A study of the influence of the mobility on the phase transitions of the synchronous SIR model

Roberto da Silva$^1$ and Henrique A Fernandes$^2$

$^1$ Instituto de Física, Universidade Federal do Rio Grande do Sul, Av. Bento Gonçalves, 9500-CEP 91501-970, Porto Alegre, Rio Grande do Sul, Brazil
$^2$ Coordenação de Física, Universidade Federal de Goiás, Campus Jataí, BR 364, km 192, 3800-CEP 75801-615, Jataí, Goiás, Brazil

Received 7 November 2014
Accepted for publication 3 May 2015
Published 3 June 2015

Online at stacks.iop.org/JSTAT/2015/P06011
doi:10.1088/1742-5468/2015/06/P06011

Abstract. By using an appropriate version of the synchronous SIR model, we studied the effects of dilution and mobility on the critical immunization rate. We showed that, by applying time-dependent Monte Carlo (MC) simulations at criticality, and taking into account the optimization of the power law for the density of infected individuals, the critical immunization necessary to block the epidemic in two-dimensional lattices decreases as dilution increases with a logarithmic dependence. On the other hand, the mobility minimizes such effects and the critical recovery probabilities are greater when the probability of movement of the individuals increases. Moreover, we studied the dynamic critical exponent $\theta$ which governs the growing of the density of infected individuals under dilution and mobility, when starting each lattice with all individuals as susceptible ones but the individual at the center which is set as infected one.

Keywords: finite-size scaling, phase diagrams (theory), cellular automata, epidemic modelling
1. Introduction

The study of critical phenomena in epidemic models defined on lattices has an important role in the context of statistical mechanics [1–5]. However, such approach is relatively recent since the mathematical modelling of an epidemic process was introduced via differential equations [6]. The advantages of the first approach in relation to differential equations framework are the possibility of studying fluctuations, whereas it takes into account correlations and clustering effects.

In this context, the non-equilibrium phase transitions of systems that possess absorbing states have been vastly studied, as can be seeing in the literature (see, for example, [2,3]), and can be didactically separated in two kinds: with and without recovery.

Epidemic models without recovery belong generically to the directed percolation (DP) universality class. In this case, the finite size scaling near criticality can be described by the following general scaling relation [3]:

\[ \langle i(t) \rangle \sim t^{-\beta/\nu_\parallel} f(\Delta t^{1/\nu_\parallel}, L^{-d/d/z}, d_0 t^{\beta/\nu_\parallel+\theta}) \]  

where \( i(t) = \frac{1}{L^d} \sum_{j=1}^{L^d} \sigma_j \) is the density of infected individuals in a \( d \)-dimensional lattice at the time \( t \) and \( \langle \cdots \rangle \) means the average on different evolutions of the system.

For example, the individuals denoted by the stochastic variable \( \sigma_j \) are arranged on the sites \( j \) of the lattice (where \( j = 1, \cdots, L^d \) and \( L \) is the linear size of the lattice) and can be in two different states, infected (or active) and susceptible (or inactive). When the individual is infected, one considers \( \sigma_j = 1 \) and otherwise \( \sigma_j = 0 \). The exponents \( \beta, \nu_\parallel, \text{and } \nu_\perp \) are static critical exponents, while \( z = \nu_\parallel/\nu_\perp \) and \( \theta \) are the dynamic ones. Here, \( \Delta = p - p_c \) denotes the distance of a point \( p \) to the critical point, \( p_c \), which governs the algebraic behaviors of the two independent correlation lengths: the spatial one which behaves as \( \xi_\perp \sim \Delta^{-\nu_\perp} \) and the temporal one, \( \xi_\parallel \sim \Delta^{-\nu_\parallel} \). Basically, \( \xi_\perp \) must be thought of as the average over many independent realizations of the cluster diameter while \( \xi_\parallel \) is the same average of the required time to reach the absorbing state. Here \( \beta \) is related to the stationary density of infected individuals in the active phase according to \( i_{\text{stat}} \sim \Delta^{\beta} \).
A study of the influence of the mobility on the phase transitions of the synchronous SIR model

