Susceptible-infected-removed and susceptible-exposed-infected models

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(Dated: July 19, 2010)

Two stochastic epidemic lattice models, the susceptible-infected-recovered and the susceptible-exposed-infected models, are studied on a Cayley tree of coordination number k. The spreading of the disease in the former is found to occur when the infection probability b is larger than $b_c = k/2(k-1)$. In the latter, which is equivalent to a dynamic site percolation model, the spreading occurs when the infection probability p is greater than $p_c = 1/(k-1)$. We set up and solve the time evolution equations for both models and determine the final and time-dependent properties, including the epidemic curve. We show that the two models are closely related by revealing that their relevant properties are exactly mapped into each other when $p = b/[k-(k-1)b]$. These include the cluster size distribution and the density of individuals of each type, quantities that have been determined in closed forms.
PACS: 05.40.-a, 02.50.Ey, 87.10.Hk

I. INTRODUCTION

The development of a priori models in epidemiology was made possible when the spreading mechanism of the infectious disease was discovered [1]. Since then the spreading of an infectious disease among a community of individuals has been described by several types of models either deterministic or stochastic [1–10]. Special attention has been given to the susceptible-infected-recovered (SIR) model that describes the spreading of an epidemic in which a susceptible individual becomes spontaneously immune or recovered after being infected by a contagious disease. A deterministic approach based on a set of ordinary differential equations for the numbers of susceptible, infected and recovered individuals has been advanced by Kermack and McKendrick [11, 12]. Based on a general stochastic formulation of processes in epidemiology introduced by Bartlett [13], a stochastic approach to the SIR model has been developed by Bailey [14]. This stochastic approach is a birth and death Markovian process in which the number of each type of individuals, treated as a stochastic variable, may increase or decrease by a unity. A more detailed description, in which the spatial structure is taken into account, is provided by stochastic lattice models [15–27] in which each site of a lattice, representing the space where the individuals live, is occupied by just one individual that can be either susceptible (S), or infected (I), or recovered (R). In this approach, a susceptible individual becomes infected (S→I) with a rate that is proportional to the number of neighboring infected individuals, an autocatalytic reaction, and an infected individual becomes recovered (I→R) spontaneously.

The general features of the SIR model are as follows. When the disease is set in a community of susceptible individuals, the number of infected individuals increases during a certain period of time after which it decreases due to spontaneous immunization and, in the long term, there will be no infected individuals: any individual either have had become recovered or have had remained susceptible. In other words, the epidemic ends before all the susceptibles have got the disease. For small infection rates there will be no spreading of epidemic in the sense that only a finite number of individuals becomes infected and eventually recovered. If the rate of infection is large enough, the epidemic spreads, that is, the number of infected individuals that become recovered increases without bounds. The transition from the non-spreading to spreading regime, that is, the threshold of epidemic spreading, is regarded as a continuous phase transition. The critical behavior around the phase transition places the model in the universality class of dynamical percolation (DynP) [15–17], a feature that has been confirmed by numerical simulations [23–28].

Here we are concerned not only with the SIR model but also with a standard typical example of a model exhibiting the DynP critical behavior. This prototype model is a stochastic lattice model and corresponds to an asynchronous version of the model introduced by Alexandrowicz [29] to generate site percolation clusters. Using the epidemiological language, it is called susceptible-exposed-infected (SEI) model and is defined as follows. A susceptible individual in contact with an infected individual either becomes infected or becomes exposed (E), an individual that has got the disease but is not infectious. Infected and exposed individuals remain forever in the same state. Susceptible individuals become infected or exposed with rates that are proportional to the number of neighboring infected individuals. The first reaction (S→I) is autocatalytic whereas the second (S→E) is catalytic. A clusters of infected individuals is grown by starting the dynamics with a lattice full of susceptibles with the exception of one single infected individual. The dynamics comes to a halt when all the I sites have no S neighbors. The final I clusters generated by this procedure can be shown to be identical to clusters of occupied sites of the (isotropic and static) site percolation model [29], the I and E sites playing the roles of occupied and

empty sites, respectively.

Apart from being in the DynP universality class, the stochastic SIR lattice model has an even closer relationship [3, 15, 28, 30–32] with percolation models [33–36], particularly with the SEI model as we show here. The clusters generated by the rules of the SIR model turns out to have the same properties of clusters occurring in (isotropic and static) percolation models [28].

In the present paper we study the SIR and SEI models on a Cayley tree and show that a direct relationship can indeed be established between them. By studying the growth of a single cluster of infected individuals on a Cayley tree of coordination k, we show that the infection probability p of the SEI model is related to the infection probability b of the SIR model by

$$p = \frac{b}{k-(k-1)b}. \tag{1}$$

We also show that the critical infection probability b_c is given by

$$b_c = \frac{k}{2(k-1)}, \tag{2}$$

which, combined with equation (1), gives [34–36]

$$p_c = \frac{1}{k-1}, \tag{3}$$

the well known critical value of percolation on a Cayley tree of coordination number k.

The motivation to study models on a cycle-free structure such as a Cayley tree is twofold. In the first place, the solution of models on a Cayley tree can be considered as a good approximation to the solution on a regular lattice of the same coordination. For instance, the solution of equilibrium models on a Cayley tree is known to be identical to the Bethe approximation. In the second place, an epidemic model defined on a Cayley will give an appropriate description of an epidemic that sets in a community in which the contacts among individuals do not form cycles or if they do they do only on a local level.

The text that follows is divided into two parts according to the presence or absence of epidemic spreading. In the first part, corresponding to sections II and III, we analyze the growth of a single cluster in an infinite Cayley tree. The equations are written in terms of the numbers of individuals of each type and are appropriate to describe the regime where there is no spreading of the disease. In the second part, corresponding to sections IV-VIII, we study the properties of the models by means of equations written in terms of densities. This is the appropriate approach to analyze the regime where the spreading of the disease occurs. In a regular lattice this approach corresponds to study the properties of the model obtained by taking the thermodynamic limit.

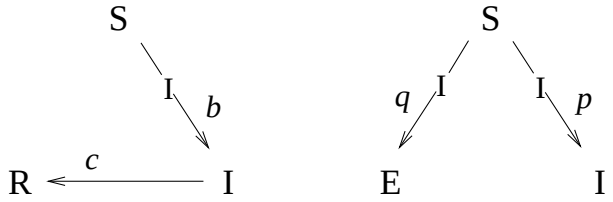

FIG. 1: Diagram showing the transitions between the several types of individuals, susceptible (S), infected (I), recovered (R), and exposed (E), in the SIR (left panel) and SEI (right panel) models. In both models, the transition S→I is an autocatalytic reaction. In the SIR model, the reaction I→R is spontaneous. In the SEI model the reaction S→E is catalytic, I being the catalyzer. The parameters b, c, p and q are the probabilities associated to the each reaction.

II. GROWTH OF A SINGLE CLUSTER

A. SIR model

Let us consider a community of individuals living on the sites of a lattice. Each site of the lattice is occupied by just one individual that can be S, I or R. The dynamic rules of the SIR model, illustrated in figure 1, are as follows. An I site chooses one of its neighbors to infect. If the chosen site is an S site it becomes I with rate β. An I site becomes an R site spontaneously with rate γ. The parameters β and γ are the infection and recovery rates, respectively.

