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A stochastic model as a survival strategy for an infected population

Um modelo estocástico como estratégia de sobrevivência de uma população infectada

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Complex Systems is a branch of Statistical Mechanics that has gained great notoriety in recent years. In particular, Cellular Automata are a simple way to represent complex dynamical systems in which space and time are discrete. In addition to the high degree of nonlinearity, the Boltzmann-Gibbs formalism fails due to the non-extensibility of the systems. In some cases, Complex Systems appear at the typical scale, such as stock market fluctuations for example. In the case of epidemic modeling, cellular automata are used in the description of contagion processes, such phenomena are complex and have large-scale correlations. In this sense, cellular automata present a robust and precise tool for quantifying the spread of diseases in a population provided. In our work, we reported the temporal evolution of an infection in the square network, counting process is to introduce an interaction between first neighbors and the population in which the infection acts remains constant. We obtained, through the fourth-order Binder's cumulative, the instant of time $t$when the peak of the infection occurs, we also carried out the characterization of the type of passage through which the system goes through. We also analyzed the impact that the parameter causes on the temporal evolution of the infection.
Keywords: cellular automata, phase transition, Epidemiology.

Sistemas Complexos é um ramo da Mecânica Estatística que ganhou grande notoriedade nos últimos anos. Em particular, Autômatos Celulares são uma maneira simples de representar sistemas dinâmicos complexos em que espaço e tempo são discretos. Além do alto grau de não linearidade, o formalismo de Boltzmann-Gibbs falha devido a não-extensividade dos sistemas. Em alguns casos os Sistemas Complexos apresentam ausência de escala típica, como as flutuações da bolsa de valores, por exemplo. No caso da modelagem de epidemias, os autômatos celulares são utilizados na descrição de processos de contágio, tais fenômenos são complexos e possuem correlações em larga escala, neste sentido os autômatos celulares apresentam uma ferramenta robusta e precisa para a quantificação da difusão de doenças em uma determinada população. Em nosso trabalho reportamos a evolução temporal de uma infecção na rede quadrada, processo de contado é caracterizado por uma interação entre primeiros vizinhos e população a qual a infecção atua se mantém constante. Realizamos medidas do cumulante de Binder de quarta ordem no instante de tempo t em que ocorre o pico da infecção, realizando a caracterização do tipo de transição pela qual o sistema passa. Analisamos o impacto do parâmetro α na evolução da infecção.
Palavras-chave: autômatos celulares, transição de fase, Epidemiologia.

1. INTRODUCTION

The branch of Physics entitled Statistical Mechanics gained new impetus in the area of Complex Systems. These systems made up of a large number of components, simple when isolated, present a very complicated collective behavior. They have a high degree of non-linearity, and non-extensivity, where the application of the Boltzmann-Gibbs formalism often fails. In some cases, Complex Systems lack a typical scale, such as those presented in avalanches, earthquakes, and stock market fluctuations. When this happens, random events happen to obey power laws. The corresponding distributions form fractal or multi-fractal geometric structures. Thus, terms such as fractality, non-extensivity, R/S analysis, wavelets, non-linearity, turbulence, chaos,

self-organized criticality, anomalous diffusion, Levy processes, growth models, and power law, are common in the field of Complex Systems. These new concepts extrapolated the domain of Physics developed until just before the end of XIX. These concepts are applied to the Economy, stock market fluctuations, capital volatility, etc; Biology in cell evolution, tumor growth, damage spread, disease; Genetics in the study of DNA, genetic inheritance, genetic mutations, etc; Neural Networks in the study of brain function; Neurology in nervous system analysis, encephalogram analysis; Meteorology in the study of climate, weather forecasting; Geophysics in understanding earthquakes, avalanches; Cellular Automata in application to biological systems, population dynamics, hydrodynamics; among others, putting an end to the division between the various Sciences, no longer existing a problem of a specific scientific field. The main feature is multidisciplinarity. The difference that exists now is the technique used. This constitutes the modern area of Complex Systems [1-18].