Representing this universality class, one have for example, the susceptible-infected-susceptible (SIS) model which corresponds to the Domany–Kinzel cellular automaton for a particular case of the parameters when taking into account the synchronous update, as well as to the contact process when one considers the asynchronous update. The SIS model represents diseases for which the infection does not confer immunity, i.e. the individual return to the susceptible class after recovering from the infection. For this model, we expect a crossover between two power-law behaviors when starting the simulation with a small density of infected sites, \( i(t = 0) = i_0 \approx 0 \), at criticality \( \Delta = 0 \):

\[
\langle i(t) \rangle = \begin{cases} 
  t^\theta & \text{if } t < t_0 \\
  t^{-(\beta/\nu z + \theta)} & \text{elsewhere}
\end{cases}
\]

(2)

where the crossover time depends on \( t_0 \sim i_0^{-(1/\beta/\nu z + \theta)} \). This critical initial slip is very similar to the behavior of magnetic systems when they are quenched from a high temperature to the critical one \([7]\).

Such behaviors can be studied from Monte Carlo (MC) simulations. The first one (when \( t < t_0 \)) is obtained by putting only one infected individual at the center of the lattice and all other sites are occupied by susceptible ones \( (i_0 = 1/L^d) \). The second behavior can be obtained by making \( i_0 = 1 \) (representing a fully infected lattice). However, in models with recovery, the initial condition \( i_0 = 1 \) does not reproduce the second power law. Actually, in this case, an exponential relaxation is expected.

In addition to the SIS model, a range of other models can be studied in order to represent a desired epidemic. For instance, one can consider the susceptible-infected (SI) model to study the human immunodeficiency virus (HIV) whereas there is no recovery. However, when the disease is such that the individual can recover and be immune to the disease, at least for some time, one must consider a new class of recovered individuals, R. If, after recovering from the disease, the individual becomes immune to reinfection, the epidemic can be studied through the susceptible-infected-recovered (SIR) model. Nevertheless, if the individual can be reinfected with the disease after some time, one can consider the SIRS model \([8]\). In addition, there are other models which demand other classes such as exposed (E), hidden (H), and maternally-derived immunity (M), in order to represent infectious diseases.

The first studies about lattice-based models for epidemic growth is due to Grassberger \([1]\), who considered a simple cellular automata to show that exists a critical contamination value such that, below this point, no infinite epidemic is possible, i.e. the epidemic does not percolate. In his pioneering work about epidemic model with recovery, Grassberger \([1]\) raised important questions about epidemic process, and one of them, in particular, caught our attention: ‘... A somewhat more subtle question is whether one can allow also for mobility of individuals...’). Unfortunately, no work has explored the phase transitions and the preservation of some scaling relations for epidemic models with immunization despite this excellent tip. Some authors have explored dynamics of the SIR and reaction-diffusion processes in meta-population models with heterogeneous connectivity patterns via analytical results \([9]\). In a similar way, Belik et al \([12]\) performed an analysis of dynamical features of epidemic on regular and complex topologies and showed the differences to ordinary reaction-diffusion process and effective force of infection models. In \([11]\), the authors found the integral of motion for a deterministic SIR model with strong
A study of the influence of the mobility on the phase transitions of the synchronous SIR model coupling to neighbor lattice sites. Other interesting study explores how the recurrent mobility patterns mediates the contagion process via theoretical framework corroborated by real human commuting data [10].

However, a study via time-dependent and independent MC simulations of the phase diagrams by considering diluted lattices with mobility of individuals deserves attention.

