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A Full Cellular Automaton to Simulate Predator-Prey Systems*

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Abstract. A Cellular Automaton (CA) describing a predator–prey dynamics is proposed. This model is fully local, i.e., without any “spurious” Monte Carlo step during the movement phase. A particular attention has been addressed to the comparison of the obtained simulations with the discrete version of the Lotka–Volterra equations.

1 Introduction

Nonlinear ordinary differential equations are still a fundamental tool in the analysis of Predator–Prey systems [5, 8]. The limit due to lack of information about the spatial distribution during the time evolution of the populations have pushed the research, since the early 1990’s, toward lattice models. These systems evolves in discrete time steps by means of the application of some rules to the lattice sites. Most of the proposed lattice models are based on Monte Carlo (MC) simulation methods [9, 7, 11, 4, 1, 6, 10]. This approach is usually paired with mean-field equation analysis. The rules used to define the hunting process, i.e. the strictly local predator-prey interaction, are in many cases deterministic. Sometimes this local interaction does not assume the exclusion principle, so many entities may stay in the same lattice site [6, 11, 7]. More important, in the MC methods the movement phase of the species is a non local process. Let us stress that the random unbounded jumps between lattice sites may be unlikely w.r.t. the real movement capabilities of the individuals. In effects in many MC lattice models the focus on the biological semantics of the predation is somehow considered a secondary aspect. In [2] the predation phase is suitably treated but the MC modelling of the movement is not completely satisfactory from a biological point of view.

Cellular Automata (CA) models [12, 3] give a better biological approach to simulate predator-prey interactions. In the CA context all the lattice sites are updated in a synchronous way and, generally, the local evolution rule is simpler than the MC versions. The small cardinality of the CA neighborhood grants to model properly the individual movements.

* This work has been supported by the MIUR PRIN project “Formal Languages and Automata: Mathematical and Applicative Aspects”.

We propose a CA model to simulate predator-prey systems. The probabilistic predation rule, inspired by [2], has been designed by ecological motivations. We have defined a truly local movement phase, where wishes and fears of each species have been taken into account. A comparison between the simulations obtained by our CA approach and dynamical systems is exposed.

2 Discrete Time Dynamical Systems

Let us consider a single population within a closed environment. We denote by the variable $x(t) \in \mathbb{R}_+$ the population magnitude at time $t \in \mathbb{N}$ and by $r : \mathbb{N} \mapsto \mathbb{R}$ the growth rate function of the population. The system evolves according to the equation $x(t + 1) - x(t) = r(t) \cdot x(t)$. We consider the logistic case where $r(t) = k(1 - x(t)/L)$ with $k \geq -1$ and $L \in \mathbb{R}_+$. The parameter L is the capacity, i.e., the maximum number of individuals allowed by the system in order to maintain the population in equilibrium. The variation of the parameter k in the domain $-1 < k < 3$ determines different dynamical behaviors modifying the features of the equilibrium points 0 and L .

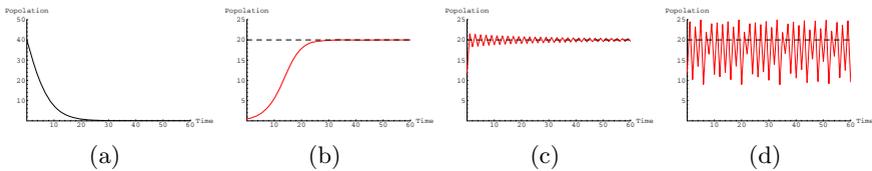


Fig. 1. Dynamics in the cases: (a) $-1 < k = -0.2 < 0$ (0 attracting, $L = 100$ repelling), (b) $0 < k = 0.23 < 1$ (0 repelling, $L = 20$ attracting), (c) $1 < k = 1.98 < 2$ (0 repelling, $L = 20$ attracting with possible oscillations) and (d) $2 < k = 2.6 < 3$ (0 and $L = 20$ repelling)

