PHYSICAL REVIEW E **79**, 052104 (2009)

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

Peter Grassberger
John-von-Neumann Institute for Computing, Forschungszentrum Jülich, D-52425 Jülich, Germany
and Department of Physics and Astrophysics, University of Calgary, Alberta, Canada T2N 1N4

(Received 7 April 2009; published 26 May 2009)

We simulate directed site percolation on two lattices with four spatial and one timelike 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 reweighing, and improved estimators) as described by Grassberger [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.

DOI: 10.1103/PhysRevE.79.052104 PACS number(s): 64.60.ae, 64.60.ah, 05.40.−a, 64.60.Ht

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 also has 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 such as self-avoiding walks (SAWs) or percolation, where one does not need to simulate the entire lattice, but only the 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 the next-to-leading terms in the field-theoretic treatment could be calculated.

In the present Brief Report we study directed percolation (DP). There, the upper critical dimension is five. When interpreted as a spreading phenomenon, this corresponds to four 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 [4], so that we have a good theoretical prediction to compare with.

We only study site percolation, but on two lattices, the simple hypercubic (shc) lattice in four dimensions and the body-centered hypercubic (bchc) lattice. The former has $2d=8$ neighbors which can be infected in each time step, the latter has $2^d=16$ neighbors. We use the standard spreading paradigm where we start with a single infected site and infect in each time step neighboring sites with probability p. Sites stay infective for one time step, after that they become susceptible again. We measure the average number $N(t)$ of infected sites, the rms 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 5.5×10^7 clusters for the shc lattice and 1.5×10^7 clusters for the bchc lattice, both with $t_{\max}=8000$.

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 reweighing, 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 reweighing [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 offsprings per active site (and their estimated distances). These estimates are made by counting the number of free-neighboring 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 not only that the improved estimator gave smaller variances than the standard estimator but also that the covariances between the two happened to be negative (we have no explanation for this lucky coincidence). Thus

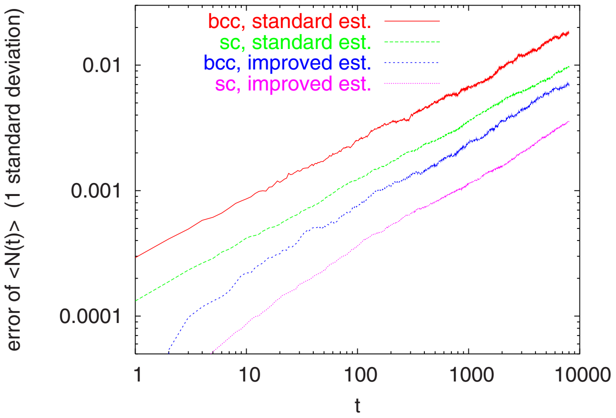

FIG. 1. (Color online) Log-log plot of statistical errors (one σ) of $N(t)$ against t. The upper curves are for the usual estimates, the lower ones are for the optimized improved estimates.

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 of 3, corresponding to a reduction in CPU time by a factor of 10. The improvement was even larger (factor of ≈ 4) for $R(t)$. For $P(t)$ no similar improved estimator seems to exist.

II. RESULTS

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

The results of [4] can be rewritten as

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

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

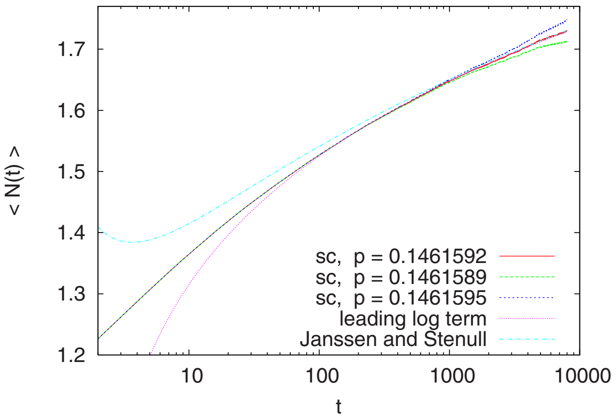

FIG. 2. (Color online) Average number of infected sites, $N(t)$, for the shc lattice. The three noisy curves are for $p = p_c$ and for $p = p_c \pm \Delta p_c$. The other two curves show the leading log term ($\propto [\ln(t/t_0')]^{1/6}$ with $t_0' = 2$) and the full prediction of Janssen and Stenull [4], Eq. (1) with $t_0 = 0.5$, $t_1 = 1.0$.

