Pair connectedness and shortest-path scaling in critical percolation

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Abstract.   We present high statistics data on the distribution of shortest path lengths between two near-by points on the same cluster at the percolation threshold. Our data are based on a new and very efficient algorithm. For $d = 2$ they clearly disprove a recent conjecture by M Porto *et al* 1998 *Phys. Rev.* E **58** R5205. Our data also provide upper bounds on the probability that two near-by points are on different infinite clusters.

1. Introduction

Although percolation is a problem which has been studied in great detail during the last few decades [1], and although many exact results are already known, there are still open questions which either have not been studied at all, or which have yet to be understood.

   In the present paper we study the spreading of percolation in the form of an epidemic process [2]. In the physics literature, this is often called the Leath growth of clusters [3]. In this process (which we assume to proceed in discrete time steps) one starts with an infected seed as a single 'growth site', and keeps at each time a list of growth sites. In the next time step, the list consists of all wettable sites which are nearest neighbours to any of the present growth sites, while the old list is cancelled. A site is wettable if it had not been a growth site before, and if it can be occupied (in site percolation), or if it is connected to the present growth site by an occupied bond (in bond percolation). It is well known that the distribution of growth sites satisfies at the critical point and for large times t the scaling law [2,4]

$$\rho(x, t) = \frac{1}{t^{1+2\beta/\nu_t}} \phi(r/t^z). \tag{1}$$

Here, β is the well known critical exponent governing the fraction of sites occupied by the infinite cluster [1], ν_t is the critical exponent governing the correlation time if one goes off-critical, and $z = \nu/\nu_t$ is the dynamical exponent. The inverse of the latter is often called $d_{\min}$. Finally, $\phi(\zeta)$ is a universal scaling function. In a purely geometrical interpretation of equation (1), t is often called the 'chemical distance' between the site x and the origin, as it counts the number of lattice steps *on the cluster* needed to reach x from the origin (i.e. the length of the shortest 'chemical path').

   The main problem we want to study is the behaviour of the scaling function $\phi(\zeta)$ for small ζ. This has been studied recently by Porto *et al* [5] (see also [6]). As usual one expects a power law,

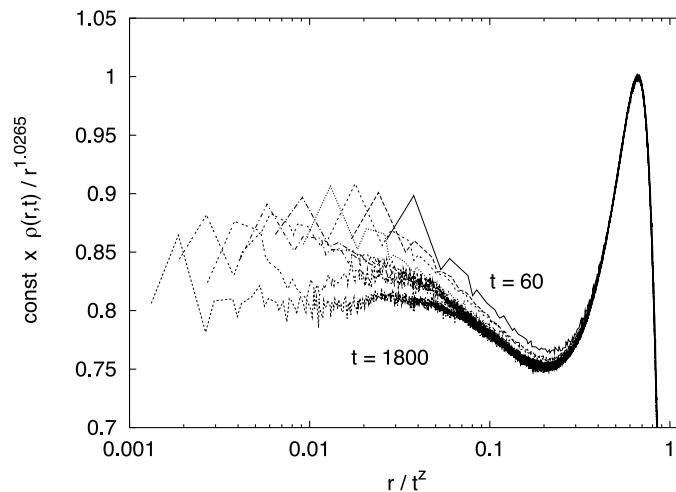$$\phi(\zeta) \sim \zeta^{g_1} \qquad \zeta \to 0. \tag{2}$$

Figure 1. Radial density of sites infected at time t, with arbitrary normalization, plotted against r/t^z with $z = 0.8844$ (corresponding to $d_{\min} = 1.1307 \pm 0.0004$; [10]). In order to enhance the significance of the plot, each curve corresponds to times $\in]0.9t, t]$, and the data are divided by $r^{d_{\min} - \beta/\nu}$. The curves correspond to $t = 60, 100, 140, 200, 300, 500, 800, 1200$ and 1800.

The authors of [5] used an analogy with self-avoiding random walks (SAW) to conjecture

$$g_1 = d_{\min} - \beta/\nu \qquad \text{(conjectured)} \tag{3}$$

where d is the dimension of the lattice in which the cluster is embedded. This conjecture was then checked numerically and found to be satisfied†.

There are, however, a number of problems associated with that analysis. The first is that the analogy with SAW is not very stringent. The analogous equation to (3) was derived by deGennes [7] using the fact that the endpoint density is the order parameter field in the SAW problem. Therefore, there is no anomalous critical exponent for the number of self-avoiding loops (which have no endpoints), and this then gives an expression for the probability that a SAW nearly forms a loop which formally seems to involve mean-field exponents. The authors of [5] essentially used these 'mean-field' arguments, although there is no analogous underlying field theory (the field theory for percolation is Potts like [8]), and we see no logical basis for equation (3).