On the other hand, the behavior of two species $x_1(t) \geq 0$ (preys) and $x_2(t) \geq 0$ (predators) in competition in the same environment is summarized by the following discrete time difference equation generalization of the standard Lotka–Volterra differential equations system with $a_{ij} \geq 0$

$$\begin{cases} x_1(t + 1) = x_1(t)[(1 + k_1) - a_{11}x_1(t)] - a_{12}x_1(t)x_2(t) \\ x_2(t + 1) = x_2(t)[(1 + k_2) - a_{22}x_2(t)] + a_{21}x_1(t)x_2(t) \end{cases} \quad (1)$$

The study of the equation 1 shows that prey and predator populations exhibit an evolution consisting of oscillations.

3 The CA Model of Predator–Prey Dynamics

The automaton we consider in this paper is based on the $2D$ discrete rectangular lattice space $\mathcal{L} = \{0, \dots, M - 1\} \times \{0, \dots, N - 1\}$ consisting of M cells in the

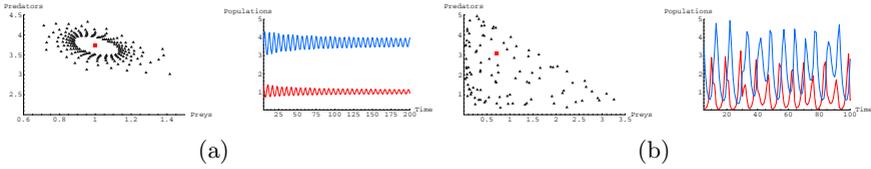


Fig. 2. (a) and (b): dynamics for $k_1 = 2.8, k_2 = 0.5, a_{12} = a_{21} = 0.5$. (c) and (d): dynamics for $k_1 = 2.8, k_2 = 0.5, a_{12} = a_{21} = 0.7$.

horizontal direction and N cells in the vertical one with periodical boundary conditions (toroidal geometry). Each cell can assume a value in $Q = \{0a, 1, 2a\}$, where $0a, 1$ and $2a$ mean that either the cell is empty, it contains a prey or it contains a predator, respectively. A *configuration* \underline{c} of the automaton is a function $\underline{c} : \mathcal{L} \mapsto Q$ which assigns to each cell $(x, y) \in \mathcal{L}$ a state $\underline{c}(x, y) \in Q$, implemented as a $M \times N$ two dimensional array. In this paper we present two CA models. The second model, as an improvement of the first one, corresponds to better (and in some sense optimal) results in comparison with the difference equations discussed in section 2. The enhancement regards the possibility of prey death in cells whose neighborhood contains a great number of other preys in absence of predators. The uniformly applied local transition CA rule consists of two steps: *reaction* and *movement*.

The reaction step is composed by two sub-phases: the attack and the reproduction (including also death processes). They depend on the following 4 parameters: b_p (prey birth probability), d_p (prey natural death probability), b_h (predator birth probability), and d_h (predator death probability). In both these sub-steps the involved neighborhood is the Von Neumann one. Let us introduce two temporary further states: $0b$ which means that the cell becomes empty after the attack sub-step and $2b$ meaning the cell contains a predator which ate. In this way, we have obtained a new state set $Q_0 = \{0a, 0b, 1, 2a, 2b\}$. For the attack we consider a cell state $s \in Q$ in the position $(x, y) \in \mathcal{L}$. If it is a prey ($s = 1$) we have two possible transitions towards a new state $s' \in Q_0$. If there are no predators in its neighborhood the cell remains prey ($s' = 1$). Otherwise, it is alive ($s' = 1$) with probability $(1 - d_p)^{n_{pt}(x,y)}$ where $n_{pt}(x, y)$ is the number of predators in its neighborhood. If the prey dies the state of the cell becomes $s' = 0b$. If the cell is a predator ($s = 2a$), the predator fails the hunt (and in this case $s' = 2a$) with probability $(1 - d_p)^{n_{pr}(x,y)}$ where $n_{pr}(x, y)$ is the number of preys in its neighborhood. If the hunt succeeds the state of the cell becomes $s' = 2b$. Let us consider now a cell of state $s \in Q_0$ in the position $(x, y) \in \mathcal{L}$. During the reproduction sub-step if the cell is a prey ($s = 1$), its state does not change ($s' = 1$). If the cell is a predator ($s = 2a/2b$), it can die with probability d_h . In this case the cell becomes empty ($s' = 0a$), otherwise the new state is $s' = 2a$. Let us now treat the situation of an empty cell $s = 0a$. If either there are some predators or there are no preys in its neighborhood, the cell remains empty ($s' = 0a$). Otherwise it becomes prey ($s' = 1$) with probability $(1 - b_p)^{n_{pr}(i)}$. In the case $s = 0b$ (corresponding to the fact that in the previous sub-phase the cell