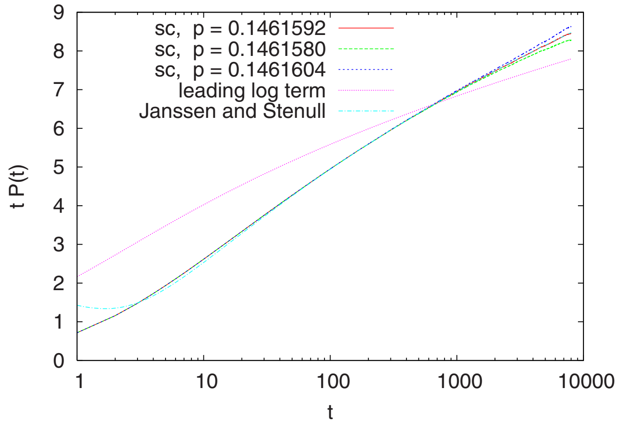

FIG. 3. (Color online) Cluster survival probability multiplied by t, $tP(t)$, for the shc lattice. The meaning of the curves is as for Fig. 2, except that the leading log term is $\propto [\ln(t/t_0')]^{1/2}$ and that the three data curves are separated by $4\Delta p_c$. The values for t_0, t_1, and t_0' are the same as in Fig. 2.

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

the exponents α_i are equal to

$$\alpha_1 = 1/6, \quad \alpha_2 = 1/2, \quad \alpha_3 = 1/12, \qquad (3)$$

the other known quantities are $b = 1.302\,04$, $a_1 = 0.1831$, $a_2 = -1.5193$, $a_3 = -1.7010$, 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 Ansätze $X_i = X_i^{(0)}[\ln\frac{t}{t_0}]^{\alpha_i}$, we would overestimate α_P and α_R by roughly 50%. The constant t_0 can be chosen such that a nearly perfect fit 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 variable which depends most sen-

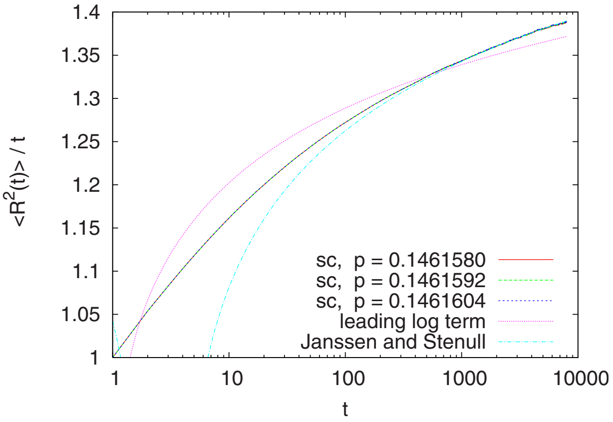

FIG. 4. (Color online) Squared cluster radius divided by t, $R^2(t)/t$, for the shc lattice. The meaning of the curves is again as for Fig. 3, except that the leading log term is $\propto [\ln(t/t_0')]^{1/12}$.

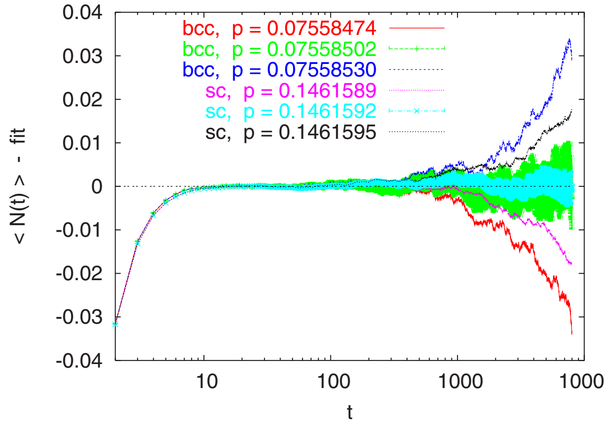

FIG. 5. (Color online) Difference between the average number of infected sites $N(t)$ and optimized fits with Eq. (1), both for the shc and for the bchc lattice. In the fit optimal values for t_0 and t_1 are used, although these values would give poor fits when used for $P(t)$ and $R(t)$.