To find the critical infection probability b_c above which the epidemic spreads, we examine the growth of the epidemic on a Cayley tree of coordination number k, as illustrated in figure 2, which initially is full of susceptible individuals with the exception of a single infected individual placed at the center. According to the rules stated above, the time evolution equation for the mean number N_I of infected and for the mean number of N_R of recovered are given by

$$\frac{d}{dt}N_I = \frac{\beta}{k}N_{IS} - \gamma N_I, \tag{4}$$

$$\frac{d}{dt}N_R = \gamma N_I, \tag{5}$$

where N_{IS} is the mean number of pairs of neighboring infected and susceptible individuals.

To find the time evolution for N_{IS} we proceed as follows. First we observe that the pairs of type IS only occur at the border of the cluster composed by I and R sites as can be seen in figure 2. When a site S next to a site I becomes I the number N_{IS} increases by $(k-1)$ units. At the same time there is a decrease by one unit so that the net rate of increase in N_{IS} equals $(\beta/k)(k-2)N_{IS}$. The number N_{IS} also decreases when the infected individual of a pair IS becomes R. This occurs spontaneously so that the rate of decrease in N_{IS} will be γN_{IS}. The time

evolution in the number of neighboring pairs of type IS is then

$$\frac{d}{dt}N_{IS} = \frac{\beta}{k}(k-2)N_{IS} - \gamma N_{IS}. \tag{6}$$

The evolution equation for the average number N_{RS} of pairs of type RS is easily found. A pair of this type occurs only at the border of the cluster formed by I and R sites. It increases by a unit when an I site next to an S site becomes R. The rate of increase in N_{RS} is then γN_{IS} so that

$$\frac{d}{dt}N_{RS} = \gamma N_{IS}. \tag{7}$$

The solution of equation (6) is

$$N_{IS} = ke^{(\gamma_c - \gamma)t}, \tag{8}$$

where

$$\gamma_c = \frac{k-2}{k}\beta. \tag{9}$$

The integration constant was found by using the initial condition $N_{IS} = k$. From equation (8), it follows that N_{IS} increases without bounds when $\gamma < \gamma_c$. In the case $\gamma \geq \gamma_c$, N_{IS} is finite. If we define the infection probability b and the recovery probability c by

$$b = \frac{\beta}{\beta+\gamma}, \qquad c = \frac{\gamma}{\beta+\gamma} = 1 - b, \tag{10}$$

the threshold of infection on a Cayley tree is given by the critical infection probability

$$b_c = \frac{k}{2(k-1)}. \tag{11}$$

Substituting expression (8) into (4) and solving it we get

$$N_I = \frac{k}{k-2}e^{(\gamma_c-\gamma)t} - \frac{2}{k-2}e^{-\gamma t}, \tag{12}$$

where the constant of integration was found by using the initial condition $N_I = 1$. The number of infected increases without bounds when $\gamma < \gamma_c$. When $\gamma > \gamma_c$, the number of infected is finite and vanishes exponentially in the limit $t \to \infty$. At the critical point, $\gamma = \gamma_c$, it is also finite but the final number does not vanish being equal to $N_I = k/(k-2)$.

The number of recovered individuals N_R is determined by substituting (12) into equation (5). After integration, it follows that N_R also increases without bounds when $\gamma < \gamma_c$. In the opposite regime, that is, $\gamma > \gamma_c$, it is finite, the final number being given by

$$N_R = \frac{k}{k-2}\,\frac{\gamma}{\gamma-\gamma_c} - \frac{2}{k-2}. \tag{13}$$

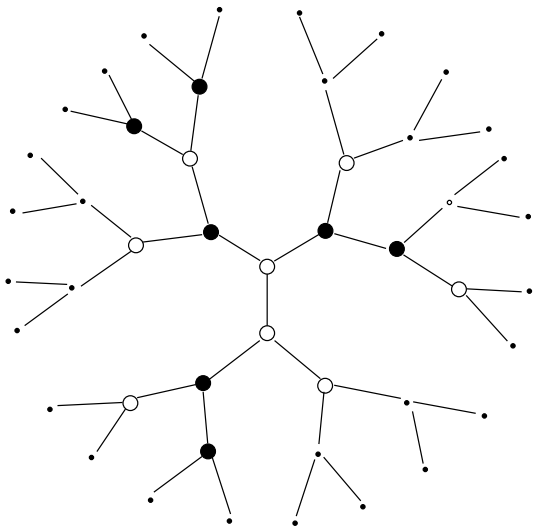

FIG. 2: A configuration of the SIR model on a Cayley tree of coordination number $k = 3$, obtained by starting with a single I site on a lattice full of S sites. Each site can be S (dot), I (full circle), or R (open circle). The I and R sites make up a connected cluster. The growth stops when the border of the cluster consists of R sites only. When this happens all I sites eventually become R sites.

As one approaches the critical point the final number of recovered individuals diverges as

$$N_R \sim (\gamma - \gamma_c)^{-1}. \tag{14}$$

At the critical point, it follows from the integration of (5) that N_R diverges linearly with time as

$$N_R = \beta\, t. \tag{15}$$

We notice that when $k = 2$, corresponding to the one-dimensional case, the first term on the right-hand site of equation (6) vanishes and N_{IS} decreases as

$$N_{IS} = 2e^{-\gamma t}, \tag{16}$$

regardless of the value of the infection rate β. The number of infected individuals is given by

$$N_I = (1 + \beta t)e^{-\gamma t}, \tag{17}$$

and vanishes in the limit $t \to \infty$. The single cluster is finite and there is no spreading of the disease in this case with the exception of the marginal case $\gamma = 0$. The number of recovered individuals is determined by integrating (5),

$$N_R = (1 + \frac{\beta}{\gamma}) - (1 + \frac{\beta}{\gamma} + \beta t)e^{-\gamma t}, \tag{18}$$

the final number being finite and equal to $N_R = (1+\beta/\gamma)$. When $\gamma = 0$, the equations (4), (5), and (6) give $N_{IS} = 2$, $N_I = 1 + \beta t$, and $N_R = 0$.

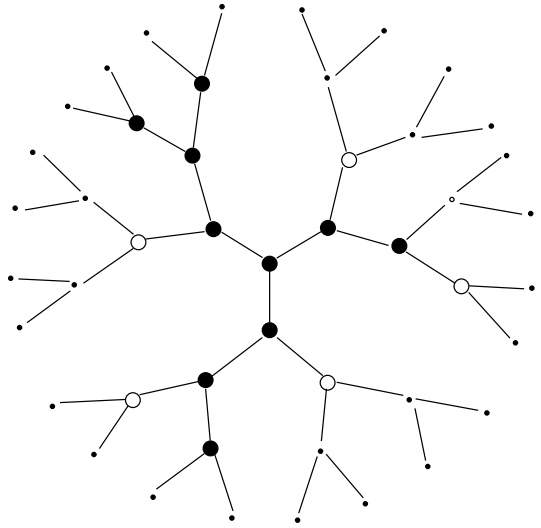

FIG. 3: A configuration of the SEI model on a Cayley tree of coordination number $k = 3$, obtained by starting with a single I site on a lattice full of S sites. Each site can be S (dot), I (full circle), or E (open circle). The I sites make up a connected cluster. The growth stops when the border of the I-cluster are connected to E sites only.