In this work, we elaborate a detailed study of the influence of the mobility of individuals on the phase transitions of the SIR model. For that, we separate our main contributions in three parts as follows:

(1) Elaboration of a refinement procedure to determine the critical parameters via time-dependent Monte Carlo Simulations for models with absorbing states;

(2) The influence of dilution on the finite size scaling behavior of the synchronous SIR model and the dependence of the critical parameters on the density of individuals in the lattice;

(3) The study of the mobility and its effects on the parameters at the transition point, more precisely, the critical recovery probability ($c$).

Our work is divided in sections as follows: In the next section, we present the SIR model implemented as cellular automata and show how to add the dilution and mobility in this model. Moreover, we show how to adapt a refinement procedure, developed in [13] (when studying spin systems in the context of time dependent MC simulations), in order to determine the critical parameters of models with absorbing states. In section 3 we present our main results. Finally, a brief discussion of the results as well as some conclusions of our findings are presented in section 4.

2. Sir model with dilution and mobility and time-dependent simulations

The susceptible-infected-recovered (SIR) model [6] is a paradigmatic model in the theory of epidemics, and can be considered as a good and simple model to mimic some infectious diseases including measles, mumps, and rubella. Defining $S(t)$ as the number of susceptible individuals at time $t$ in a population, $I(t)$ the number of infected ones, and $R(t)$ the number of recovered (immune) ones, a deterministic (mean-field) approach of the traditional SIR model considers the following set of differential equations:

$$\frac{dS}{dt} = -\lambda I(t)S(t)$$
$$\frac{dI}{dt} = \lambda S(t)I(t) - \mu I(t)$$
$$\frac{dR}{dt} = \mu I(t),$$

where $\lambda$ is the contact rate which takes into account the probability of getting the disease in a contact between a susceptible and an infected subject, and $\mu$ is simply the recovering rate of infected individuals. This originally non-linear problem was proposed by Kermack and
MacKendrick [6] and no generic analytic solution is known so far. However, an interesting analytical solution in the Cayley tree with arbitrary coordination were obtained by Tome and Oliveira [14].

Naturally, we can note that \( \frac{d}{dt}(S + I + R) = 0 \) which means that \( N = S + I + R \) is a constant of the problem: the total number of individuals. More precisely, this version of the SIR model does not suppose vital dynamics, i.e. an epidemic where a single epidemic outbreak moves faster than the normal birth/death rates.

In order to take into account the correlation and cluster effects in an epidemic spreading, Grassberger [1] considered a synchronous probabilistic (cellular automaton) version of the epidemic model on a regular lattice. A particular and interesting version of the synchronous SIR model is obtained when the rates \( \lambda \) and \( \mu \) are given by the probabilities \( b \), the infection probability, and \( c \), the recovered one respectively. In addition, in this particular version \( b + c = 1 \) as it should [15].

In this version, each site can be in the following states: occupied by a susceptible, an infected or an immune individual. The stochastic dynamic is governed by the following rules: The infection can occurs when a susceptible individual, which occupy a given site of the square lattice, has at least one neighbor occupied by an infected individual. This process occurs with probability \( b/4 \) times the number of infected individuals in its neighborhood. The recovering process occurs spontaneously with probability \( c \) when the site is occupied by an infected individual.

This version of the SIR model was proposed by Arashiro and Tome [15] as a particular case of the prey-predator cellular automaton [16]. In that work, they showed that when keeping the recovery probability \( c \) plus infection probability \( b \) exactly equal to 1 and considering every site of the lattice occupied with a susceptible, infected or recovered individual, a transition between the active and inactive phases occurs for \( c_c = 0.22 \). This is the critical value of the infection probability, where occurs the transition from a phase where the density of recovered individuals, \( r(t) \), is different from zero (meaning that \( b \) is high enough such that the whole population, after contaminated, become recovered) to a phase where \( r(t) = 0 \) (whereas \( b \), in this case, is low enough such that only few individuals, or even no one of them, become recovered). The authors performed several independent runs of a lattice completely filled with susceptible individuals except by one infected site at the center of the lattice and the system evolved according to the synchronous update. After a reasonable number of steps, any one of the infinitely many absorbing states can be reached and consequently, the number of immune individuals at the steady state varies from run to run. The simulation is finished when the system enters in an absorbing state. Then, the number of recovered individuals (attack ratio) is calculated. The mean value of this quantity, divided by the total number of individuals, is the density of immune individuals at the steady state, \( \langle r(t) \rangle \), as presented above.