In particular, Cellular Automata are a simple way to represent complex dynamical systems in which space and time are discrete. From a computer science perspective, they are computable models for complex phenomena with large-scale correlations that result from very simple short-range interactions, for example, fluids, neural networks, ecological systems, molecular dynamics, economics, military command networks, modeling of epidemics, etc. [14-25]. These systems can undergo phase transitions. Their quantitative descriptions can eventually be expressed by exact calculations, that is, without the need for approximations or adjustments to numerical data. In this context, the use of computers is relevant to obtaining numerical results, using specific techniques for each problem [19, 21].

In modeling epidemics, Cell Automata is used to describe the contagion of a given disease, configuring a precise tool for modeling and quantifying the spread of diseases in a given population [21].

A disease passes from individual to individual following the network of contacts within a given population [22]. The pattern of propagation in host-pathogen systems is a combination of local transmission from the focus of infection and long-distance transmission. Several models describe aspects related to an epidemic situation, including models that address the evolution of densities of population groups, and the existence of threshold values for the spread of the infection. The use of Stochastic Cell Automata to study the dynamics of infectious diseases is an important tool to understand the epidemiological process [23-25].

An important feature of epidemic models is that they can show phase transitions. A population made up of healthy individuals can transition to a sick population, exhibiting a phase transition from the healthy state to the sick state. Phase transitions in population systems, considering correlations and clustering effects, which have absorbing states is the subject of our study. We performed Monte Carlo simulations to observe the temporal effect of an epidemic on a population. To achieve our goal, we modeled this scenario using Stochastic Cell Automata in a square network. In this network, we performed density measurements typical of the system.

2. MATERIAL AND METHODS

Cellular automata are useful machines for the study of patterns in the formation of a vast class of complex systems such as fluids, neural networks, molecular dynamics systems, ecological systems, economics, phase transitions, etc. They are mathematically, spatially, and temporally represented, discrete, deterministic, and characterized by local interaction and inherent parallel evolution [26-28].

These systems are characterized by presenting a) discrete mesh formed by cells: one, two, three, or more dimensions; b) homogeneity: all cells are equivalent; c) interactions are local: each cell interacts only with cells in its vicinity; d) discrete dynamics: at each discrete time, each cell updates its current state according to a transition rule, taking into account the states of neighboring cells [20-28].

Each cell consists of a finite number of states, the evolution of the system occurs in discrete time according to a uniform local transition rule, or even as a function whose arguments are the states of neighboring cells at time t (and possibly the state of the considered cell itself).

Populations can transition from a healthy state to a sick one (due to the spread of a disease), undergoing a phase transition, a behavior that can be appropriately modeled using Cell Automata [19, 21].

A disease passes from individual to individual following the network of contacts within a given population [22]. For many host-pathogen systems, the pattern of spread is a combination of local transmission from the source of infection and long-distance transmission, which establishes new foci. Numerous models describe various aspects related to an epidemic situation, including models that describe the evolution of densities of population groups involved, and the existence of threshold values for the spread of infection. The use of stochastic models to study the dynamics of infectious diseases is an important tool to understand the epidemiological process. [26-28].

The study of critical phenomena in epidemic models makes it possible to study fluctuations, considering correlations and clustering effects. In this context, phase transitions in out-of-equilibrium systems, that is, systems that have absorbing states, have been widely studied in two different types of cases: with and without recovery [25].

