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Autor(en): **Kamphorst Leal da Silva, J. / Droz, M.**

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Scaling of the pair connectedness for site directed percolation

J. Kamphorst Leal da Silva[1]) and M. Droz

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Départment de Physique Théorique, Université de Genève, 1211 Genève 4, Switzerland

Abstract. We consider the pair connectedness Γ for site directed percolation on a square two dimensional lattice. Computing Γ exactly for small cells and assuming a scaling form for it, one extracts the percolation threshold p_c and the parallel exponents $\upsilon_{\parallel}$ and $\eta_{\parallel}$. The anisotropy exponent θ is obtained by computing the expected cluster size for the small cells. The results are compared with other approaches.

1. Introduction

In the usual percolation problem, one considers a regular d-dimensional lattice in which the sites are occupied with a probability p and empty with a probability $(1-p)$ (site percolation) or in which the bonds are nonzero with a probability p' and zero with probability $(1-p')$ (bond percolation). The aim of the percolation theory is to describe the properties of the connected pieces of the network. The probability that two sites, separated by a distance r, are linked decays as $\exp -r/\xi$. The correlation length ξ is finite below the percolation threshold p_c and diverges like $\xi \sim (p_c - p)^{-\nu}$ for $p \to p_c$. ν is the correlation length exponent.

The directed percolation problem differs from the usual one by the fact that now we introduce a privileged direction in the problem. The bonds have an arrow directed towards the privileged direction. One relevant question is now what is the probability that two sites separated by a distance r are linked by a path which follows the arrows. This probability does not depend anymore only on r. On the average, one can only link the origin of the lattice O, to the points within the domain sketched in Fig. 1. This domain is characterized by two correlation lengths. The one along the main diagonal of the lattice $\xi_{\parallel} \sim (p_c - p)^{-\nu_{\parallel}}$ and the one perpendicular to the main diagonal $\xi_{\perp} \sim (p_c - p)^{-\nu_{\perp}}$. p_c is here the percolation threshold for directed percolation. $\nu_{\parallel}$ and $\nu_{\perp}$ are the longitudinal and perpendicular correlation length exponents. They are independent and belong to a different universality class then ν, the exponent for the usual percolation. The main new feature of directed percolation is thus the anisotropy between the longitudinal and transverse directions. Such anisotropy is met in another context, namely in critical dynamics [1]. Here, space and time variables rescale differently. This suggests that the longitudinal direction of directed percolation may be considered as a time

[1]) Permanent address: Departamento de Fisica, Universidade Federal de Minas Gerais, CP 702, 30000 Belo Horizonte, Minas Gerais, Brazil

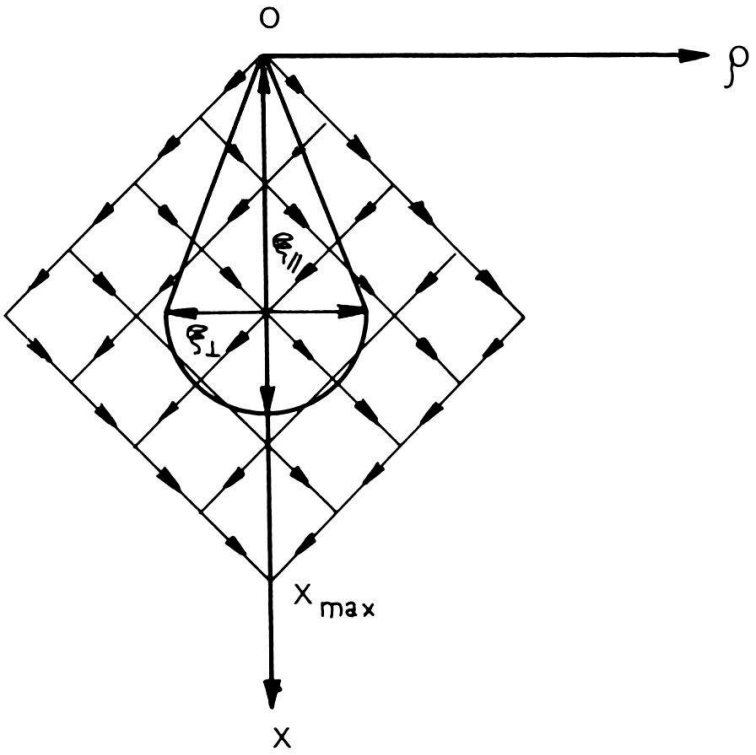

Figure 1
Typical cell considered. x is the parallel direction and ρ the transverse one. $\xi_{\|}$ and $\xi_{\perp}$ are respectively the parallel and perpendicular correlation lengths.