B. SEI model

The dynamics of the SEI model, illustrated in figure 1, are defined as follows. Each site of a lattice of coordination number k is occupied by just one individual that can be S, I or E. An S site may be transformed into an I site or into an E site. The I and E sites remain forever unchanged. An I site chooses one of its neighbors to infect. If the chosen site is an S site it becomes I with rate β or becomes E with rate α. The parameters β and α are the infection and exposition rates, respectively. It is useful to define the infection probability p and the exposition probability q by

$$p = \frac{\beta}{\beta + \alpha}, \qquad q = \frac{\alpha}{\beta + \alpha} = 1 - p. \tag{19}$$

The SEI model has a remarkable property regarding its final state, valid for any lattice. Starting from a single infected site in a lattice full of susceptible individuals, the dynamics of the SEI model generates a growing cluster of I sites. The process of growing eventually stops and a final cluster is reached. The final clusters obtained by this procedure are exactly the same clusters of site percolation in which sites are occupied independently with probability p given by equation (19). From the property that a cluster of occupied sites percolates the whole lattice when p is equal to or greater than the critical value p_c, the same will happen to the I cluster of the SEI model so that the epidemic spreading will occur when $p \geq p_c$. When $p < p_c$ the clusters are finite and there is no epidemic spreading.

Let us examine the growth of the epidemic on a Cayley tree as illustrated in figure 3. Initially the lattice is full of susceptible individuals with the exception of a single infected individual placed at the center. According to the rules of the SEI model and using arguments similar to those used for the SIR model, we get the following evolution equations for the N_I, N_E and N_{IS},

$$\frac{d}{dt}N_I = \frac{\beta}{k}N_{IS}, \tag{20}$$

$$\frac{d}{dt}N_E = \frac{\alpha}{k}N_{IS}, \tag{21}$$

$$\frac{d}{dt}N_{IS} = \frac{\beta}{k}(k-2)N_{IS} - \frac{\alpha}{k}N_{IS}. \tag{22}$$

From this last equation it follows that N_{IS} increases without bounds when $\alpha < \alpha_c$ where

$$\alpha_c = (k-2)\beta. \tag{23}$$

Using the definition (19) for the infection probability p, this condition becomes equivalent to $p > p_c$ where

$$p_c = \frac{1}{k-1}, \tag{24}$$

the well known critical probability of site percolation on a Cayley tree [34–36].

If we compare equations (6) and (22) we see that they are the same if we perform the association

$$\gamma = \frac{\alpha}{k}. \tag{25}$$

Using relations (10) and (19), this association is equivalent to the following relation between the infection probability b of the SIR model and the infection probability p of the SEI model,

$$p = \frac{b}{k - (k-1)b}. \tag{26}$$

Setting $p = p_c$ in this equation we get b_c given by equation (11).

If we use the same initial condition for both models, with a single infected individuals in a lattice full of susceptibles, then the number of nearest-neighbor pairs of type IS will be the same for both models. Using the same initial condition we may draw in addition the following conclusions. The number of infected sites of the SEI model equals the sum of infected and recovered sites of the SIR model and the number of exposed sites of the SEI model equals the number of pairs of type RS of the SIR model. Indeed, if we sum equations (4) and (5) and compare the result with equation (20), we see that they are the same equation. If we compare equations (7) and (21) they are also the same equation.

III. CLUSTER SIZE DISTRIBUTION

A. SEI model

In this section we consider the statistics of the clusters generated by a single infected site in a lattice full of susceptibles. We treat the SEI model first and begin by observing that the I sites make up a connected cluster as can be seen in figure 3. The possible configurations generated by the initial single infected site may be classified by the number n of I sites and the number of active sites m. By an active site we mean the S site of a pair IS. To each active site there corresponds just one pair IS so that m is identified as the number of pairs IS. The active sites as well as the E sites are found only on the border of the connected I cluster. On a Cayley tree the number of sites on the border of a connected cluster depends only on the number of sites of the cluster and equals $n(k-2)+2$. Therefore, given n and m, the number of E sites becomes specified.

Let us consider a certain configuration with n I sites and m active site. The rate of transition from this configuration to any other configuration with $n+1$ I sites and $m+k-2$ active sites is the same and equals $(\beta/k)m$. Also, the rate of transition to any other configuration with n I sites and $m-1$ active sites is the same and equals $(\alpha/k)m$. The transition rates do not depend on the detail of the configurations but only of the numbers n and m. This property allows us to define a birth and death master equation for the probability $\mathcal{P}_{n,m}(t)$ of finding a cluster with exactly n I sites and exactly m pairs of type IS, at time t. It is given by

$$\frac{d}{dt}\mathcal{P}_{n,m} = \frac{\beta}{k}(m-k+2)\mathcal{P}_{n-1,m-k+2} +$$

$$+\frac{\alpha}{k}(m+1)\mathcal{P}_{n,m+1} - \frac{\beta+\alpha}{k}\,m\mathcal{P}_{n,m}. \qquad (27)$$

The variable n takes the values $1, 2, \ldots$ and m runs from 0 until $n(k-2)+2$. Outside this range the probability $\mathcal{P}_{n,m}$ is assumed to vanish. From this equation we may get the evolution equation (22) for $N_{IS} = \langle m \rangle$ and time evolution equation (20) for $N_I = \langle n \rangle$.

For convenience we rewrite the master equation as

$$\frac{d}{dt}\mathcal{P}_{n,m} = p(m-k+2)\mathcal{P}_{n-1,m-k+2} +$$

$$+q(m+1)\mathcal{P}_{n,m+1} - m\mathcal{P}_{n,m}, \qquad (28)$$

where we have used the definitions (19) and rescaled time according to $t \to t(\beta+\alpha)/k$.

To solve the master equation, we begin by defining the generating function

$$G(x,y) = \sum_{n=1}^{\infty}\sum_{m=0}^{n(k-2)+2} x^n y^m \mathcal{P}_{n,m}, \qquad (29)$$

to get the equation

$$\frac{\partial G}{\partial t} = (q + pxy^{k-1} - y)\frac{\partial G}{\partial y}. \qquad (30)$$

This equation should be solved by using the initial $G = xy^k$ since at time $t = 0$ there is just one infected sites and k active sites so that $\mathcal{P}_{1k} = 1$.

Equation (30) can be solved by the method of characteristics. For the case $k = 3$ an explicit solution can be given

$$G = x\left[\frac{(f_2 - f_1\varepsilon)y - f_1 f_2(1-\varepsilon)}{(1-\varepsilon)y - (f_1 - f_2\varepsilon)}\right]^3, \qquad (31)$$

where f_1 and f_2 are functions of x, given by

$$f_1(x) = \frac{1+\sqrt{1-4pqx}}{2px}, \qquad (32)$$

and

$$f_2(x) = \frac{1-\sqrt{1-4pqx}}{2px}, \qquad (33)$$

and ε is a function of x and t, defined by

$$\varepsilon = e^{-gt}, \qquad g(x) = \sqrt{1-4pqx}. \qquad (34)$$

Let us consider the limit $t \to \infty$. In this case

$$G = x[f_2(x)]^3 = \frac{1}{8p^3x^2}\left(1-\sqrt{1-4pqx}\right)^3, \qquad (35)$$

which does not depend on y. Therefore, the only surviving probabilities $\mathcal{P}_{n,m}$ are those for which $m = 0$. That is, in the limit $t \to \infty$ there is no active sites, as it should.