We defined a discrete system consisting of N elements, arranged in a one-dimensional discrete mesh, with local interactions and stochastic dynamics. The stochastic dynamic is determined by the stochastic variable η_i, associated with each element i of the system: can take four values, $\eta_i = \{0,1,2,3\}$. The values of $\eta_i = \{0,1,2,3\}$ they correspond to the susceptible (S), infected (I), recovered (R) and dead (D) states, respectively. The form of contagion is modeled as a probabilistic process, the dynamic used disregards births and deaths, not due to the disease, that is, the total number of the population to be considered is constant, that is,

$$S + I + R + D = N \tag{1}$$

It is considered at the initial moment t_0, that a percentage of system elements are infected. every instant of time t, an element of the system is randomly chosen, then the following local state transition rules are applied:

1. A susceptible individual can be infected according to the probability of infection: $P(0 \rightarrow 1)$ if at least one of your closest neighbors is infected. The probability is given by:
$$P(0 \rightarrow 1) = \alpha \frac{n}{\tau}, 0 < \alpha \leq 1 \tag{2}$$
where n is the number of nearest neighbors infected and τ, the number of neighbors to be considered. For example, in a square network each site i in the network has four neighbors.
2. An infected individual recovers spontaneously, with no reinfection, from an interval of days limiting the infection d_i or the same occurs with probability of recovery $P(1 \rightarrow 2) = \gamma$.
3. Death occurs with probability $P(2 \rightarrow 3) = \beta$.

3. RESULTS AND DISCUSSION

We performed our simulations using square-sized grid $N = L \times L$. Initially we took values for the linear size of the network L in 16, 24, 32, 40, 48. We considered that about 5% of the individuals in the network are infected.

We defined $\alpha = 0{,}8$, $\gamma = 0{,}02$, $\beta = 0{,}003$ e $d_i = 30$, that is, after 30 days of infection, the individual is cured. During the simulation, a random site i of the network is chosen, it is verified if it is infected, a random number p between 0 and 1 is generated. As the network is square, we verified that the maximum number of first is 4, therefore $\tau = 4$, so we have the following local rules for state transition:

1. If the individual is not infected and $p < \frac{n}{4}, n$ is the number of infected neighbors, it is measured by the infection.
2. If the individual is infected and $\beta < p \leq \gamma$, the individual is healed.
3. If the individual is infected and $p \leq \beta$, the individual is dead.

Figure 1 illustrates the temporal evolution of individuals susceptible to infection. In this graph, we could see that not every population is infected by the disease. We could also note that for $t > 20$, the infection is stopped.

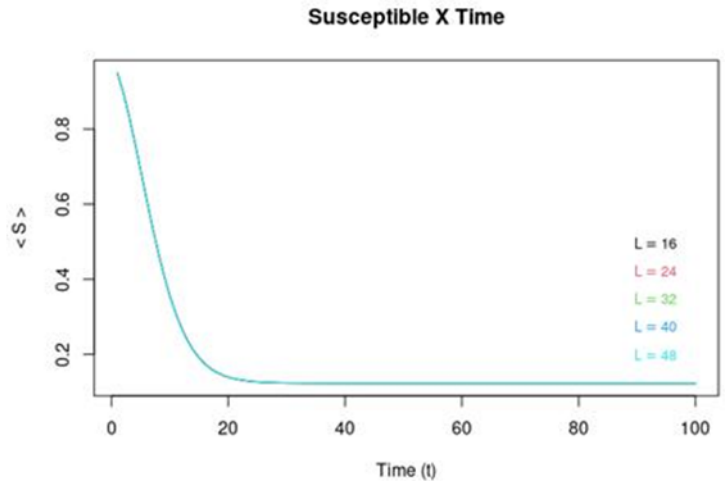

Figura 1: Curve of Susceptible Individuals and related to the time.

In Figure 2 we reported the temporal evolution of infected individuals in the network. Concerning to Figure 2, we notice that, over time, the proportion of susceptible starts to fall, as the number of infected people increases simultaneously. It is also noted that the peak of infection occurs in t next to 20.