Similarly, the simulations used in [5] seem far from conclusive. In these simulations, clusters have been studied with $t \leqslant 1800$ in $d = 2$ and with $t \leqslant 800$ in $d = 3$. In both cases, 'more than 100 000' clusters have been analysed, at several fixed values of t. In figure 1 we show results for $d = 2$ obtained by their method. Each curve is based on more than 3×10^6 clusters. In addition, in order to enhance the statistics, we have lumped together data with $0.9t < t' \leqslant t$ in each curve. In this way we arrive at statistics at least 10^3 larger than those of [5]. In order to see more details we do not show simple scaling laws as in [5], but show data multiplied by a suitable power of r/t^z. If equation (3) holds, we expect to see a horizontal line

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† In the present paper, $\rho(x, t)$ is the density averaged over *all* clusters containing the origin, not only over the infinite one. It seems that the authors of [5] wanted their argument to apply to the incipient infinite cluster only. They implemented this by analysing only clusters with chemical radius $t_{max} > 2000$, from which they presented results for chemical distances up to 1800. If there were a substantial dependence on the chemical radius, this would lead to spurious violations of scaling since t_{max} introduces a new scale. But this dependence seems to be weak, as also assumed in [6].

for small x-values. Although our data are certainly not in contradiction with this, the very large statistical and systematic deviations from such a line render any precise statement impossible.

If we want a significant test of equation (3), we have thus to proceed differently. Indeed, for fixed r there is a much faster numerical method. While the above simulations need a CPU time $\propto t^{1.6}$ in order to analyse one cluster, our improved method is faster by roughly one power of t.

Let us assume we want to test whether two sites x and y on a regular (hypercubic) lattice are on the same cluster, and want to measure the length of the shortest connecting path if they are. Let us assume furthermore that the distance between x and y, measured as the sum of the coordinate distances, is even (the case of odd distances will be discussed below). Instead of growing a single cluster from a seed at either x or y, we grow two clusters *simultaneously*, one starting from x and the other from y. We stop the growth in any of the following cases:

(1) Both clusters have a common growth site. If this happens at time t, then there exists a path of length $2t$ passing through this growth site and connecting x with y. Since this is the shortest such path (otherwise the growth would have stopped before), in this case the chemical distance between x and y is $2t$.

(2) The cluster growing from x dies (i.e., has no more growth sites). In that case, there cannot be a path from x which is long enough to reach y, and x and y are on different clusters. Notice that both clusters cannot overlap. They cannot overlap in a site which has the same chemical distance from both seeds, because they would then have been killed by rule (1) above. And they cannot overlap in a site which, say, has a smaller chemical distance from x than from y. Such a site would first have been wetted by x. In order to be wetted also from y, it must have at least one other wettable neighbour which was not wetted, however, at the time step following its first wetting. This is not possible.

(3) The cluster growing from y dies.

(4) t reaches some upper bound T specified at the beginning. In this case x and y are either on different clusters, or the shortest path has length $> 2T$.

If the distance between x and y is odd, we have to replace (1) by:

(1′) A growth site of the first cluster at time t coincides with a growth site of the other cluster at time $t-1$. In this case, the chemical distance is $2t-1$.

Let us denote by $p(t)$ the probability that an event dies because of rule (1). It is equal to the probability that two sites at a distance $r = |x-y|$ have chemical distance $2t$, which according to equations (1)–(3) is given by

$$p(t) = \frac{\rho(x-y, 2t)}{\sum_{t'=0}^{\infty} \rho(x-y, t')} \sim t^{-\lambda} \tag{4}$$