Although this model has been considered for the case where the density of individuals is \( \rho = 1 \), i.e. no vacancies are presented in the lattice, in many real applications some sites of the lattice can be empty, affecting therefore the critical properties of the model. Previous studies in other statistical mechanical models (see for example diluted Ising model [17, 18]) show that phase transitions are changed when \( \rho \neq 1 \). By extending the applications for other diluted lattices, Vainstein et al [19] explored not only the influence of dilution on the cooperation among prisoner dilemma players but also the effects of the mobility of players. Vainstein et al [19] considered the mobility simulated by a simple
random walk in a two-dimensional lattice. In their prescription, each player can only jump (with probability $p$) to its nearest neighbor at random and when there is at least one nearest-neighbor site empty. Otherwise, the player remains where it is. 

For an epidemic process, it is not different, i.e. infections must be changed not only by dilution but mainly by mobility! In this paper, we analyse the influence of the mobility of individuals on the phase diagrams of the SIR model. For this task, we consider its synchronous version implemented according to [15]. On the other hand, the mobility was implemented according to the prescription used in [19].

For the refinement process of the critical parameters, we use a method developed in [13] and vastly explored in our previous contributions in which we studied magnetic systems [20–22]. To our knowledge, this is the first time that this kind of refinement is applied to a model without a defined Hamiltonian.

Basically, we perform time dependent simulations by starting system with a completely filled lattice by susceptible individuals but the individual at its center which is contaminated with the disease. By considering $N_{\text{runs}}$ different runs, we calculate the average time of the density of infected individuals through the equation

$$\langle i(t) \rangle = \frac{1}{N_{\text{run}}} \sum_{k=1}^{N_{\text{run}}} \sum_{l=1}^{L} \sum_{j=1}^{L} \sum_{k=1}^{L} m_{l,j,k}(t) \delta_{1,\sigma_{l,j,k}(t)} \sum_{l=1}^{L} \sum_{j=1}^{L} m_{l,j,k}(t).$$

Here, $L$ is the linear size of a square lattice and $m$ is 0 when the site $(l,j)$ is empty or 1 when it is occupied by an individual at the time $t$ of the $k$–th run. In addition, $\sigma$ denotes the state of an individual: susceptible ($\sigma = 0$), infected ($\sigma = 1$), or recovered ($\sigma = 2$), and $l = 1, \ldots, L$ $(j = 1, \ldots, L)$ stands for the $l$–th line $(j$–th column) of the lattice.

Since at criticality it is expected that $\langle i(t) \rangle \sim t^\theta$, the method/algorihm changes the values of the recovery probability, $c$, according to a resolution $\Delta c$ from $c_{\text{min}}$ up to $c_{\text{max}}$ in order to find its best value, i.e. the critical recovery probability, $c_c$. Then, we calculate the known coefficient of determination [23]

$$\alpha = \frac{\sum_{t=t_{\text{min}}}^{t_{\text{MC}}} \left( \ln \langle i(t) \rangle - a_1 - a_2 \ln t \right)^2}{\sum_{t=t_{\text{min}}}^{t_{\text{MC}}} \left( \ln \langle i \rangle - \ln \langle i(t) \rangle \right)^2}$$

for each value of $c = c_{\text{min}} + i \Delta c$, where $i = 1, \ldots, \lfloor (c_{\text{max}} - c_{\text{min}})/\Delta c \rfloor$ and $N_{\text{MC}}$ is the number of MC steps. Here $a_1$ and $a_2$ come from the linear fit of $\ln \langle i(t) \rangle$ versus $\ln t$, and $\ln \langle i \rangle = (1/(N_{\text{MC}} - t_{\text{min}} + 1)) \sum_{t=t_{\text{min}}}^{N_{\text{MC}}} \ln \langle i \rangle (t)$. In addition, $t_{\text{min}}$ is the number of disregarded MC steps at the beginning of the simulation. The coefficient $\alpha$ has a very simple explanation: It measures the ratio (expected variation)/(total variation). The bigger the $\alpha$, the better the linear fit in log scale, and therefore, the better the power law which corresponds to the critical parameter excepted for an error $O(\Delta c)$.

