Logarithmic corrections in (4+1)-dimensional directed percolation

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We simulate directed site percolation on two lattices with 4 spatial and 1 time-like dimensions (simple and body-centered hypercubic in space) with the standard single cluster spreading scheme. For efficiency, the code uses the same ingredients (hashing, histogram re-weighing, and improved estimators) as described in Phys. Rev. E 67, 036101 (2003). Apart from providing the most precise estimates for $p_c$ on these lattices, we provide a detailed comparison with the logarithmic corrections calculated by Janssen and Stenull [Phys. Rev. E 69, 016125 (2004)]. Fits with the leading logarithmic terms alone would give estimates of the powers of these logarithms which are too big by typically 50%. When the next-to-leading terms are included, each of the measured quantities (the average number of sites wetted at time $t$, their average distance from the seed, and the probability of cluster survival) can be fitted nearly perfectly. But these fits would not be mutually consistent. With a consistent set of fit parameters, one obtains still much improvement over the leading log - approximation. In particular we show that there is one combination of these three observables which seems completely free of logarithmic terms.

I. INTRODUCTION

Although it is well known that all critical phenomena have logarithmic corrections at their upper critical dimensions, and although the leading terms are easily calculated from the renormalization group, it is in general not easy to verify these predictions numerically. In equilibrium models, one reason is that it is difficult to simulate a sufficiently large system in high dimensions, both because of storage and of CPU requirements. The other reason is that, together with powers of the logarithm of the system size $L$, one usually has also terms of type $\log \log L$ etc. If these are not known explicitly (and their computation is much more demanding), one has hardly any chance to verify the leading terms.

The situation is somewhat better in models with long range interactions [1] and in tricritical phenomena [2] where the upper critical dimension is lower than in ordinary critical phenomena. It is also better in models like self-avoiding walks or percolation, where one does not need to simulate the entire lattice, but only fractal objects with much lower dimension. For SAWs, e.g., it was possible to verify the structure of logarithmic corrections quite in detail [3], since there one only has to simulate walks with dimension two, and since the next-to-leading terms in the field theoretic treatment could be calculated.

In the present paper we study directed percolation (DP). There, the upper critical dimension is 5. When interpreted as a spreading phenomenon, this corresponds to 4 spatial dimensions. Critical clusters then have spatial fractal dimension $D_f = 2$, i.e. then it becomes also feasible to study systems with very large correlation lengths. In addition, the leading and next-to-leading logarithmic terms have been calculated recently from field theory [3], so that we have a good theoretical prediction to compare with.

We study only site percolation, but on two lattices: the simple hypercubic (shc) lattice in 4 dimension, and the body-centered hypercubic (bhc) lattice. The former has $2d = 8$ neighbours which can be infected in each time step, the latter has $2d = 16$ neighbours. We use the standard spreading paradigm where we start with a single infected site and infect in each time step neighbouring sites with probability $p$. Sites stay infective for one time step, after that they become again susceptible. We measure the average number $N(t)$ of infected sites, the r.m.s. distance $R(t)$ of infected sites from the seed site, and the probability $P(t)$ that there is still at least one infected site (i.e., that the cluster is still alive) at time $t$. The total sample sizes are $5.5 \times 10^7$ clusters for the shc lattice, and $1.5 \times 10^7$ clusters for the bhc lattice, both with $t_{\text{max}} = 8000$.

The code used to simulate this is very similar to the one used in [5] for high-dimensional ordinary percolation: 1) We used hashing to store very large virtual lattices. 2) In addition to the straightforward averages we also estimated in each run two averages obtained by re-weighing, corresponding to one $p$-value slightly above and to one $p$-value slightly below the point at which we simulate. This is equivalent to histogram re-weighing [6, 7], but avoids the need for storing huge histograms. 3) We used improved estimators for $N(t)$ and $R(t)$, as described in [5]. These estimators were found to lead to large variance reduction (the same concept was used recently also for random walks with memory, where it also gave substantial improvements [8]). These estimators were found to lead to large variance reduction. Essentially, the idea is not to measure the actual number of offsprings in each generation (and their distances from the seed), but to measure the estimated number of off-
springs per active site (and their estimated distances).
These estimates are made by counting the number of free neighbouring sites and multiplying it by $p$. This eliminates the fluctuations in the actual number of wetted sites resulting from the random number generator. Indeed, we found that the improved estimator gave not only smaller variances than the standard estimator, but that the covariances between the two happened to be negative (we have no explanation for this lucky coincidence). Thus we can optimize the estimator by taking that particular linear combination which has the smallest variance. The resulting errors for $N(t)$ are shown in Fig. 1. We see a reduction by roughly a factor 3, corresponding to a reduction of CPU time by a factor 10. The improvement was even larger (factor $\approx 4$) for $R(t)$. For $P(t)$ no similar improved estimator seems to exist.