direction, since steps against it are forbidden. In order to illustrate this analogy explicitly, let us imagine that our system modeled a hydraulic network. Water is poured at the origin O and flows across the network towards the bottom. The 'state' of the network at the level x (see Fig. 1) is determined by enumerating which sites belonging to this level are 'wet' and which sites are 'dry'. The state at the level $(x+1)$ will depend only upon the state at the level x. In the dynamical picture, this means that the evolution of the system at time t depends only upon the state of the system at time $(t-1)$. There is no memory effects, this is a markovian evolution. More precisely, the directed percolation problem can be mapped onto a particular model of cellular automaton [2]. Cellular automaton theory describes a system consisting of an homogeneous array of 'cells'. Each cell is endowed with a finite number of states, and evolves in discrete time according to an uniform local transition rule. Uses of cellular automaton in chemistry, biology have been numerous [see [3] and references therein]. Accordingly, the problem of directed percolation is closely related to several problems of chemistry, population dynamics and high energy physics [see [4] and references therein]. Estimations of p_c, $\nu_{\|}$ and $\nu_{\perp}$ have been obtained in two dimensions by finite-size renormalization group approach [5]. p_c and $\nu_{\|}$ have also been estimated by Monte Carlo simulations [6], series expansion [7] and real space renormalization group [8].

In the framework of ordinary site percolation several interesting results have been obtained using real space renormalization group approach for finite cells of sizes b and eventually by extrapolating the results for $b \to \infty$ [9]. For small sizes $(b \leq 5)$, the recursion relations were obtained in a closed form while for larger b, they were obtained by Monte Carlo simulation. In this approach, the occupation

probability of a site p is renormalized in $p' = R(b, p)$. Note however that the renormalization group transformation R contains some arbitrariness related to the criterion chosen for a percolating cell [10]. Despite this fact, results obtained even for small cells, i.e. $b \leq 5$, are quite good.

In view of the additional directional constraint present in directed percolation, one may expect that results obtained by studying small cells will be even better for the directed percolation than for the ordinary one.

Moreover, in order to eliminate the arbitrariness in the definition of the renormalization group transformation, it is legitimate to look for a quantity uniquely defined. A good candidate is the pair connectedness $\Gamma(\vec{R}, p)$ defined as the probability that a pair of sites at the origin O and at an arbitrary point $\vec{R}$ of the lattice are connected by a path of bonds that can be traversed in the direction of the arrows. Assuming scaling for the pair connectedness, information about the critical region can be obtained by comparing cells of several sizes. In order to test the validity of this approach, we restrict ourselves to small cells for which $\Gamma(\vec{R}, p)$ can be computed analytically.

The paper is organized as follows. In Section 2, we recall the scaling assumption for the pair connectedness and show how to extract the desired information. In Section 3, we quote the results obtained and discuss a complementary approach to obtain information about the perpendicular direction. The conclusions are drawn in Section 4.

2. Scaling for the pair connectedness in two dimensions

Let $\vec{R} = (x, \rho)$ a point of the lattice (see Fig. 1). x is the longitudinal component and ρ the transverse one. According to the scaling hypothesis [4], the pair connectedness $\Gamma(x, \rho, p)$ behaves, for p close to p_c, and $x, \rho > a$ the lattice constant as:

$$\Gamma(x, \rho, p) = (p - p_c)^{2\beta} f(x/\xi_{\parallel}, \rho/\xi_{\perp}) \tag{1}$$

with

$$\xi_{\parallel} = A_{\parallel}(p - p_c)^{-\nu_{\parallel}} \quad \text{and} \quad \xi_{\perp} = A_{\perp}(p - p_c)^{-\nu_{\perp}} \tag{2}$$

β is the critical exponent governing the fraction of the sites belonging to the percolating cluster $P_\infty(p)$:

$$P_\infty(p) \sim (p - p_c)^{\beta} \tag{3}$$

Integrating $\Gamma(x, \rho, p)$ over (x, ρ), one obtains the average cluster size

$$\chi = \int dx\, d\rho \Gamma(x, \rho, p) \sim (p - p_c)^{-\gamma} \tag{4}$$

The above critical exponents are related through the hyperscaling relation, which reads in two dimensions:

$$\gamma + 2\beta = \nu_{\perp} + \nu_{\parallel} \tag{5}$$

Let us first consider the longitudinal case, i.e. $\rho = 0$. From (1) and (2) one gets for