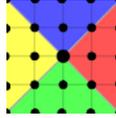


Fig. 3. The 4 quadrants of the radius 2 Moore neighborhood of a cell

was occupied by a prey and in its neighborhood there was predators) the cell remains empty (with $s' = 0a$) with probability $(1 - b_h)^{n_{pt2}(x,y)}$, where $n_{pt2}(x,y)$ is the number of predators which have eaten. Otherwise the cell becomes predator ($s' = 2a$).

In order to describe the movement phase let us introduce the mapping $T : Q \times \mathcal{L} \mapsto \{0, 1\}$ defined as follows:

$$T(v; x, y) = \begin{cases} 1 & \text{if the state of the cell } (x, y) \text{ is } v \in Q \\ 0 & \text{otherwise} \end{cases} \tag{2}$$

We can associate to any cell of position (x, y) and to each state $v \in Q$ the following quantities

$$\begin{aligned} n_N^{(r)}(v; x, y) &= \sum_{i=1}^r \sum_{j=-i}^i T(v, x + j, y + i) & n_S^{(r)}(v; x, y) &= \sum_{i=1}^r \sum_{j=-i}^i T(v, x + j, y - i) \\ n_E^{(r)}(v; x, y) &= \sum_{i=1}^r \sum_{j=-i}^i T(v, x + i, y + j) & n_W^{(r)}(v; x, y) &= \sum_{i=1}^r \sum_{j=-i}^i T(v, x - i, y + j) \end{aligned}$$

which represent the number of cells of state v in the North, South, Est, and West, respectively, quadrant of the radius r Moore neighborhood centered in the cell (x, y) (see figure 3). On the basis of these numbers it will be possible to determine the movement intentions of the individuals. If a cell contains a prey, the associated direction is the one corresponding to the quadrant containing the minimum number of predators. If many quadrants contain the same minimum value, then the direction is chosen with uniform probability. If there are not predators in the whole Moore neighborhood there is no movement. Analogously, a predator cell direction is directed toward the quadrant with the maximum prey number. Once the intentions are set, the movement is modelled so that the individuals move towards available empty cells in their Von Neumann neighborhood. If the same available empty cell is pointed by many creatures then a random choice is performed.

4 Simulations

In order to make a first test about the validity of the proposed model, we have considered the two opposite situations of preys without predators and vice versa. In the former (see the fig. 4b), the simulations show an increase of the population which is similar to the behavior of the logistic difference equation under

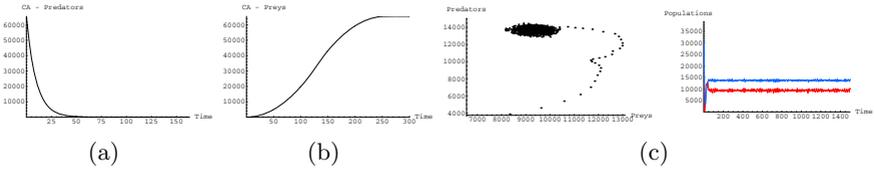


Fig. 4. CA dynamics of (a) predators in absence of preys and (b) preys in absence of predators. (c) CA dynamics with prey and predators ($b_p = .6, d_p = .7, b_h = .3, d_h = .2$).