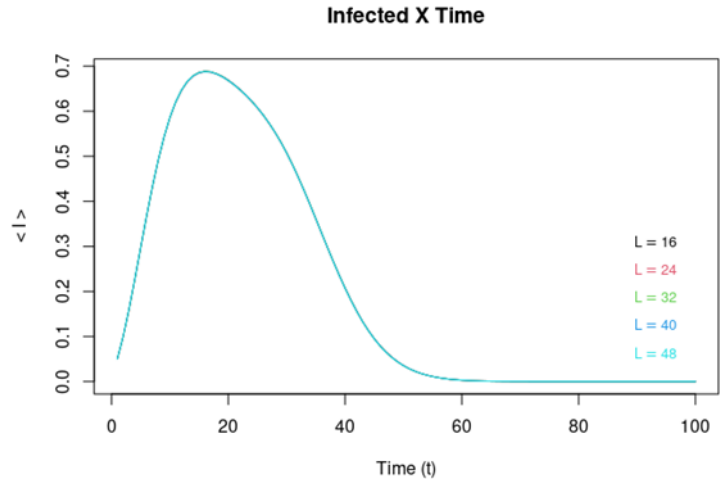

Figura 2: Curve of Infected Individuals over time.

In Figure 3, we showed how the individuals in the network are cured, we see that about 80% of the individuals are cured. In comparison with Figure 2, we could conclude that the infection stops at $t > 60$.

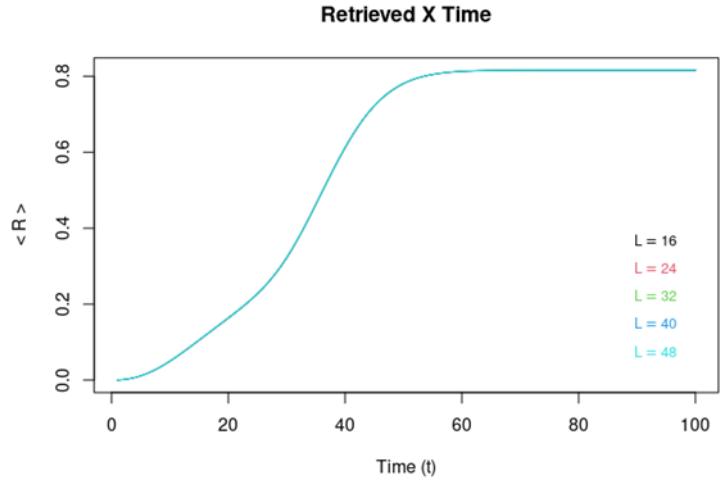

Figura 3: Curve of Recovered Individuals over time.

In Figure 4, we showed the behavior of deaths caused by the disease over time.

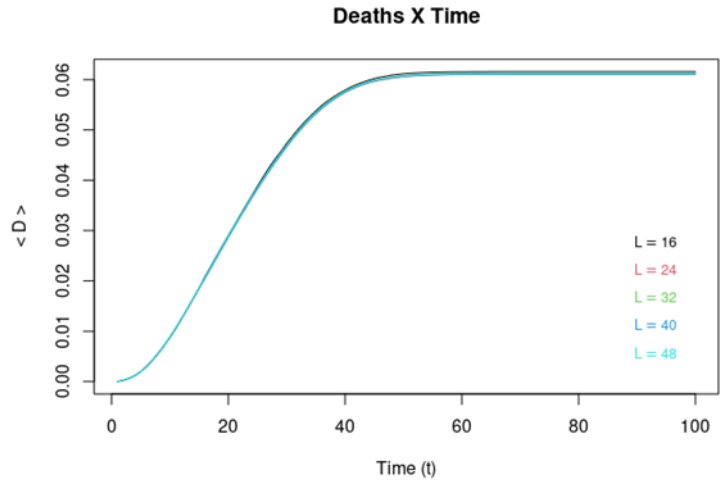

Figura 4: Curve of Dead Individuals over time.