$p = p_c + \delta p$

$$\Gamma(x, 0, \delta p) = \frac{1}{x^{2\beta/\nu_\parallel}} g\left(\frac{x\delta p^{\nu_\parallel}}{A_\parallel}\right) \tag{6}$$

at p_c,

$$\Gamma(x, 0, p_c) \sim \frac{1}{x^{\eta_\parallel}} \tag{7}$$

where $\eta_\parallel = 2\beta/\nu_\parallel$ is the longitudinal pair connectedness exponent. Under a change of scale l, we have

$$\Gamma(lx, 0, \delta p l^{-1/\nu_\parallel}) = l^{-\eta_\parallel}\Gamma(x, 0, \delta p) \tag{8}$$

For the perpendicular case, we have (x fixed)

$$\Gamma(x, \rho, \delta p) = \frac{1}{\rho^{2\beta/\nu_\perp}} g_1\left(\frac{x\delta p^{\nu_\parallel}}{A_\parallel}, \frac{\rho\delta p^{\nu_\perp}}{A_\perp}\right) \tag{9}$$

at p_c,

$$\Gamma(x, \rho, p_c) \sim \frac{1}{\rho^{\eta_\perp}} \tag{10}$$

where $\eta_\perp = 2\beta/\nu_\perp$ is the transversal pair connectedness exponent. Under a change of scale l, we have

$$\Gamma(l^{1/\theta}x, l\rho, l^{-1/\nu_\perp}\delta p) = l^{-\eta_\perp}\Gamma(x, \rho, \delta p) \tag{11}$$

where

$$\theta = \nu_\parallel/\nu_\perp \text{ is the anisotropy exponent.} \tag{12}$$

How to extract useful information from the above relations ? Note at first that the scaling relation (1) is strictly valid for large distances. On the other hand, analytic calculation are possible only at short distances. Thus, we will assume that the above scaling relations can be extended for short distances. A similar hypothesis has shown to be sensible for two and three dimensional Ising models [11].

By computing $\Gamma(x_{\max}, 0, p)$ for three different cells with respectively $N_1 = L_1 \times L_1$, $N_2 = L_2 \times L_2$ and $N_3 = L_3 \times L_3$ sites ($x_{\max}$ is the the opposite corner of O, see Fig. 1), we obtain from (8) the values of p_c, $\nu_\parallel$ and $\eta_\parallel$. Knowing p_c, we can then extract $\eta_\perp$ from (10). Note however that (10) is an asymptotic form valid for ρ large as compared to x. For x comparable to ρ, the complete scaling form (11) should be used. However this form is not suitable for small cells because the point $(l^{1/\theta}x, l\rho)$ should be a site of the lattice, which restricts drastically the possible values of θ. Thus it is not possible to extract meaningful information about the perpendicular exponents by studying small cells. However this difficulty can be overcome by looking at another quantity, the expected size of a cluster

$$n(p) = \sum_{s \geq 1} sP(s, p) \sim (p - p_c)^{-\gamma} \qquad p \to p_c - 0 \tag{13}$$

where $P(s, p)$ is the probability that the origin belongs to an (oriented) cluster of s sites. Note that $n(p)$ is proportional to χ defined by (4). In terms of the parallel correlation length, one has

$$n(p) \sim \xi_{\parallel}^{\gamma/\nu_{\parallel}} \qquad p \to p_c - 0 \tag{14}$$

and thus under a rescaling by $l = (L_1/L_2)$ in the parallel direction

$$n_{L_1}(p_c) \sim \left(\frac{L_1}{L_2}\right)^{\gamma/\nu_{\parallel}} n_{L_2}(p_c) \tag{15}$$

By comparing $n_L(p_c)$ for two different cells, one computes $\gamma/\nu_{\parallel}$. Using the scaling relation (5) and knowing β and $\nu_{\parallel}$ we can then compute $\nu_{\perp}$ and the anisotropy exponent θ.