We are interested particularly in determining the probability $\mathcal{P}_n(t)$ of finding a cluster with exactly n infected sites, at time t. To this end we first determine its generating function. If we set $y = 1$ in the expression (29) for the $G(x,y)$, we get

$$G(x,1) = \sum_{n=1}^{\infty} x^n \mathcal{P}_n, \qquad (36)$$

because $\mathcal{P}_n$ is a marginal distribution obtained from $\mathcal{P}_{n,m}$. Thus $G(x,1)$ turns out to be desired generating function. For the case $k = 3$, $G(x,1)$ is obtained by setting $y = 1$ in equation (31). In the limit $t \to \infty$, wee see that the generating function coincides with expression (35).

To determine $\mathcal{P}_n$ explicitly for the case $k = 3$ we expand the expression (35) in powers of x to get

$$\mathcal{P}_n = \frac{3q^2}{p}\frac{(2n)!}{(n-1)!(n+2)!}(pq)^n. \qquad (37)$$

For large values of n we get

$$\mathcal{P}_n = \frac{3q^2}{p\sqrt{\pi}}n^{-3/2}(4pq)^n. \qquad (38)$$

Taking into account that $p_c = 1/2$ we may write the following scaling form, valid for small values of $p_c - p$,

$$\mathcal{P}_n \sim n^{-3/2}e^{-n(p_c-p)^2/4}. \qquad (39)$$

B. SIR model

We begin by noticing that the I and R sites make up a connected cluster as can be seen in figure 2. The possible configurations of a cluster can be classified by the number ℓ of infected sites, the number j of recovered sites and the number m of active sites. Following the same reasoning used in the case of the SEI model we reach the following birth and death master equation for the cluster probability $\mathcal{P}_{\ell,j,m}$

$$\frac{d}{dt}\mathcal{P}_{\ell,j,m} = \frac{\beta}{k}(m-k+2)\mathcal{P}_{\ell-1,j,m-k+2}$$

$$+\gamma(m+1)\mathcal{P}_{\ell+1,j-1,m+1} + \gamma(\ell+1-m)\mathcal{P}_{\ell+1,j-1,m}$$

$$-(\frac{\beta}{k}+\gamma)\, m\mathcal{P}_{\ell,j,m} - \gamma(\ell-m)\mathcal{P}_{\ell,j,m}. \qquad (40)$$

We remark that from equation (40) one may obtain the evolution equations (4), (5), and (6) for the averages $N_I = \langle \ell \rangle$, $N_R = \langle j \rangle$, and $N_{IS} = \langle m \rangle$.

If we sum the left-hand side and the right-hand side on the variables ℓ and j subject to the constraint $\ell + j = n$ we find the evolution equation for the probability $\mathcal{P}_{n,m}$ which turns out to be identical to the master equation (27) provided $\gamma = \alpha/k$, which is the relation (25) found earlier. It follows that the sum of the number of infected sites and the recovered sites of the SIR model equals the number of infected sites in the SEI model. The expressions found in the previous subsection are therefore also valid for the SIR model provided we give the proper interpretation of n as the sum of the numbers of infected and recovered individuals. In particular the equations (37), (38), and (39) give the final distribution of recovered individuals because no infected individuals are left.

IV. SPREADING REGIME: SIR MODEL

A. Evolution equations

If we consider initial conditions with several infected sites random placed among the susceptible sites, there might be several clusters of infected sites instead of just one. Although equations (4) and (5) remain unchanged, the evolution equation for the number of pairs IS, will not be that given by equation (6). In this section, we will set up evolution equations that will be valid for an arbitrary initial condition. We consider a finite lattice with N sites and formulate the problem in terms of the probabilities.

Let P_S, P_I, and P_R the probabilities that a site is occupied by a susceptible, an infected, or by a recovered individual, respectively. According to the rules of the SIR model, the evolution equation for these probabilities are

$$\frac{d}{dt}P_S = -\beta P_{IS}, \qquad (41)$$

$$\frac{d}{dt}P_I = \beta P_{IS} - \gamma P_I, \qquad (42)$$

$$\frac{d}{dt}P_R = \gamma P_I, \qquad (43)$$

where P_{IS} is the probability of occurrence of a pair IS. More properly, given two nearest neighbor sites i and j, P_{IS} is the probability that site i is in state I and site j in state S. Note that the last equation is not independent of the other two because P_R is not independent of P_S and P_I due to the constraint $P_S + P_I + P_R = 1$. If we multiply equations (42) and (43) by N they will be identified as equations (4) and (5). To see this it suffices to bear in mind the relations $N_I = P_I N$, $N_R = P_R N$ and $N_{IS} = kNP_{IS}$.

To find the time evolution equation for P_{IS} we proceed as follows. Let us focus on two nearest neighbor sites of the lattice with labels 1 and 0 and let us find the variation in time of the probability P_{IS} that site 1 is in state I and site 0 is in state S. First, we suppose that site 1 is in state I and site 0 is in state S. The probability P_{IS} will decrease with rate β/k if S turns into I, implying a decrease equal to $(\beta/k)P_{IS}$. The probability P_{IS} will also decrease if another nearest neighbor of site 0, say site 2, is in state I. Since there are $k-1$ sites of this type, the decrease will be equal to $(\beta/k)(k-1)P_{ISI}$ where P_{ISI} is the probability that sites 1, 0, and 2 are in states I, S, and I, respectively. Let suppose now that both sites 1 and 0 are in state S. The probability P_{IS} will increase if another nearest neighbor of site 1, say site 3, is in state I. This is so because the state S of site 1 turns into state I with rate β/k. Since there are $(k-1)$ sites of this type, the increase will be equal to $(\beta/k)(k-1)P_{ISS}$ where P_{ISS} is the probability that sites 3, 1, and 0 are in states, I, S, and S, respectively. Finally, the probability P_{IS} decreases because I becomes R spontaneously with rate γ. The decrease in this case is γP_{IS}. Collecting all the possibilities we may write the following equation for the time evolution of P_{IS},

$$\frac{d}{dt}P_{IS} = \beta\mu P_{ISS} - \beta\mu P_{ISI} - \frac{\beta}{k}P_{IS} - \gamma P_{IS}, \qquad (44)$$

where μ is defined by

$$\mu = \frac{k-1}{k}. \qquad (45)$$

Proceeding in an analogous manner we find the following equations for the time evolution of P_{RS}, the probability of a pair RS,

$$\frac{d}{dt}P_{RS} = -\beta\mu P_{ISR} + \gamma P_{IS}, \qquad (46)$$

and of P_{IR}, the probability of a pair IR,

$$\frac{d}{dt}P_{IR} = \beta\mu P_{ISR} + \gamma P_{II} - \gamma P_{IR}. \qquad (47)$$