We used the fourth-order Binder cumulative for the number of susceptible individuals, to determine when the peak of infection occurs, the same is given by:

$$U_4(S) = 1 - \frac{\langle S \rangle^4}{\langle S^2 \rangle^2} \tag{3}$$

In Figure 5, we displayed typical fourth-order Binder Cumulant measures for susceptible individuals $U_4(S)$ as a function of time t for different network sizes. From the cumulative graph it can be seen that the change of state in the system is characterized by a second-order transition. We also reported that, for $\alpha = 0.8$ that the peak of the infection occurs in $t = 16$.

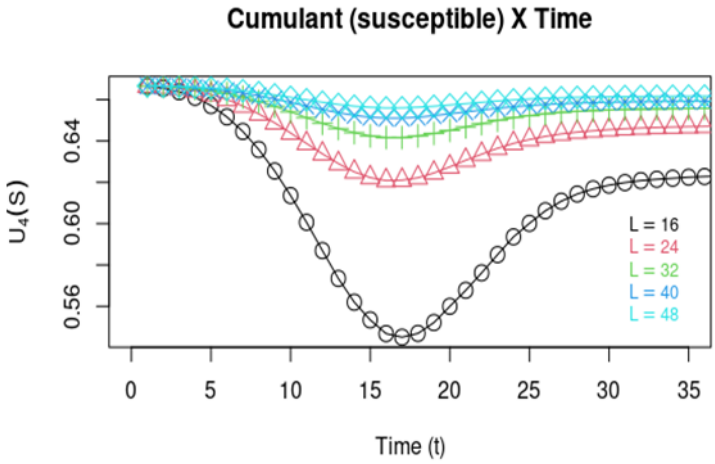

Figura 5: Fourth-order Binder cumulative for susceptible individuals.

Setting the Grid Size Parameter $N = L \times L = 48$, we varied $\alpha = \{10^{-3}, 0.25, 0.50, 0, 75, 1.0\}$, in order to analyze the impact of the parameter on the spread of the infection. In Figure 6, we presented typical measures of the mean infected. We observed that with increasing α, the expected value for the mean infected grows faster, as well as reaching its peak faster.

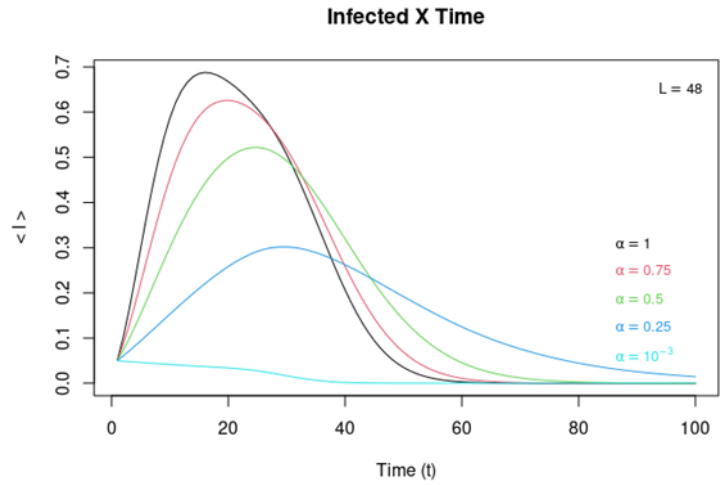

Figura 6: Infection diffusion in relation to the parameter $\boldsymbol{\alpha}$.

4. CONCLUSION

We studied an automata system, a square network, this system aims to model the temporal evolution of an epidemic in a population of N individuals. We used Monte Carlo processes to measure typical system densities. We observed that as time passes the system changes from susceptible to infected, and that after the peak of the infection, the population becomes mostly cured, with a small percentage of dead individuals, such behavior was already expected, since $\beta < \gamma$. Our stochastic results, whether deterministic or stochastic, are in line with those of models already in the literature. It is also noted that our model has two absorbing states, recurred (R) and the dead ones (D). We estimated the peak of infection using the fourth-order Binder Cumulative for the number of susceptible individuals $U_4(S)$. We also obtained that with the increase of α the average infected increases.

5. ACKNOWLEDGMENTS

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