with

$$\lambda = 1 + \frac{2\beta}{\nu_t} + zg_1. \tag{5}$$

Inserting here the conjectured equation (3), we arrive at

$$\lambda = 2 + \frac{\beta}{\nu_t} \qquad \text{(conjectured)}. \tag{6}$$

During these simulations, we not only collect a histogram $n(t)$ of the times t when rule (1) applies (which gives the distribution $p(t)$ when normalized), but also a histogram of times when the growth stops due to *any* reason or, equivalently, a histogram $N(t)$ indicating how many events have survived at least t time steps. The numer $N(T)$ of events surviving until the
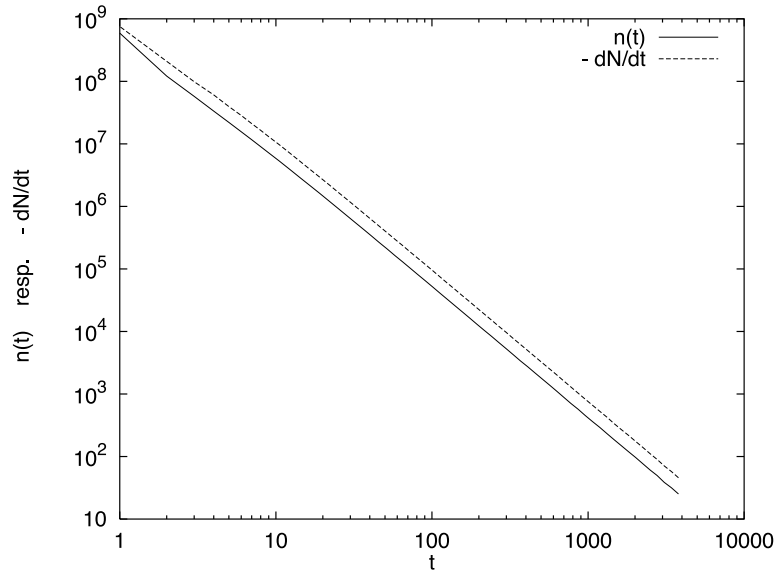
Figure 2. Histograms of $n(t)$ and $-\mathrm{d}N(t)/\mathrm{d}t$ for $d = 2$ bond percolation with $x - y = (1, 1)$. In order to reduce statistical fluctuations, data are averaged over intervals $[0.98t, t]$.

very end gives an upper bound on the probability that x and y are on different *infinite* clusters, $P_{\mathrm{diff}} < N(T)/N$. If $P_{\mathrm{diff}} = 0$ (which we expect for $d < 6$; there are several infinite clusters for any $d \geqslant 2$, but the chance that they come close to each other should be zero), we expect $N(t)$ also to decay with a power law,

$$N(t) \sim t^{-\mu} \tag{7}$$

with exponent $\mu \leqslant \lambda - 1$. This should be compared with the power with which single clusters survive, $-\beta/\nu_t$ [2,4]. Thus, according to the conjecture, the difference in the powers is exactly 1, suggesting that the present algorithm is faster by one power of t.

In figure 2 we show, for $d = 2$ and $x - y = (1, 1)$, both $n(t)$ and $|\mathrm{d}N(t)/\mathrm{d}t|$. We used bond percolation where $p_c = \frac{1}{2}$ exactly. We see large deviations from power laws, but these deviations are the same for both curves. Obviously, if a pair of clusters dies, the chance that it dies because of rule (1) is finite and tends to a constant, and therefore

$$\mu = \lambda - 1. \tag{8}$$

If we accept this, we can obtain the most precise estimate of λ from $N(t)$. In any case, even if this is not correct, we obtain from $N(t)$ a lower bound on λ. Since we shall see that this lower bound is larger than the value conjectured by [5], this is sufficient to exclude the conjecture.

Results for $N(t)$ for $d = 2$ are shown in figure 3, for $x - y = (1, 1)$ and for $x - y = (1, 0)$. Each curve is based on $> 10^9$ runs with $T = 4000$, and took about 90 h CPU time on a fast workstation. In order to compare it with equation (6), we multiplied $N(t)$ by $t^{1+\frac{\beta}{\nu_t}}$, using the exact value $\beta = \frac{5}{36}$ [1] and the estimate $\nu_t = 1.5075 \pm 0.0004$ (corresponding to $d_{\min} = 1.1306 \pm 0.0003$). This estimate is based on new simulations which follow exactly the lines of [10], but have four times higher statistics. It is fully compatible with [10]. We see clearly that equation (6) is wrong since it gives too small a value. A precise estimate of λ is hampered by the very strong corrections to scaling visible in figure 3. Fitting these corrections by terms $\sim 1/t$ relative to the leading term and assuming that $n(t) \propto N(t)$, we arrive at