3. Results

By using the optimization method presented in the previous section, we determined the critical recovery probability ($c_c$) for different values of dilution $0 \leq \rho \leq 1$ and mobility.
A study of the influence of the mobility on the phase transitions of the synchronous SIR model

Figure 1. (a): Values of the coefficient of determination $\alpha$ as function of $c$ for the case $\rho = 1$. (b): Density of recovered individuals as function of $c$ for different values of $L$. The phase transition is observed in $c = 0.22$. (c): The search for a power law behavior of $\langle i(t) \rangle$ for different values of $c$ around $c_c = 0.22$ via time-dependent MC simulations. The value of $c$ which corresponds to the curve with linear behavior corroborates the value found in (a) and (b).

$0 \leq p \leq 1$. For time-dependent simulations, we used $t_{\text{min}} = 100$ MC steps and $N_{\text{MC}} = 800$ MC steps. Let us start with the simplest case where $\rho = 1$ which corresponds to the critical value $c_c = 0.22$ obtained by Arashiro and Tomé [15] whereas there is no empty site in the lattice. As shown in figure 1 (a), our simulations pointed out for a maximum of $\alpha$ corresponding to $c = 0.2200(25)$ which corroborates the value from literature. Basically, our refinement process changes $c$ with a precision $\Delta c = 0.0025$ and in addition, the time-dependent simulations are performed with $N_{\text{run}} = 2400$ runs for each value of $c$.

Figure 1(b) shows that the model presents a phase transition for $c = 0.2200(25)$ corroborating the value found in figure 1(a). This is shown by calculating $\langle r \rangle$, the average of the density of recovered individuals, in the steady state (absorbing state). For these simulations, we considered $N_{\text{run}} = 4000$ and the maximum number of MC steps $N^{(\text{max})}_{\text{MC}} = 3000$ to ensure that the steady state is reached for each value of $c$. Such a result corroborates the result obtained by the refinement process (figure 1(a)). The optimization described by figure 1(a) can be visually observed in figure 1(c).

Since we observed that the optimization method described in section 2 works for the standard case, we decided to apply this approach to study the phase transitions of the SIR model when there is dilution of the lattice and mobility of the individuals. First of all, it is worth to describe how the dilution effects can change the critical recovery probabilities. In order to study the dependence of $c_c$ with $\rho$ when $p = 0$ (static scenarios), we changed $\rho$ from 1 up to 0.70 by considering $\Delta \rho = 0.05$. We applied the refinement process and determined the best $c$ (corresponding to the highest $\alpha$) for each $\rho$-value.

Figure 2 (a) shows the behavior of $c$ as function of $\ln \rho$. We observed a logarithm law for $p = 0$ where $c_c = a + b \ln \rho$. For $a = 0.2196(5)$ and $b = 0.434(2)$, one obtains a very good fit: $\alpha = 0.9998$. The plot (b) of figure 2 shows the optimization curve ($\alpha \times c$) for the more diluted case ($\rho = 0.7$).

Since we have already studied the case $p = 0$ (without mobility), now we turned our attention to the mobility of the individuals in the lattice. By using the same procedure for each value of $\rho$, we performed simulations in order to obtain the critical recovery probability $c$ as function of $p$. Firstly, we can observe in figure 3 (a) the phase diagram for the case where $\rho = 0.85$ and $p = 0.30$.