Note also that we have two possible interpretations for the rescaling factor l:

i) One stays on the original lattice and compute the quantities of interest for cells of several sizes on this lattice. For example, one computes $\Gamma(x, 0, p)$ and $\Gamma(x_2 = lx_1, 0, p)$. The rescaling factor is obviously l. This procedure is called (PI) in the next section.

ii) One considers that going from a cell of $N_1 = (L_1 \times L_1)$ sites to one with $N_2 = (L_2 \times L_2)$ sites corresponds to a renormalization group transformation. Assuming that the transformation is linear and maps the initial one parameter problem into a new one parameter problem, then we can use the above scaling forms with a rescaling factor $l = (N_1/N_2)^{1/2}$. This procedure, called (PII) implies extra assumptions about the existence of such a renormalization group transformation. Note that the usual connectivity rule used in ordinary and directed percolation maps also a one parameter problem into another one parameter problem [10]. Moreover, as we shall see later, the pair-connectedness exponents $\eta_{\parallel}$ and $\eta_{\perp}$ are not small. Fitting the results within the approximation $\eta_{\parallel} = \eta_{\perp} = 0$ leads only to the trivial fixed points $p^* = 0$ or 1.

3. Results

Let us consider first the longitudinal case. The analytical expressions for $\Gamma(x_{\max}, 0, p)$ for clusters of size $L \times L$, $L = 1$ to 5 are given in Table 1.

Using (8) for three different values of L, we extract p_c, $\nu_{\parallel}^{-1}$ and $\eta_{\parallel}$. The results are quoted in Tables 2, 3 and 4 for the procedures PI and PII. The above results

Table 1
Values of the pair connectedness function $\Gamma(x_{\max}, 0, p)$ for several cells of size $L \times L$.

L	$\Gamma(x_{\max}, 0, p)$
1	p
2	$-p^4 + 2p^3$
3	$p^9 - p^8 + p^7 - 6p^6 + 6p^5$
4	$2p^{15} - 8p^{14} + 6p^{13} + 2p^{12} + 4p^{11} - 7p^{10} + 12p^9 - 30p^8 + 20p^7$
5	$p^{23} - 8p^{22} + 21p^{21} - 49p^{20} + 107p^{19} - 110p^{18} + 26p^{17} - p^{16} + 10p^{15} + 3p^{14} + 31p^{13} - 50p^{12} + 90p^{11} - 140p^{10} + 70p^9$

Table 2
Values of the percolation threshold obtained from the cells of sizes $L_1 \times L_1$, $L_2 \times L_2$ and $L_3 \times L_3$ with the procedures PI and PII.

L_1,	L_2,	L_3	p_c (PI)	p_c (PII)
3	2	1		0.5634
4	2	1		0.5859
5	2	1		0.6002
4	3	1		0.6135
5	3	1		0.6242
5	4	1		0.6364
4	3	2	0.7399	0.6541
5	3	2	0.7345	0.6596
5	4	2	0.7281	0.6660
5	4	3	0.7195	0.6738

show clearly a monotonous evolution as a function of the number of sites involved in a given three point fit. However an extrapolation scheme is clearly needed. The usual extrapolation scheme, based on finite size scaling theory [12], shows how to extrapolate a set of data $s(l)$ associated with a well defined rescaling factor l. In our case, the situation is not so simple. Indeed the values $p_c(l)$, $\nu_{\|}^{-1}(l)$ and $\eta_{\|}(l)$, listed in Tables 2, 3 and 4 are obtained from a three-point fit with rescaling factors $l_1 = L_1 - 1$; $l_2 = L_2 - 1$; $l_3 = L_3 - 1$. For the small values of L considered, it is not obvious to assign an effective rescaling factor l_{eff} to our data. It turns out that the best effective rescaling factor is $l_{\text{eff}} = l_1 \cdot l_2 \cdot l_3$. The fit $p_c(l_{\text{eff}}) - p_c \sim l_{\text{eff}}^{-1/\nu_{\|}}$ leads to

$$\begin{aligned} p_c(\text{PI}) &= 0.703 \qquad \nu_{\|}(\text{PI}) = 1.71 \\ p_c(\text{PII}) &= 0.716 \qquad \nu_{\|}(\text{PII}) = 1.70 \end{aligned} \tag{16}$$

to be compared with the best estimation [4] $p_c = 0.7058$ and $\nu_{\|} = 1.73$.