II. RESULTS

Our main results are shown in Figs. 2 to 4. In each of them we show our results for the sc lattice together with the leading logarithmic term and with a fit based on the full analytic results of Janssen and Stenull. The integration constants $t_i$ appearing in the logarithms are the same for all three observables.

The results of Janssen and Stenull can be rewritten as

$$X_i = X_i^{(0)} \left[ \ln \frac{t}{t_0} - b \ln \ln \frac{t}{t_1} + a_i \right]^\alpha_i \times (1 + O((\ln \ln t/\ln t)^2, \ln \ln t/\ln^2 t, 1/\ln^2 t))$$

with $i = 1, 2,$ and $3$. Here,

$$X_1 = N(t), \quad X_2 = tP(t), \quad X_3 = R^2(t)/t,$$

the exponents $\alpha_i$ are equal to

$$\alpha_1 = 1/6, \quad \alpha_2 = 1/2, \quad \alpha_3 = 1/12,$$

the other known quantities are $b = 1.30204, a_1 = 0.1831, a_2 = -1.5193, a_3 = -1.7010,$ and $t_0$ and $t_1$ are unknown integration constants from the renormalization group flow. Notice that $t_0$ and $t_1$ are not universal (they differ between models), but they are the same for all observables within one model – although using different values of $t_i$ for different observables could effectively take into account of higher order corrections.

The first observation is that the leading logarithms alone are not sufficient to describe the data. Using only these terms, i.e. making ansatzes $X_i = X_i^{(0)}[\ln \frac{t}{t_0}]^{\alpha_i}$, we would overestimate $\alpha_P$ and $\alpha_R$ by roughly $50\%$. The constant $t_0$ can be chosen such that a nearly perfect fit

\[\text{FIG. 1: (color online) Log-log plot of statistical errors (one $\sigma$) of } N(t) \text{ against } t. \text{ The upper curves are for the usual estimates, the lower ones are for the optimized improved estimates.}\]

\[\text{FIG. 2: (color online) Average number of infected sites, } N(t), \text{ for the sc lattice. The three noisy curves are for } p = p_c \pm \Delta p_c. \text{ The other two curves show the leading log term } (\propto (\ln(t/t_0)^1/6 \text{ with } t_0 = 2) \text{ and the full prediction of Janssen and Stenull } [\text{I}], \text{ Eq. (1)} \text{ with } t_0 = 0.5, t_1 = 1.0.\]

\[\text{FIG. 3: (color online) Cluster survival probability multiplied by } t, \text{ } tP(t), \text{ for the sc lattice. The meaning of the curves is as for Fig. 2, except that the leading log term is } (\propto (\ln(t/t_0)^1/2 \text{ and that the three data curves are separated by } 4\Delta p_c. \text{ The values for } t_0, t_1, \text{ and } t_0' \text{ are the same as in Fig. 2.}\]
is obtained for $N(t)$ at large $t$. But this value of $t_0$ gives
bad results for the other two variables. Also, $N(t)$ is the
tool which depends most sensitively on the exact
value of $p_c$. It is mainly for the latter that we need high
statistics. Without a good estimate of $p_c$ we could not
get a decent estimate of the logarithmic corrections from
the leading terms alone. The same results were obtained
for the bchc lattice (not shown here). Our estimates for
$p_c$ are

$$p_c = 0.0755850 \pm 0.0000003 \quad \text{(bchc)},$$

$$p_c = 0.1461592 \pm 0.0000003 \quad \text{(shc).} \tag{4}$$

This is to be compared to Ref. [9], where the authors
studied steady state DP with a weak rate $h$ for “immigra-
tion” (i.e., sites are turned infective with a rate $h$, even
when they have no infected neighbour) and then
considered the limit $h \to 0$. The observable measured
in [9] was the density of infected sites. Such simul-
ations are of course much more cumbersome. In addition
to corrections from the limit $h \to 0$ one also has finite
size corrections which are completely absent in spread-
ing simulations. Indeed, the estimate for $p_c$ given in [9],
$p_c = 0.075582 \pm 0.000017$ for the bchc lattice, has an er-
ror about 60 times larger than ours. Nevertheless, very
good agreement was found in [9] when comparing with
the leading log terms only. We believe that this is a bit
fortuitous.