The phase transition occurs for $c_c = 0.1750(25)$ which is corroborated by time-dependent simulations as can be observed in the plot (b) of figure 3. According to

doi:10.1088/1742-5468/2015/06/P06011
A study of the influence of the mobility on the phase transitions of the synchronous SIR model

Figure 2. (a): Critical recovery probability ($c_c$) versus the density of individuals ($\rho$) for $p = 0$. We can observe a linear dependence on $\ln \rho$. (b): Illustration of the refinement process for $p = 0$ and $\rho = 0.7$.

Figure 3. (a): Behavior of the density of recovered individuals as function of $c$, for $\rho = 0.85$ and $p = 0.30$. (b): Illustration of the time-dependent simulations for $\rho = 0.85$ and $p = 0.30$.

Table 1. Exponents obtained from curves of critical recovery probability $c_c$ as function of $p$ for different density of individuals.

| $\rho$ | 1.0  | 0.95 | 0.90 | 0.85 | 0.80 | 0.75 | 0.70 |
|--------|------|------|------|------|------|------|------|
| $\gamma$ | 0.22 | 0.210(1) | 0.200(1) | 0.191(1) | 0.182(1) | 0.172(1) | 0.164(1) |
| $\beta$   | 0.00 | 0.024(3) | 0.048(3) | 0.074(4) | 0.109(4) | 0.151(2) | 0.200(1) |

our previous study, when $p = 0$, and for the same value of $\rho$ ($\rho = 0.85$), we obtained $c_c = 0.1500(25)$. Hence, it suggests that the critical recovery rates must depend on $p$ for fixed values of $\rho$. We explore such a dependence as can be seen in figure 4. The explanation is straightforward: the lattice dilution makes possible the infected individuals to reach sites previously inaccessible and the recovering rate must increase to block the epidemic.

In this figure, we can see that $c$ increases as $p$ increases. This means more mobility for the same dilution and makes possible the infected individuals reach sites previously inaccessible. In addition, the recovering rate must increase to block the epidemic. For a fixed value of $\rho$, $c_c$ was empirically fitted by a power function $c(\rho) = \gamma(\rho)p^{\beta(\rho)}$. The values $\gamma(\rho)$ and $\beta(\rho)$ are reported in table 1.

doi:10.1088/1742-5468/2015/06/P06011
Figure 4. Study of mobility effects on the critical immunization probabilities. Good fits with power functions $c(\rho) = \gamma(\rho)p^\beta(\rho)$ are observed.

So, we can assert that critical immunizations increase as $p$ increases. However, for $\rho \neq 1$, $c_c$ never is greater than 0.22 which corresponds to $\rho = 1$, even for maximum mobility ($p = 1$). Since we have estimated all critical parameters $c_c$ corresponding to a given the pair $(\rho, p)$, we extend our studies of phase transition of the SIR model by estimating the exponent $\theta$ for each $c_c$. For this task, we used a simple optimization procedure: we simulated the density of infected sites in order to obtain time series averaged over $n_{\text{run}} = 4000$ runs, which are repeated with $n_{\text{bin}} = 5$ different seeds. With these $n_{\text{bin}} = 5$ different time series in hand, we are able to obtain error bars. Moreover we included an additional ingredient to estimate the critical exponent whereas the exponent is very dependent on the time lag of the time series. We consider lags $[t_{\text{min}}, t_{\text{max}}]$, with $t_{\text{min}}$ changing from 10 up to 300 and $t_{\text{max}}$ changing from $t_{\text{min}}$ up to $N_{\text{MC}} = 800$ MC steps (which is the maximum number of MC steps used in this work as previously reported for the time dependent simulations). In order to avoid time correlations between successive measures of the density of infected sites, as well as the underestimated error bars, we always fixed in our analysis the same number of points ($n_{\text{point}}$) for each considered interval $[t_{\text{min}}, t_{\text{max}}]$. This means that we did not use all points of the interval. Instead, the points are equally spaced and described by $t_i = t_{\text{min}} + i \cdot \frac{t_{\text{max}} - t_{\text{min}}}{n_{\text{points}}}$ with $i = 1, \ldots, n_{\text{points}}$. In this work, we used $n_{\text{points}} = 20$ (a similar procedure was used to calculate the dynamic critical exponents of the Potts model, as shown in [24]).