We may also write the equations for the probability of other pairs, P_{SS}, P_{II}, and P_{RR}. But they will not be independent of the equations (44), (46) and (47) because these quantities are not independent of the previous variables whose equations have already been introduced above due to the following constraints

$$P_{II} + P_{IS} + P_{IR} = P_I, \tag{48}$$

$$P_{IS} + P_{SS} + P_{RS} = P_S, \tag{49}$$

$$P_{IR} + P_{RS} + P_{RR} = P_R. \tag{50}$$

The evolution equations (41), (42), (44), (46), and (47), just set up are exact equations that can be deduced from the master equation describing the evolution of the joint probability distribution referring to all sites [19]. However, they do not constitute a closed set of equations for the variables P_S, P_I, P_{IS}, P_{IR} and P_{RS}. Nevertheless, they become closed equations if we use a truncation scheme consisting in using the following relations between a three-site probability and two-site and one-site probabilities,

$$P_{ISS} = \frac{P_{IS}P_{SS}}{P_S}, \tag{51}$$

$$P_{ISI} = \frac{P_{IS}P_{IS}}{P_S}, \tag{52}$$

$$P_{ISR} = \frac{P_{IS}P_{RS}}{P_S}. \tag{53}$$

These relations are the same as those used in the pair mean-field approximations [19, 22, 37] and are exact relations for some systems defined on a Cayley tree as is the case of equilibrium lattice models with nearest-neighbor interactions [38, 39]. For nonequilibrium models, such as the ones studied here, these relations cannot be guaranteed regarding the time-dependent solution but it turns out to be valid regarding the stationary solution. That is, these relations becomes asymptotically correct in the limit $t \to \infty$. As we shall see, the use of relations (51), (52) and (53) lead us to the exact results (11), (24), and (26), concerning the SIR and SEI models on a Cayley tree.

Using relations (51), (52), and (53), the evolution equations for the two-site probabilities are written in the form

$$\frac{d}{dt}P_{IS} = \beta\mu\frac{P_{IS}P_{SS}}{P_S} - \beta\mu\frac{P_{IS}P_{IS}}{P_S} - \frac{\beta}{n}P_{IS} - \gamma P_{IS}, \tag{54}$$

$$\frac{d}{dt}P_{RS} = -\beta\mu\frac{P_{IS}P_{RS}}{P_S} + \gamma P_{IS}, \tag{55}$$

$$\frac{d}{dt}P_{IR} = \beta\mu\frac{P_{IS}P_{RS}}{P_S} + \gamma P_{II} - \gamma P_{IR}. \tag{56}$$

B. Solution of the evolution equations

Before starting to find the solution of the evolution equations, we need to known what the initial conditions are. We use here initial conditions with a lattice containing only susceptible and infected individuals. The initial number of infected, however, is negligible when compared to the number of susceptible individuals. This amounts to consider an initial condition such that $P_I \to 0$, $P_S \to 1$, $P_{IS} \to 0$, $P_{RS} = 0$, and $P_{IR} = 0$.

For convenience we use a set of variables defined by $x = P_S$, $y = P_I$, $v = P_{IS}$, $u = P_{RS}$, and $w = P_{IR}$, to write down the evolution equation as

$$\frac{dx}{dt} = -\beta v, \tag{57}$$

$$\frac{dy}{dt} = \beta v - \gamma y, \tag{58}$$

$$\frac{dv}{dt} = \beta\mu\frac{v(x-v-u)}{x} - \beta\mu\frac{v^2}{x} - \frac{\beta}{k}v - \gamma v, \tag{59}$$

$$\frac{du}{dt} = -\beta\mu\frac{vu}{x} + \gamma v, \tag{60}$$

$$\frac{dw}{dt} = \beta\mu\frac{vu}{x} + \gamma(y-v-w) - \gamma w. \tag{61}$$

where we used the relation $P_{SS} = P_S - P_{IS} - P_{RS} = x - v - u$ and $P_{II} = P_I - P_{IS} - P_{IR} = y - v - w$. These equations should be solved with the initial condition $y \to 0$, $x \to 1$, $v \to 0$, $u = 0$, and $w = 0$. The variables x and y may be interpreted as the densities of susceptible and infected individuals, respectively. We also define the density of recovered individuals $z = P_R = 1 - x - y$. This set of equations can be regarded as a particular case of the set of equations for the predator-prey model [19, 27].

To solve this set of equations, we begin by taking the ratio between equations (60) and (57) to get

$$\frac{du}{dx} = \mu\frac{u}{x} - r, \tag{62}$$

where

$$r = \frac{\gamma}{\beta}, \tag{63}$$

the relative recovery rate. Equation (62) can readily be solved with the solution

$$u = K_0 x^\mu - krx, \tag{64}$$

where K_0 is a constant to be found from the initial conditions. Using the initial conditions, $u = 0$ and $x \to 1$, we get $K_0 = kr$ so that we may write

$$u = kr(x^\mu - x), \tag{65}$$

a relation that can be regarded as a conservation law, valid for any instant of time.

The substitution of the result (65) into (59) and the division of (59) by (57) lead us to the equation

$$\frac{dv}{dx} = 2\mu\frac{v}{x} + \mu kr(x^{\mu-1} - 1) - (2\mu - 1 - r). \tag{66}$$

This equation can be solved with the solution

$$v = -krx^{\mu} + (kr + 1)x + K_1 x^{2\mu}, \tag{67}$$

where K_1 is another constant to be found from the initial conditions. Using the initial conditions, $v \to 0$ and $x \to 1$, we find $K_1 = -1$ and we get

$$v = -krx^{\mu} + (kr + 1)x - x^{2\mu}, \tag{68}$$

which is another conservation law.

Let us consider the solution of the set of equations when $t \to \infty$. In this limit there will be no infected individuals because they become recovered spontaneously. Therefore, when $t \to \infty$ one should have $y = 0$ as well as $v = 0$. The stationary solution for x is then the nontrivial solution of

$$-krx^{\mu} + (kr + 1)x - x^{2\mu} = 0. \tag{69}$$

Defining $s = x^{1/k}$ and taking into account the definition (45) of μ, we may write this equation as the following algebraic equation

$$-kr + (kr + 1)s - s^{k-1} = 0, \tag{70}$$

of degree $k - 1$, which is equivalent to

$$(1 - s)(-kr + s + s^2 + \ldots + s^{k-2}) = 0. \tag{71}$$

The non trivial solution is then given by

$$s + s^2 + \ldots + s^{k-2} = kr. \tag{72}$$

In the interval $s \geq 0$, the polynomial on the left-hand side is an increasing function of s that takes vanishes at $s = 0$ and attains the value $k - 2$ at $s = 1$. Therefore a real solution of (72) in the interval $0 \leq s < 1$ exists and is the only solution as long as $r < (k-2)/k$. If $r \geq (k-2)/k$ the only solution of (71) is $s = 1$. Therefore, there is a phase transition that occurs at the critical relative recovery rate

$$r_c = \frac{k - 2}{k}. \tag{73}$$

Using the definition (63) of r and the relations (10) the parameter r can be written as

$$r = \frac{1 - b}{b}, \tag{74}$$

from which follows that the transition occurs at a critical infection probability

$$b_c = \frac{k}{2(k - 1)}. \tag{75}$$

The order parameter may be defined as the density of recovered individuals z which in the stationary state is related to x by $z = 1 - x = 1 - s^k$ since in this case $y = 0$.

The solution of (72) around $r = r_c$ gives the following behavior of the order parameter

$$z = \frac{2k^2}{(k - 2)(k - 1)}(r_c - r) \tag{76}$$

valid for $r \leq r_c$.

