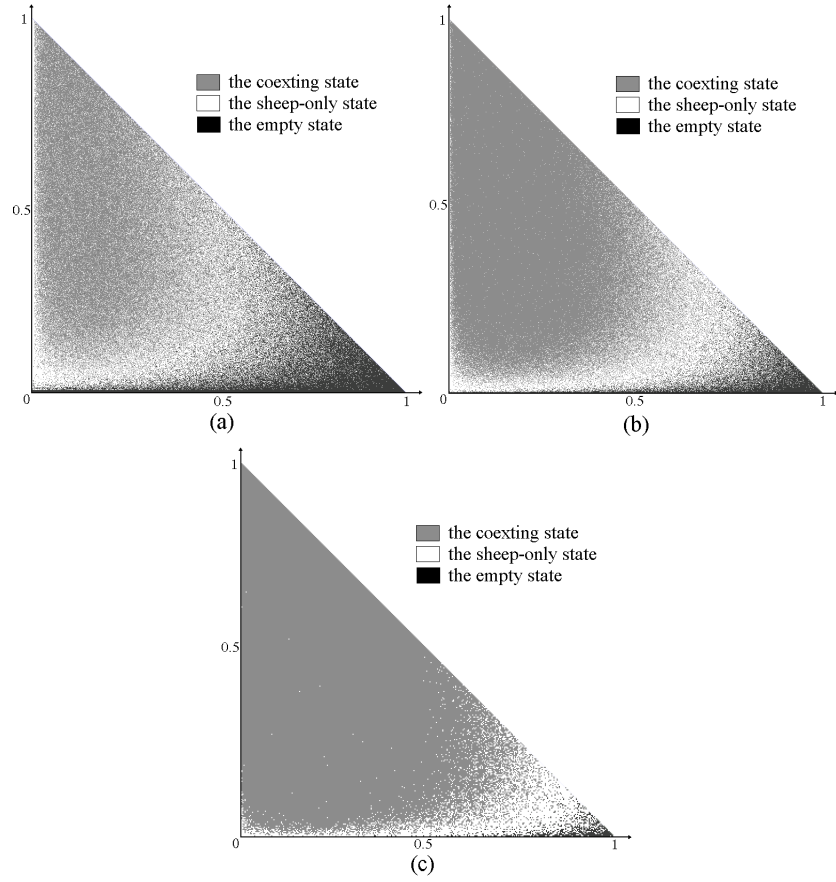


Fig. 5. (a) $L = 128$, $M = 2$. The proportion of black, gray and white respectively is 22.3%, 41.8%, 35.9%.
 (b) $L = 256$, $M = 2$. The proportion of black, gray and white respectively is 22.3%, 41.8%, 35.9%.
 (c) $L = 512$, $M = 2$. The proportion of black, gray and white respectively is 2.8%, 81.8%, 15.4%.

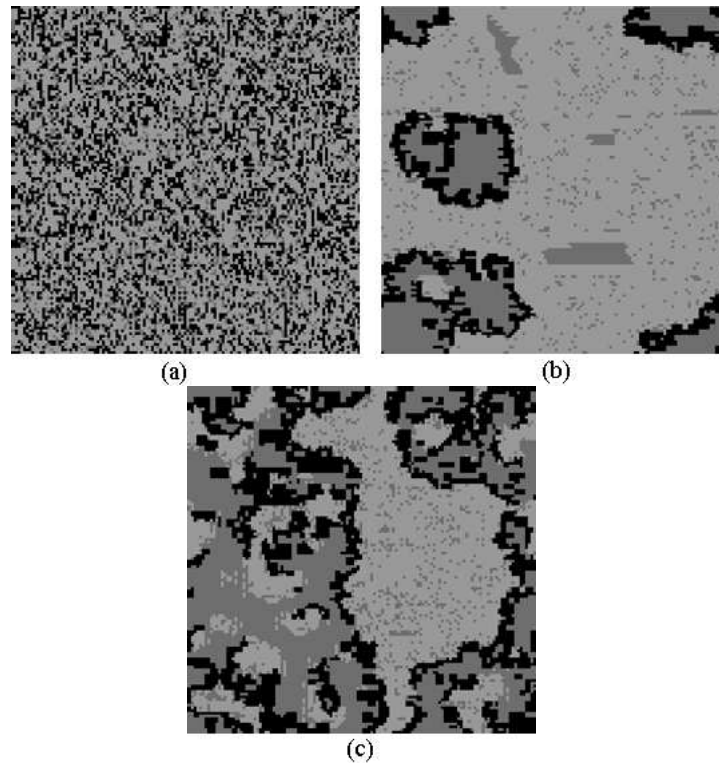


Fig. 6. (a) At the initial state the wolves and the sheep are distributed randomly.
(b) After 100 time steps, self-organization can be observed.
(c) The distribution of the grass, sheep and wolf after 200 time steps.