For $\eta_{\|}$, taking into account corrections to scaling, one expects $\eta_{\|}(l_{\text{eff}}) = \eta_{\|} + A/\ln(l_{\text{eff}})$. This leads to the extrapolating value

$$\eta_{\|}(\text{PI}) = 0.315 \tag{17a}$$

For the second procedure, reasonable extrapolated values are obtained only by

Table 3
Values of the correlation length exponent obtained from the cells of sizes $L_1 \times L_1$, $L_2 \times L_2$ and $L_3 \times L_3$ with the procedures PI and PII.

L_1,	L_2,	L_3	$\nu_{\|}^{-1}$ (PI)	$\nu_{\|}^{-1}$(PII)
3	2	1		1.0510
4	2	1		1.0010
5	2	1		0.9695
4	3	1		0.9274
5	3	1		0.9016
5	4	1		0.8678
4	3	2	0.4784	0.8629
5	3	2	0.4890	0.8401
5	4	2	0.5052	0.8103
5	4	3	0.5249	0.7932

Table 4
Values of the exponent $\eta_{\|}$ obtained from the cells of sizes $L_1 \times L_1$, $L_2 \times L_2$ and $L_3 \times L_3$ with the procedures PI and PII.

L_1,	L_2,	L_3	$\eta_{\|}$(PI)	$\eta_{\|}$(PII)
3	2	1		1.1328
4	2	1		1.0425
5	2	1		0.9877
4	3	1		0.9071
5	3	1		0.8628
5	4	1		0.8031
4	3	2	0.2009	0.6609
5	3	2	0.2104	0.6368
5	4	2	0.2251	0.6046
5	4	3	0.2527	0.5574

considering the set of datas containing the one site cell. One finds

$$\eta_{\|}(\text{PII}) = 0.314 \tag{17b}$$

These values must be compared with the best estimation [13], $\eta_{\|} = 0.314 \pm 0.002$.

The results for the expected size of a cluster are given in Table 5. Two-point fits lead to the exponents $\gamma/\nu_{\|}$ quoted in Table 6. Here, the rescaling factors are well defined. The best extrapolation is obtained by fitting the results which correspond to a rescaling factor going to one. One gets:

$$\gamma/\nu_{\|}(\text{PI}) = 1.43 \qquad \gamma/\beta_{\|}(\text{P2}) = 1.45 \tag{18}$$

Table 5
Values of the expected size of a cluster at p_c as a function of the size of the cell L.

L	n_L (0.703)	n_L (0.716)
1	0.703	0.716
2	2.144	2.180
3	3.993	4.085
4	6.146	6.321
5	8.545	8.831

Table 6
Values of $\gamma/\nu_{\|}$ obtained from cells of size $L_1 \times L_1$ and $L_2 \times L_2$ with the procedures PI and PII.

L_1,	L_2	$\gamma/\nu_{\|}$ (PI)	$\gamma/\nu_{\|}$ (PII)
2	1		1.6184
3	1		1.5927
4	1		1.5771
5	1		1.5663
3	2	0.8973	1.5489
4	2	0.9587	1.5358
5	2	0.9975	1.5268
4	3	1.0635	1.5174
5	3	1.0976	1.5093
5	4	1.1457	1.4989

Using (17) and the scaling relation (5) one gets for the anisotropy exponent,

$$\theta(\mathrm{PI}) = 1.34 \qquad \theta(\mathrm{PII}) = 1.31 \tag{19}$$

to be compared with the best estimate [13], $\theta = 1.576$.

4. Conclusions

As anticipated on physical grounds, the above results show that reasonable information can be obtained for directed percolation by studying small cells. For the parallel direction, scaling for the pair connectedness holds already at short distances. The study of the perpendicular quantities is more problematic for the reasons explained in Section 2. The computation of the expected size of a cluster for small cells, leads to a qualitatively correct description of the anisotropy of the problem. However, in view of the values obtained for the anisotropy exponent, we would conclude that short distance scaling does not hold as well for the perpendicular direction as for the longitudinal one. More precise results can obviously be obtained by considering larger cells. Unfortunately, it is not possible to study analytically such cells. One has to use Monte Carlo simulation and deal with the problem of statistics inherent to the method. During the completion of this work, someone brought to our attention the recent paper of Benzoni [13], in which an extensive Monte Carlo analysis is performed. Simulating cells of size smaller or equal to 60×60, Benzoni tests the validity of the scaling form (1). He gets a precise determination of all the components as well as an expression for the scaling function.

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