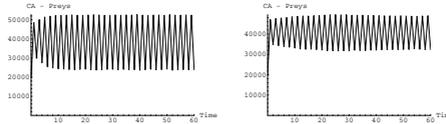


Fig. 5. CA prey dynamics with cosine function (left) and exponential function (right)

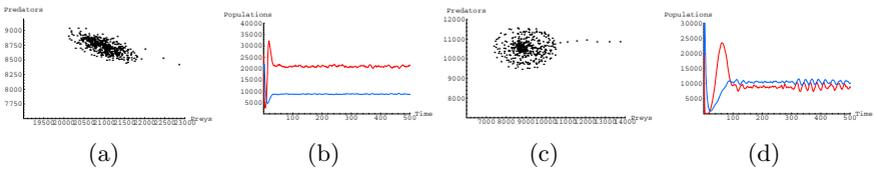


Fig. 6. CA dynamics of an interacting predator-prey system with cosine function

$0 < k < 1$ (compare with the fig. 1b). In the latter (see the fig. 4a) the decrease of predators is comparable to the logistic difference equation under $-1 < k < 0$ (compare with the fig. 1a).

These behaviors occur in any performed simulation independently by the CA parameters. Differently from the difference logistic equation behavior no oscillations appear. The figure 4b shows a simulation of a predator-prey interaction.

An improvement of the first CA model

The above discussion, with the inadequacy in obtaining oscillatory dynamics in the case of a single prey population, led us to modify the attack sub-phase for cells (x, y) containing a prey ($s = 1$). **If either** there is some predator in the Von Neumann neighborhood of the given cell and the prey is alive to the attack **or** there is no predator in its Moore neighborhood of radius r , **then** it dies ($s' = 0a$) with probability $n'_{pr}(x, y) \cdot f(b_p) / (2r + 1)^2$, where $n'_{pr}(x, y)$ is the number of preys in the Moore neighborhood of radius r and f is a pre-assigned mapping on the interval $[0, 1]$. In this paper we have adopted the two following different choices $f_1(b_p) = (1 - \cos(\pi/2 \cdot b_p))$ (cosine) and $f_2(b_p) = 1 - e^{-e \cdot b_p}$ (exponential). The figure 5 shows two oscillating prey dynamics and the figures 6 and 7 propose some simulations of interacting populations obtained by the modified model.

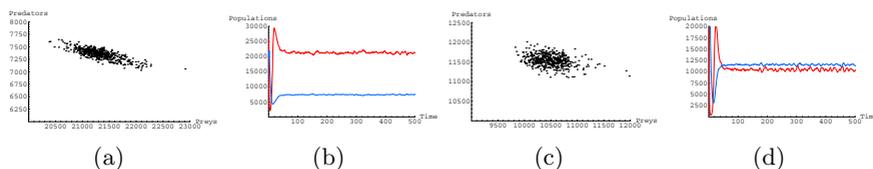


Fig. 7. CA dynamics of an interacting predator-prey system with exponential function

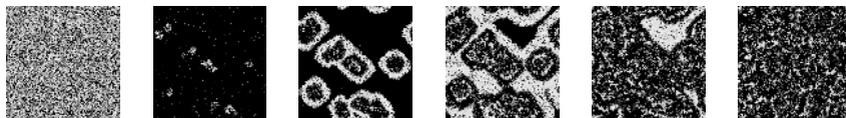


Fig. 8. Different lattice evolution steps

5 Conclusions

We have presented a full CA model of predator–prey systems whose fit with the logistic discrete time results about the dynamical evolution of the total number of individuals is very promising. Furthermore, the information about the “spatial strategies” adopted by the two species during these dynamics, information non available in the difference (but also differential) equation case, can be obtained.

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