In order to complete the optimization procedure, we calculate $\theta$ for each interval as well as its corresponding goodness-of-fit $Q$ (see, for instance, [25]) that, exactly as $\alpha$ defined by equation (5), measures the quality of fitting, but unlike, takes in to account the error bars for such a calculation. Our exponent is that one with highest goodness-of-fit. The figure 5 shows a histogram of different values of $\theta$ obtained for different time lags $[t_{\text{min}}, t_{\text{max}}]$ for a particular case: $\rho = 0.85$ and $p = 0.2$ for the sake of simplicity (the results obtained through MC simulations with other critical parameters previously found in this work are similar and therefore were not shown).

Here, $\theta$ corresponds to the value with the highest goodness-of-fit. For instance, for $\rho = 0.80$ and $p = 0.40$, we found $Q = 0.999999$ as the best goodness, corresponding
A study of the influence of the mobility on the phase transitions of the synchronous SIR model

Figure 5. Histogram for the exponent $\theta$ calculated for different time lags for the particular case $\rho = 0.85$ and $p = 0.2$.

Table 2. Values of the exponent $\theta$ obtained for each pair $(p, \rho)$ corresponding to the highest goodness-of-fit.

| $p$ \ $\rho$ | 1.0  | 0.95  | 0.90  | 0.85  | 0.80  | 0.75  | 0.70  |
|-------------|------|-------|-------|-------|-------|-------|-------|
| 0.00        | 0.589(7) | 0.62(1) | 0.69(1) | 0.72(1) | 0.77(2) | 0.87(1) | 1.00(1) |
| 0.10        | 0.589(7) | 0.61(1) | 0.68(1) | 0.66(1) | 0.70(1) | 0.74(1) | 0.78(1) |
| 0.20        | 0.589(7) | 0.62(2) | 0.68(2) | 0.73(2) | 0.64(2) | 0.71(1) | 0.75(2) |
| 0.30        | 0.589(7) | 0.64(1) | 0.68(1) | 0.64(1) | 0.75(1) | 0.66(1) | 0.71(2) |
| 0.40        | 0.589(7) | 0.68(1) | 0.66(3) | 0.75(2) | 0.69(2) | 0.66(1) | 0.74(1) |
| 0.60        | 0.589(7) | 0.67(3) | 0.67(4) | 0.67(1) | 0.63(3) | 0.66(2) | 0.71(2) |
| 0.80        | 0.589(7) | 0.56(1) | 0.52(2) | 0.65(2) | 0.66(4) | 0.68(1) | 0.60(2) |
| 1.00        | 0.589(7) | 0.61(1) | 0.64(1) | 0.59(1) | 0.66(2) | 0.65(2) | 0.66(3) |

to the interval [50, 530]. On the other hand, for $\rho = 0.70$ and $p = 1.00$, we found $Q = 0.9999999999989$ which corresponds to the interval [290, 390]. Our estimates are summarized in table 2.

For $p = 0.00$, we can see that $\theta$ increases monotonically when $\rho$ decreases. We also can see, that by fixing $\rho$, $\theta(p = 1) > \theta(p = 0)$. However, the decrease of $p$ from 0 up to 1 does not occur monotonically and such fluctuations are due to sensitivity in the calculation of the exponents. Nevertheless, more importantly than this fact is to mention that the exponent $\theta$ depends on $\rho$ and $p$, and differently from the critical parameter $c$ we do not find a monotonic function to describe such dependence.