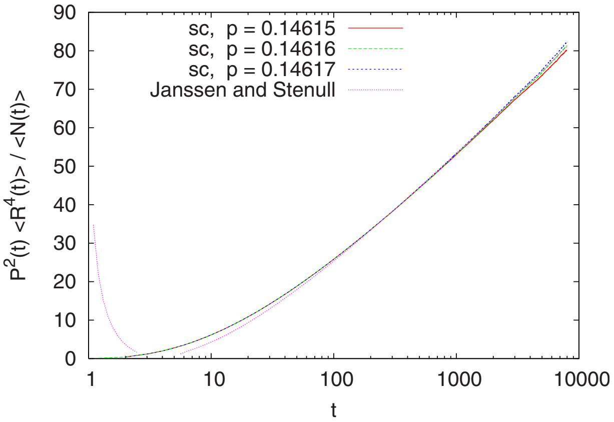

FIG. 6. (Color online) Product $P^2(t)R^4(t)/N(t)$ against t for the shc lattice. Notice that the three curves correspond to values of p whose difference is about 30 standard deviations. The leading logarithmic correction would be linear in ln t.

sitively 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

$$p_c = 0.075\,585\,0 \pm 0.000\,000\,3 \quad (\text{bchc}),$$

$$p_c = 0.146\,159\,2 \pm 0.000\,000\,3 \quad (\text{shc}). \tag{4}$$

This is to be compared to Ref. [9], where the authors studied steady-state DP with a weak rate h for "immigration" (i.e., sites are turned infective with a rate h, even when they have no infected neighbor), and then considered the limit $h \to 0$. The observable measured in [9] was the density of infected sites. Such simulations 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 spreading simulations. Indeed, the estimate for p_c given in [9], $p_c = 0.075\,582 \pm 0.000\,017$ for the bchc lattice, has an error of 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, which 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 subtracting 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 Δp_c given in Eq. (4).

Unfortunately the fits used in Fig. 5, although presumably 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 observables. As a good compromise we used $t_0 = 0.5$, $t_1 = 1.0$ in Figs. 2–4. 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 $X_i = X_i(w)$ 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 (Eq. (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

$$P^2(t)R^d(t)/N(t) \approx \text{const}. \tag{5}$$

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

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

We see in 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 nonleading 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 $\Pi_i X_i^{\mu_i}$ with $\Sigma_i \mu_i \alpha_i = \Sigma_i \mu_i \alpha_i a_i = 0$. Numerically, we thus obtain that

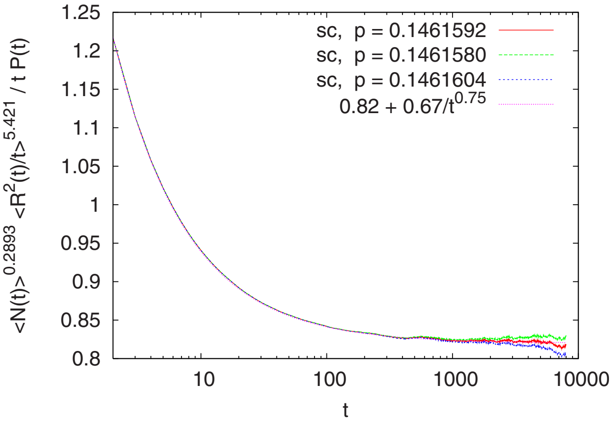

FIG. 7. (Color online) Product Eq. (7) against t for the shc lattice. The three data curves are for p_c and for $p_c \pm 4\Delta p_c$.

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

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 serious (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 Brief Report 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 nonequilibrium critical phenomena. A prerequisite for this was, however, the availability of more than the leading log terms. If we could have had only the leading terms available for comparison (as was the case for the steady-state equation of state studied in [9]), even with much more CPU time, only 1 order-of-magnitude verification would have been possible.

ACKNOWLEDGMENTS

I am indebted to Sven Lübeck and Richard Willmann for very stimulating discussions. Walter Nadler and Hannes Janssen critically read the Brief Report, and the latter pointed out some numerical mistakes. Finally, I want to thank an anonymous referee for suggesting an analysis directly based on the implicit parametric predictions of Ref. [4].

---

[1] E. Luijten and H. Messingfeld, Phys. Rev. Lett. **86**, 5305 (2001).
[2] J. Hager and L. Schäfer, Phys. Rev. E **60**, 2071 (1999).
[3] P. Grassberger, R. Hegger, and L. Schäfer, J. Phys. A **27**, 7265 (1994).
[4] H.-K. Janssen and O. Stenull, Phys. Rev. E **69**, 016125 (2004).
[5] P. Grassberger, Phys. Rev. E **67**, 036101 (2003).
[6] R. Dickman, Phys. Rev. E **60**, R2441 (1999).
[7] H. G. Ballesteros *et al.*, Phys. Lett. B **400**, 346 (1997).
[8] J. G. Foster, P. Grassberger, and M. Paczuski, New J. Phys. **11**, 023009 (2009).
[9] S. Lübeck and R. D. Willmann, J. Stat. Phys. **115**, 1231 (2004).
[10] H.-K. Janssen (private communication).