V. SPREADING REGIME: SEI MODEL

A. Evolution equations

Following the same reasoning of section IV, we find the following set of equations for the SEI model,

$$\frac{d}{dt}P_S = -(\alpha + \beta)P_{IS}, \tag{77}$$

$$\frac{d}{dt}P_I = \beta P_{IS}, \tag{78}$$

$$\frac{d}{dt}P_E = \alpha P_{IS}, \tag{79}$$

$$\frac{d}{dt}P_{IS} = -\frac{\alpha + \beta}{n}P_{IS} - (\alpha + \beta)\mu P_{ISI} + \beta\mu P_{ISS}, \tag{80}$$

$$\frac{d}{dt}P_{ES} = -(\alpha + \beta)\mu P_{ISE} + \alpha\mu P_{ISS}, \tag{81}$$

$$\frac{d}{dt}P_{IE} = \frac{\alpha}{n}P_{IS} + \alpha\mu P_{ISI} + \beta\mu P_{ISE}. \tag{82}$$

Using the relations (51), (52), and (53), the last three equations becomes

$$\frac{d}{dt}P_{IS} = -\frac{\alpha + \beta}{k}P_{IS} - (\alpha + \beta)\mu\frac{P_{IS}P_{IS}}{P_S} + \\ + \beta\mu\frac{P_{SS}P_{IS}}{P_S}, \tag{83}$$

$$\frac{d}{dt}P_{ES} = -(\alpha + \beta)\mu\frac{P_{ES}P_{IS}}{P_S} + \alpha\mu\frac{P_{SS}P_{IS}}{P_S}, \tag{84}$$

$$\frac{d}{dt}P_{IE} = \frac{\alpha}{k}P_{IS} + \alpha\mu\frac{P_{IS}P_{IS}}{P_S} + \beta\mu\frac{P_{ES}P_{IS}}{P_S}. \tag{85}$$

Using the notation $x = P_S$, $y = P_I$, $v = P_{IS}$, $u = P_{ES}$, and $w = P_{IE}$, introduced before, we may write

$$\frac{dx}{dt} = -(\alpha + \beta)v, \tag{86}$$

$$\frac{dy}{dt} = \beta v, \tag{87}$$

$$\frac{dv}{dt} = -(\alpha+\beta)\frac{v}{k} - (\alpha+\beta)\mu\frac{v^2}{x} +$$

$$+\beta\mu\frac{v}{x}(x-v-u), \tag{88}$$

$$\frac{du}{dt} = -(\alpha+\beta)\mu\frac{uv}{x} + \alpha\mu\frac{v}{x}(x-v-u), \tag{89}$$

$$\frac{dw}{dt} = \alpha\frac{v}{k} + \alpha\mu\frac{v^2}{x} + \beta\mu\frac{uv}{x}. \tag{90}$$

Again these equations should be solved with the initial condition $y \to 0$, $x \to 1$, $v \to 0$, $u = 0$, and $w = 0$.

B. Solution of the evolution equations

To solve the above set of equations we sum up the equations (88) and (89) to get the following equation for the variable $h = u + v$

$$\frac{dh}{dt} = -(\alpha+\beta)\frac{v}{k} + (\alpha+\beta)\mu\frac{v}{x}(x-2h). \tag{91}$$

Taking the ratio between this equation and equation (86) we end up with

$$\frac{dh}{dx} = 1 - 2\mu + 2\mu\frac{h}{x}, \tag{92}$$

whose solution is

$$h = x + K_0 x^{2\mu}, \tag{93}$$

where K_0 is a constant to be found from the initial conditions. The initial conditions $v \to 0$, $u = 0$, $x \to 1$ give $h \to 0$ when $x \to 1$ from which we get $K_0 = -1$ and

$$h = x - x^{2\mu}. \tag{94}$$

Taking the ratio between equation (89) and (86) and taking into account the definition of q, given by (19), we get

$$\frac{du}{dx} = \mu\frac{u}{x} - q\mu\frac{1}{x}(x-h), \tag{95}$$

or, using the result (94),

$$\frac{du}{dx} = \mu\frac{u}{x} - q\mu x^{2\mu-1}. \tag{96}$$

This equation has the solution

$$u = q(x^\mu - x^{2\mu}), \tag{97}$$

where the constant of integration was found by using the initial condition $u = 0$ and $x \to 1$. Therefore, $v = h - u$ is given by

$$v = x - qx^\mu - px^{2\mu}, \tag{98}$$

where, as before, $p = 1 - q$. In the limit $t \to \infty$, each I site of the lattice will not have an S site as one of its nearest neighbors. Therefore in this limit there will be no pairs of the type IS so that $v = 0$. The stationary solution for x will be then a root of the equation

$$x - qx^\mu - px^{2\mu} = 0. \tag{99}$$

Defining the variable $s = x^{1/k}$ an keeping in mind the definition (63) of μ, we get the algebraic equation in s of degree $k - 1$

$$s - q - ps^{k-1} = 0, \tag{100}$$

which can be written as the product

$$(1-s)[-q + p(s + s^2 + \ldots + s^{k-2})] = 0. \tag{101}$$

The nontrivial solution is the solution of

$$s + s^2 + \ldots + s^{k-2} = \frac{q}{p} \tag{102}$$

This equation has just one solution in the interval $0 \leq s < 1$ which exists as long as $q/p < k - 2$, that is, $p > 1/k - 1$. Therefore, there is a phase transition at the critical infection probability

$$p_c = \frac{1}{k-1}. \tag{103}$$

We finally notice that the densities y and z are related to x by the equations

$$y = p(1-x), \qquad z = q(1-x), \tag{104}$$

so that y and z can be obtained from s by

$$y = p(1-s^k), \tag{105}$$

$$z = q(1-s^k). \tag{106}$$

Relations (104) are obtained as follows. From equation (86) and (87) we get $dy/dx = -p$ which integrated gives $y = -px + K$. The constant of integration is found to be $K = p$ by using the condition $y \to 0$ when $x \to 1$. The density z is obtained by using the constraint $x+y+z = 1$. The density of infected sites y plays the role of order parameter, and can be understood, in the percolation language, as the probability that a site belongs to the infinite percolating cluster. Around the critical point, we find from the solution of (102) the following behavior of the order parameter

$$y = \frac{2k}{k-2}(p - p_c), \tag{107}$$

valid for $p \geq p_c$.

VI. RELATION TO STATIC PERCOLATION

In static site percolation, each site of a lattice is occupied with probability p and vacant with probability $q = 1 - p$, independently of the others. Above a critical probability p_c, an infinite percolating cluster sets in. On a Cayley tree of coordination number k, the probability P that a site belongs to the infinite percolating cluster, which is the order parameter, is given by [35]

$$P = p(1 - Q^k), \tag{108}$$

where Q obeys the equation

$$Q = q + pQ^{k-1}, \tag{109}$$

which can be written in the form

$$(1 - Q)[-q + p(Q + Q^2 + \ldots + Q^{k-2})] = 0. \tag{110}$$

The nontrivial solution, which gives a nonzero value of the order parameter, is given by

$$Q + Q^2 + \ldots + Q^{k-2} = \frac{q}{p} \tag{111}$$

Setting $Q = 1$ in this equation, it follows that the critical value of p for site percolation on a Cayley tree of coordination number k is the well known result [34–36]

$$p_c = \frac{1}{k-1}. \tag{112}$$

Now, equation (111) is identical to equation (102) of the SEI model if we make the association $Q = s$. Moreover, from equations (105) and (108) we see that the order parameter P should be identified with the density of infected individuals y of the SEI model. These results are expected since the stationary properties of the SEI model are identified with the static site percolation.