4. Summaries and conclusions

Based on two-dimensional SIR model with synchronous update, we performed (by following a suggestion of the seminal paper of Grassberger [1]) a detailed study of dilution and mobility effects on the critical immunizations $c$, i.e. values of the recovering probability for which the epidemic transits from a not controlled regime (where all individuals are
A study of the influence of the mobility on the phase transitions of the synchronous SIR model contaminated at sometime) to a controlled regime (few individuals or none at all get sick). We used a method to refine the critical parameters based on the optimization of the power law for the density of infected individuals along the time at criticality. Our work shows that the dilution of the lattice decreases the recovery probability $c$ based on a log-law. However, this effect is minimized when the individuals have the possibility to move on the lattice. In this case, for a fixed density of individuals, the greater the mobility, the bigger the immunization rate. Finally, the exponent $\theta$ was studied for some values of mobility and occupation. Our estimates show that the exponent varies according to $\rho$ and $p$ which gives a non-universal character to the model when these parameters are taking into account.

Acknowledgments

This research was partially supported by the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), under the grant 11862/2012-8. The authors would like to thank Prof. LG Brunet (IF-UFRGS) for kindly providing the computational resources from Clustered Computing (ada.if.ufrgs.br) for this work.

References

[1] Grassberger P 1983 *Math. Biosci.* **63** 157–72
[2] Marro J and Dickman R 1999 *Nonequilibrium Phase Transitions in Lattice Models* (Cambridge: Cambridge University Press)
[3] Hinrichsen H 2000 *Adv. Phys.* **49** 815
[4] Tomé T and Ziff R M 2010 *Phys. Rev. E* **82** 051921
[5] de Souza D R, Tomé T and Ziff R M 2011 *J. Stat. Mech.* P03006
[6] Kermack W O and McKendrick A G 1927 *Proc. R. Soc. Lond.* **115** 700–21
[7] Janssen H K, Schaub B and Schmittmann B Z 1989 *Z. Phys. B* **73** 539
[8] Souza D R and Tomé T 2010 *Physica A* **389** 1142
[9] Colizza V and Vespignani A 2007 *Phys. Rev. Lett.* **99** 148701
[10] Balcan D and Vespignani A 2011 *Nat. Phys.* **7** 581–6
[11] Postnikov E B and Sokolov I M 2007 *Math. Biosci.* **208** 205–15
[12] Belik V, Geisel T and Brockmann D 2011 *Phys. Rev. X* **1** 011001
[13] da Silva R, Drugowich J R and Martínez A S 2012 *Phys. Rev. E* **85** 066707
[14] Tomé T and de Oliveira M J 2011 *J. Phys. A* **44** 095005
[15] Arashiro E and Tomé T 2007 *J. Phys. A* **40** 887–900
[16] de Carvalho K C and Tomé T 2006 *Int. J. Mod. Phys. C* **17** 1647
[17] Mazzeo G and Kuhn R 1999 *Phys. Rev. E* **60** 3823
[18] Martins P H L and Plascak J A 2007 *Phys. Rev. E* **76** 012102
[19] Vainstein M, Silva A T C and Arenzon J J 2007 *J. Theor. Biol.* **244** 722
[20] da Silva R, Alves N Jr and Drugowich de Felício J R 2013 *Phys. Rev. E* **87** 012131
[21] da Silva R, Fernandes H A, Drugowich de Felício J R and Figueiredo W 2013 *Comput. Phys. Commun.* **184** 2371
[22] da Silva R, Fernandes H A and Drugowich de Felício J R 2014 *Phys. Rev. E* **90** 042101
[23] Trivedi K S 2002 *Probability and Statistics with Reliability, Queuing, and Computer Science and Applications* 2nd edn (New York: Wiley)
[24] da Silva R, Alves N A and Drugowich J R 2002 *Phys. Lett. A* **298** 325
[25] Press W H, Teukolsky S A, Vetterling W T and Flannery B P 1992 *Numerical Recipes in Fortran 77: The art of Scientific Computing* (Cambridge: Cambridge University Press)

doi:10.1088/1742-5468/2015/06/P06011