The error estimates in Eq.(4) are of course subjective,
as is true for all extrapolations and, in particular, also for
any critical exponents. To support the above estimates
we show in Fig.5 our values of $N(t)$, after having sub-
tracting from them the best fits using Eq.(1). In spite
of the very small error bars of the raw data, the fits are
perfect for $t > 20$. The lines seen in Fig.5 correspond to
$p_c \pm \Delta p_c$, with $\Delta p_c$ given in Eq.(4).

Unfortunately the fits used in Fig.5, although presum-
ably correct for large values of $t$ and therefore suitable
for estimating $p_c$, are not to be taken too seriously. This
is seen from the fact that using the same values of $t_0$ and
t_1$ would give rather poor fits for the other two observ-
able. As a good compromise we used $t_0 = 0.5$, $t_1 = 1.0$
in Figs. 2 to 4. We see that none of the three fits is
perfect, but all are quite reasonable and definitely give a
big improvement over the leading term. Thus we can
safely conclude that the field theoretic calculations of [4]
are verified by our simulations.

Equation (1) was indeed obtained in Ref.[4] by first
deriving parametric forms $X_t = X_i(w)$ and $t = t(w)$, and
then inverting the latter to $w = w(t)$. Since the
parametric representations are only to lowest orders, the inversion introduces errors which, although subdominant asymptotically, might be numerically large. Comparing directly with the parametric expressions (Eqs.(15) and the first lines of Eqs.(25), (31), and (44) in Ref. [4]) gives indeed significant further improvements for small $t$.

Before concluding, let us make two remarks. The first concerns hyperscaling. Usually, hyperscaling is formulated in terms of critical exponents. Writing $N(t) \sim t^\eta$, $P(t) \sim t^{-\delta}$, $R^2(t) \sim t^z$ at $p = p_c$, one expects for $d < d_c = 4$ that $dz/2 = 2\delta + \eta$. This is no longer true for $d > 4$ where $\eta = 0$, $\delta = 1$, and $z = 2$, but it still should hold in $d = 4$. Written in terms of the observables themselves, hyperscaling is equivalent (for $d < 4$) to

$$P^2(t)R^4(t)/N(t) \approx \text{const.}$$

From Eq.(1) we see that this should be violated by logarithmic terms at $d = 4$,

$$P^2(t)R^4(t)/N(t) \sim [\ln t]^{2\alpha_2 + 2\alpha_3 - \alpha_1} = \ln t. \quad (6)$$

We see from Fig. 6 that this product indeed increases strongly with $t$, but the increase is far from linear in $\ln t$. Thus, next-to-leading terms again are important. The corrections given in Eq.(1) give a big improvement, although they are not perfect. An interesting observation is that this product depends very weakly on $p$, making it thus an ideal test object for further non-leading logarithmic corrections.

The second remark concerns another product of $N(t), P(t)$, and $R(t)$. Using Eq.(1) we can form one combination (and of course all its powers) which contains, up to the order considered in Eq.(1), no logarithmic corrections at all. It is given by $\prod X_i^{\mu_i}$ with $\sum_1 \mu_i \alpha_i = \sum_1 \mu_i \alpha_i a_i = 0$. Numerically, we thus obtain that

$$N^{0.28931}(t) \left( \frac{R(t)}{t^{1/2}} \right)^{10.8427} / (tP(t)) \approx \text{const.} \quad (7)$$

We plot this combination in Fig. 7, together with a fit of the type $a + b/t^\Delta$. Numerically we found $\Delta = 0.75$. Of course one should not take this exponent very seriously (it could well be that the correct exponent is $1/2$ or $1$), but it seems rather convincing that logarithmic terms are completely absent. Notice that this is not trivial. A priori, we should have expected terms $\sim O(\ln \ln t/\ln t)^2, \ln \ln t/\ln^2 t, 1/\ln^2 t)$. This might hint at a special structure of the renormalization group flow, although this does not seem likely from the way in which Eq. (1) was derived [10].

III. SUMMARY

We have shown that improved algorithms for cluster spreading allow, even with rather modest effort (the total CPU time used for this paper was about 1 week on a fast PC), a rather stringent verification of logarithmic corrections at the upper critical dimension of one of the standard non-equilibrium critical phenomena. A prerequisite for this was, however, the availability of more than the leading log terms. If we would have had only the leading terms available for comparison (as was the case for the steady-state equation of state studied in [1]), even with much more CPU time only an order of magnitude verification would have been possible.

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