Next, let us compare equation (111) with equation (72) of the SIR model. The two equations are identical if we make the associations $Q = s$ and $q/p = kr$. Taking into account the relation (74) and that $q = 1 - p$, we reach the following relation between the infection probability p of SEI model and the infection probability b of the SIR model

$$p = \frac{b}{k - (k-1)b}. \tag{113}$$

Let us define $P^* = P/p$ which is an alternative definition of the order parameter and interpreted as the probability that an *occupied* site belongs to the infinite cluster. Comparing the expression $P^* = 1 - Q^k$, obtained from (108), and taking into account that $x = s^k$ we get the association $P^* = 1 - x = y + z$, that is, the order parameter is identified as the sum of the densities of infected and recovered individuals of the SIR model. In the limit $t \to \infty$, the density y of infected individuals vanishes and we may conclude that the order parameter P^* is identified as the density z of recovered individuals.

It is worth of mentioning that equation (111), or the equivalent equations (102) and (72), also appears in the theory of polymerization advanced by Flory [40–42] in which the weight fraction of the gel W is related to s by the related $W = 1 - s^k$ where k represents the functionality of the monomers making up the polymers. The same can be said about the equations (37) and (38) that give the cluster size distribution.

We remark also that the expression (39) is in agreement with the following scaling form for percolation [36]

$$\mathcal{P}_n = n^{-\tau+1}\mathcal{F}(n(p - p_c)^{1/\sigma}) \tag{114}$$

where $\tau = 5/2$, $\sigma = 1/2$ and $\mathcal{F}(x)$ is a scaling function.

VII. TIME-DEPENDENT SOLUTION

To get the time-dependent solutions of the SIR model we replace v in equation (57) by the expression (68). Equation (57) becomes

$$\frac{dx}{\beta dt} = krx^\mu - (kr + 1)x + x^{2\mu}. \tag{115}$$

We note that the same equation holds for the SEI model if in equation (86) we replace v by the expression (98) and p by the expression (113). By this expedient, the solution $x(t)$ of equation (115) will be the time-dependent solution of the SEI model as well.

It is useful to change variable from x to $s = x^{1/k}$ which allows us to write (115) in the form

$$\frac{k}{\beta}\frac{ds}{dt} = D(s), \tag{116}$$

where

$$D(s) = kr - (kr + 1)s + s^{k-1}. \tag{117}$$

This polynomial of degree $k - 1$ can be written as the product

$$D(s) = (s - 1)(s^{k-2} + \ldots + s^2 + s - kr). \tag{118}$$

An implicit solution $s(t)$ is given by the integral

$$\beta t = k \int \frac{ds}{D(s)}. \tag{119}$$

Let us consider the roots λ_i of the polynomial $D(s)$ in the interval $0 \le s \le 1$ One root is $\lambda_0 = 1$. As we have seen in section IV B, if $r < (k-2)/k$ there is another root in this interval which we denote by λ_1. No real roots exists in this interval other that λ_0 and λ_1. One expects that as $t \to \infty$, either $s \to 1$ or $s \to \lambda_1$. Linearizing equation (115) around $s = 1$, we get

$$\frac{ds}{\beta dt} = (r_c - r)(s - 1), \tag{120}$$

where $r_c = (k-2)/k$, so that the solution $s = 1$ is unstable when $r < r_c$ and the solution for $t \to \infty$ in this case must be $s = \lambda_1$.

To get an approximate solution of (116) for the case $r < r_c$, we expand the polynomial $D(s)$ around $s = \lambda_1$ to get

$$\frac{ds}{dt} = A(s-1)(s-\lambda_1), \tag{121}$$

where $A > 0$. Integrating

$$t = \frac{1}{B}\int \frac{ds}{s-1} - \frac{1}{B}\int \frac{ds}{s-\lambda_1}, \tag{122}$$

where $B = A(1-\lambda_1) > 0$. Performing the integration and writing s as a function of t, we get

$$s = \frac{\lambda_1 + Ce^{-Bt}}{1 + Ce^{-Bt}}, \tag{123}$$

where $C > 0$ is a constant to be determined from the initial conditions. Since the initial gives $x \to 1$ at $t = 0$ or $s \to 1$ at $t = 0$, it follows that $1/C$ should very small but nonzero.

When $t \to \infty$, it is clear that $s \to \lambda_1$ and $x \to \lambda^k$. From the solution (123) it follows that the derivative $-ds/dt$ as a function of t is a bell shaped curve and so is the epidemic curve, $\zeta = -dx/dt$ versus t, that is, the density of susceptible individuals that are being infected per unit versus time, as shown in figure 4.

A. The case $k = 3$

Let us consider the simplest nontrivial case namely $k = 3$. In this case

$$D(s) = (s-1)(s-3r), \tag{124}$$

and

$$\frac{3}{D(s)} = \frac{3}{1-3r}\left(\frac{1}{s-1} - \frac{1}{s-3r}\right). \tag{125}$$

Substituting this expression in (119) and performing the integration we get,

$$(r_c - r)\beta t = \ln|1-s| - \ln|s-3r| + K, \tag{126}$$

where $r_c = 1/3$ and K is a constant. Solving for s we obtain

$$s = \frac{3r + Ce^{-(r_c-r)\beta t}}{1 + Ce^{-(r_c-r)\beta)}}, \tag{127}$$

where C is to be determined by the initial conditions. From this solution we get $x(t)$ and the epidemic curve, that is, the density of susceptible individuals that are being infected per unit time $\zeta = -dx/dt$ versus t, shown in figure 4.

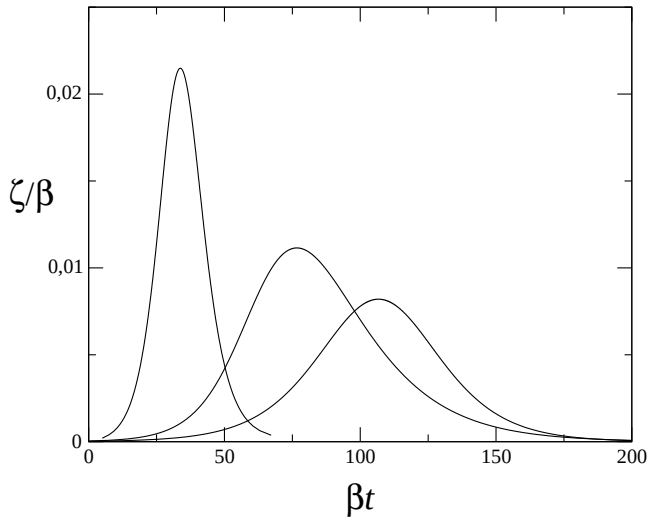

FIG. 4: Epidemic curve for the SIR model: density of susceptible individuals that are being infected per unit time $\zeta = -dx/dt$ versus time t, for $r/r_c = 0.8$. The leftmost curve was obtained by solving equation (150). The middle and rightmost curves come from the solutions corresponding to $k = 4$ and $k = 3$, respectively. The area below the curves give the final density of recovered individuals z, which are 0.371, 0.453, and 0.488, respectively.