$$\mu = 1.1055 \pm 0.0010 \qquad \lambda = 2.1055 \pm 0.0010 \qquad g_1 = 1.041 \pm 0.001. \tag{9}$$
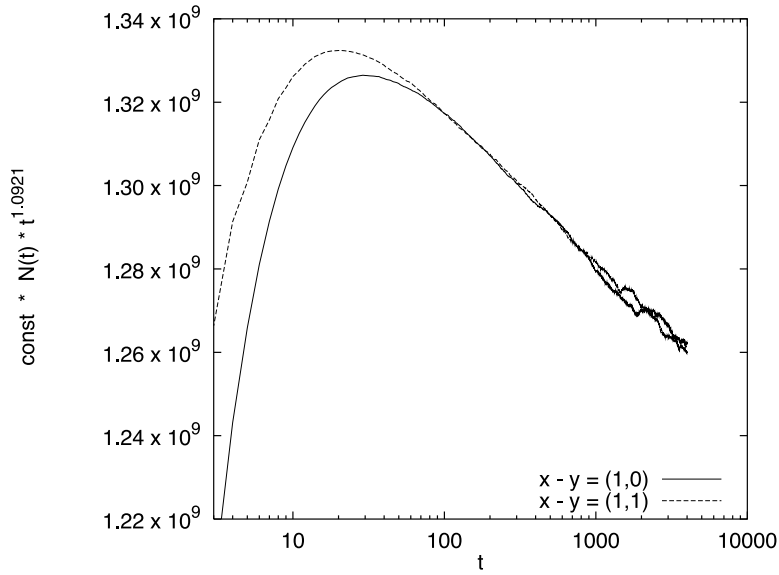
Figure 3. Plot of $N(t)t^{1.0921}$ for $d = 2$ with $x - y = (1, 0)$ (lower curve) and for $x - y = (1, 1)$ (upper curve). The numbers of configurations were chosen such that both curves coincide for large t. The exponent $1.0921 = 1 + \beta/\nu_t$ is such that the curves should become flat for large t, according to the conjecture of [5]. Relative statistical errors are $\approx 1/\sqrt{N(t)}$. For $t = 4000$, they are $\approx 2.6 \times 10^{-3}$.
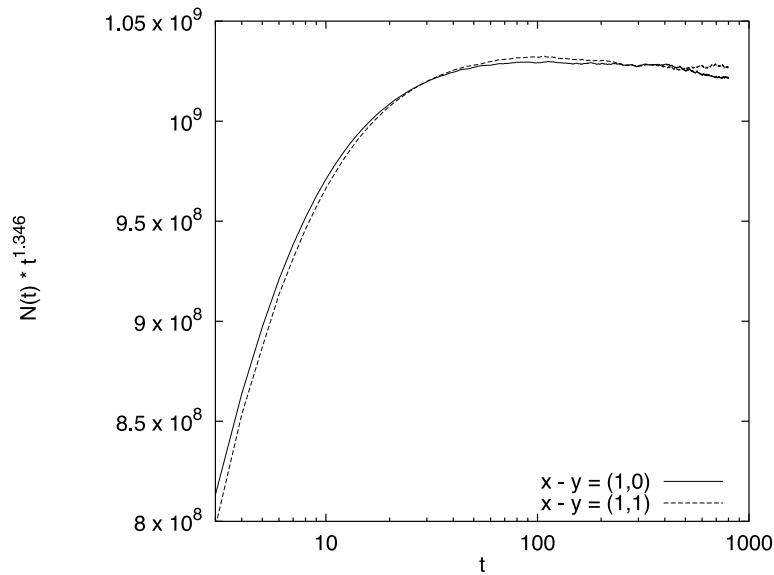

Figure 4. Similar to figure 3, but for $d = 3$. This time we used $\beta/\nu_t = 0.3467 \pm 0.0028$ from [4,9]. Relative errors for $N(t = 800)$ are $\approx 3 \times 10^{-3}$.

If we based the analysis on $n(t)$ instead of $N(t)$, we would get $\lambda = 2.105 \pm 0.002$, $g_1 = 1.041 \pm 0.003$.

A similar analysis for $d = 3$ is shown in figure 4. This time $T = 800$. For p_c we used the

value 0.248 8126 of [9]. The most precise value of β/ν_t can be obtained either by combining the value of z from [4] with the value of τ from [9,11], or by using directly the estimate of β/ν_t from [4]. The first gives $\beta/\nu_t = 0.3472 \pm 0.002$, the latter $\beta/\nu_t = 0.345 \pm 0.004$. In addition, we performed further simulations using the method of [4]. Together, all these combine to our final estimate $\beta/\nu_t = 0.347 \pm 0.002$. As seen from figure 4, the corrections to scaling are even worse than for $d = 2$, and the disagreement with equation (6) is much less pronounced. It seems that equation (6) is just barely compatible with our data which give, after taking into account the corrections to scaling,

$$\mu = 1.353 \pm 0.003 \qquad g_1 = 0.905 \pm 0.008. \tag{10}$$

We also tried to fit $N(t)$ by an exponential plus a constant, the latter corresponding to events where the two starting points are on different infinite clusters. We obtained $P_{\text{diff}} < 10^{-6}$ for $d = 2$ and $P_{\text{diff}} < 2 \times 10^{-6}$ for $d = 3$, both for $\boldsymbol{x} - \boldsymbol{y} = (1, 0)$ and for $\boldsymbol{x} - \boldsymbol{y} = (1, 1)$.

Finally, we should point out that the advantage of our two-seed algorithm over the naive one using a single seed is even more pronounced for supercritical percolation. There, the survival chance for an event decays exponentially with t, while it would not decay at all for the growth of a single cluster.

Acknowledgment

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