We may draw the following conclusions concerning the limit $t \to \infty$. If $r < r_c$, then $s \to 3r$, otherwise, $s \to 1$. Notice that, the critical point occurs when $r = 1/3$ or $b = 3/4$ in agreement with (73) and (75). In this case, $x = s^3$ and the stationary value of the density of susceptible individuals is $x = (3r)^3$ and the order parameter, the density of recovered individuals $z = 1 - x$ is

$$z = 1 - (3r)^3 \tag{128}$$

The order parameter vanishes linearly with the distance from the critical point $b_c = 3/4$,

$$z = 9(r_c - r). \tag{129}$$

B. The case $k = 4$

In this case

$$D(s) = (s-1)(s^2 + s - 4r), \tag{130}$$

which can be written as

$$D(s) = (s-1)(s-\lambda_1)(s-\lambda_2), \tag{131}$$

where

$$\lambda_1 = \frac{-1 + \sqrt{1+16r}}{2}, \tag{132}$$

$$\lambda_2 = \frac{-1 - \sqrt{1+16r}}{2}. \tag{133}$$

Now, it is possible to write

$$\frac{4}{D(s)} = \frac{2}{1-2r}\left(\frac{1}{s-1} - \frac{A_1}{s-\lambda_1} + \frac{A_2}{s-\lambda_2}\right), \quad (134)$$

where the coefficient of the fractions are

$$A_1 = \frac{1-\lambda_2}{\lambda_1-\lambda_2} = \frac{3+\sqrt{1+16r}}{\sqrt{1+16r}}, \quad (135)$$

$$A_2 = \frac{1-\lambda_1}{\lambda_1-\lambda_2} = \frac{3-\sqrt{1+16r}}{\sqrt{1+16r}}. \quad (136)$$

The integration of equation (119) gives

$$(r_c - r)\beta t =$$

$$= \ln|1-s| - A_1 \ln|s-\lambda_1| + A_2 \ln|s-\lambda_2| + K, \quad (137)$$

where $r_c = 1/2$ and K is a constant to be determined by the initial conditions. From $s(t)$ we obtain $x(t)$ and the epidemic curve, $\zeta = -dx/dt$ versus t, shown in figure 4.

Let us consider the limit $t \to \infty$. When $r < r_c = 1/2$, $A_2 > 0$ and since $A_1 > 0$ then the dominant term in the right-hand site is the second and

$$(r_c - r)\beta t = -A_1 \ln|s-\lambda_1| + K'. \quad (138)$$

Therefore, when $r < r_c$, s approaches λ_1 in the limit $t \to \infty$. The critical point occurs at $r_c = 1/2$ or $b_c = 2/3$ in agreement with (73) and (75). The stationary density of susceptible individuals is then $x = s^4 = \lambda_1^4$ and the density of removed individuals, or the order parameter, $z = 1 - x$ is then

$$z = 1 - \left(\frac{-1+\sqrt{1+16r}}{2}\right)^4. \quad (139)$$

The order parameter vanishes linearly near the critical point as

$$z = \frac{16}{3}(r_c - r) \quad (140)$$

VIII. KERMACK AND MCKENDRICK EQUATIONS

To make contact with the previous works on the SIR model related to deterministic equations, we consider here a simpler approach to the evolution equations in which only the one-site probabilities are taken into account. We replace the two-site probability P_{IS} on the right-hand side of equations (41) and (42) by the product $P_I P_S$. Equations (41), (42) and (43) become then

$$\frac{dx}{dt} = -\beta xy, \quad (141)$$

$$\frac{dy}{dt} = \beta xy - \gamma y, \quad (142)$$

$$\frac{dz}{dt} = \gamma y, \quad (143)$$

which are the equations introduced by Kermack and McKendrick [11].

To solve these equations we take the ratio between (143) and (141) to get

$$\frac{dz}{dx} = -\frac{r}{x}, \quad (144)$$

where r is the relative recovery rate, defined by (63), whose solution is

$$z = -r \ln x + K, \quad (145)$$

where K is a constant to be found by the initial conditions $z = 0$ and $x \to 1$. It follows that $K = 0$ and we get

$$z = -r \ln x, \quad (146)$$

which is a conservation law, that can be written also as

$$y = 1 - x + r \ln x, \quad (147)$$

or

$$y = 1 - z - e^{-z/r}, \quad (148)$$

since $x + y + z = 1$.

In the limit $t \to \infty$ the epidemics ends which means to say that $y = 0$. The final density of recovered individuals, which may be considered as the order parameter, will be then the root of

$$z = 1 - e^{-z/r}, \quad (149)$$

which is the equation found by Kendall [12]. For $r \geq 1$ the only root is $z = 0$ corresponding to the non-spreading regime. For $r < 1$, there is in addition a non trivial root $z^* < 1$ corresponding to the spreading regime. In this regime, $z \to z^*$ when $t \to \infty$. The threshold of epidemic occurs then at $r = r_c 1$ around which the order parameter behaves as $z^* = 2(r_c - r)$.

To obtain the time dependent solution we substitute the result (147) into equation (141) to get

$$\frac{dx}{\beta dt} = x(x - 1 - r \ln x), \quad (150)$$

and consequently

$$\beta t = \int \frac{dx}{x(x - 1 - r \ln x)}. \quad (151)$$

This equation can be integrated numerically to get t as a function of x and, by inversion, to get x as a function of t and finally y as a function of t by the use of (147). Figure 4 shows the epidemic curve, $\zeta = -dx/dt$ versus t, obtained by this numerical procedure.

The scheme used in this section may also be understood as the limit of infinite coordination number. Indeed, if we take the limit $k \to \infty$ in equation (115) and bearing in mind that $\mu = (k-1)/k$, we get equation (150).

IX. CONCLUSION

We have studied the stochastic SIR and SEI lattice models on a Cayley tree of a generic coordination number k. Two approaches have been considered concerning the spreading and no spreading regimes. In the first, we have analyzed the growth of a single cluster which was generated by using an initial condition with a single infected site on a lattice full of susceptible individuals. Exact equations for the time evolution where set up and exact solutions were obtained for any value of k. From the exact solution we have determined the threshold of epidemic spreading as a function of k and the numbers of individuals of each type as well as the final values of these quantities. The cluster size distribution has been also determined.

In the second approach, we have considered the properties that in a regular lattice are obtained by taking the thermodynamic limite. By using relations (51), (52), and (53), we have set up and solved the evolution equations for both models pointing out the close relationship between them. The solution was made possible by the use of some conservation laws that have been obtained in advance. We have shown that in the stationary state the order parameter of both models are the same as that of site percolation on a Cayley tree, a result that indicates that the relations (51), (52), and (53), becomes asymptotically correct. From the time solution of the evolution equation for the density of susceptible individuals we have determined the time-dependent properties including the epidemic curve, showing its bell shaped behavior. Explicit solutions concerning the final density of recovered individuals were found for the cases $k = 3$ and $k = 4$.

Acknowledgment

We wish to acknowledge the financial support from the Brazilian agency CNPq and INCT/CNPq of Complex Fluids.

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