Local persistence in 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, AB, T2N 1N4, Canada
E-mail: p.grassberger@fz-juelich.de

Received 23 July 2009
Accepted 31 July 2009
Published 24 August 2009

Abstract. We reconsider the problem of local persistence in directed site percolation. We present improved estimates of the exponent of persistence in all dimensions from $1 + 1$ to $7 + 1$, obtained using new algorithms and using improved implementations of existing ones. We verify the strong corrections to scaling for $2 + 1$ and $3 + 1$ dimensions found in previous analyses, but we show that scaling is much better satisfied for very large and very small dimensions. For $d > 4$ ($d$ is the spatial dimension), the persistence exponent depends non-trivially on $d$, in qualitative agreement with the non-universal values calculated recently by Fuchs et al (2008 J. Stat. Mech. P04015). These results are mainly based on efficient simulations of clusters evolving under the time reversed dynamics with a permanently active site and a particular survival condition discussed by Fuchs et al. These simulations suggest also a new critical exponent $\zeta$ which describes the growth of these clusters conditioned on survival, and which turns out to be the same as the exponent, $\eta + \delta$ in standard notation, of surviving clusters under the standard DP evolution.

Keywords: critical exponents and amplitudes (theory), percolation problems (theory), persistence (theory)
1. Introduction

In general, persistence \[1\]–\[3\] in time-dependent critical phenomena is the probability that some observable does not cross its long-time expectation until some finite time \(t\). In particular, we will deal with the order parameter, which in directed percolation is the density and satisfies \(\langle \rho \rangle \to 0\) at the critical point. Local persistence \(P(r, t)\) is the probability that the local order parameter at position \(r\) does not cross this value up to time \(t\). In directed percolation it is thus equal to zero when the site \(r\) was active in the initial configuration, while it is positive and equal to the chance that it is not yet activated at \(t\) when it was inactive originally. In the following we shall only consider homogeneous systems in which case \(P(r, t)\) does not depend on \(r\) and will be written as \(P(t)\).

In general, local persistence decays according to a power law
\[
P(t) \sim t^{-\theta},
\]
(1)
where \(\theta\) is a new universal critical exponent, independent of the standard exponents. In particular, it is in general not related to the dynamical critical exponent \(z\) \[1\]–\[4\].

Previous studies of persistence (in the following we will only deal with local persistence) in the directed percolation (DP) universality class \[4\]–\[6\] have given somewhat contradictory results. In particular, superuniversality was suggested in \[6\], i.e. the possibility that \(\theta\) is independent of dimension. This was later refuted in \[4\]. For \(d = 1\), a connection with spreading of DP clusters in the presence of a wall was pointed out in \[5\], although no direct relation between \(\theta\) and critical boundary exponents for DP could be established.

In the following we shall again study this problem by means of numerical simulations. In spite of doubts concerning the universality of \(\theta\) \[4\], we restrict ourselves to site percolation on simple hyperbolic lattices. We use a new sampling strategy which is more time efficient than the standard strategy in low dimensions, and more space efficient in high dimension. In addition, we also made (for intermediate dimensions) simulations with a highly efficient implementation of the standard strategy. Finally, since it was crucial to simulate exactly at the critical point, we made new estimates of \(p_c\) (the percolation threshold) in dimensions \(1 + 2\) to \(1 + 7\). One of our findings is that \(\theta\) not only is not superuniversal, but also depends also non-trivially on dimension above the critical dimension for DP (which is \(d_c = 4\); in the following, we will always denote the spatial
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dimension by \( d \). The latter had been predicted in [4], where it was also suggested that \( \theta \) might be not universal at all for \( d > d_c \).

Our new sampling strategy suggests immediately a new critical exponent, called \( \zeta \) in the following. This exponent describes the growth of clusters under a modified evolution, where time is reversed, a permanent source of activity is added at the site at which persistence is measured, and a rule is added that clusters die when they hit the baseline [4,5]. The growth of the mass of such clusters, conditioned on their survival, can be described using an exponent \( \zeta \). As pointed out by Hinrichsen after this paper was written [7], a heuristic argument relates \( \zeta \) to a combination of standard DP exponents which can be rewritten, using hyperscaling and the standard notation for DP exponents [8], as

\[
\zeta = \eta + \delta. \tag{2}
\]

The rhs is the exponent which describes the mass growth of surviving critical DP clusters under normal (forward time, single-site seed) dynamics.

2. Algorithms and the exponent \( \zeta \)

In all simulations we used helical boundary conditions, i.e. the site is indexed by a single integer \( i \in [0, \ldots, N-1] \), where \( N \) is the size of the lattice. In all cases, \( N \) is chosen as a power of 2. Neighbors of \( i \) are indexed by \( i \pm 1, i \pm L_1, \ldots, i \pm L_{d-1} \), all modulo \( N \). The integers \( L_k \) are of order \( N^{1/d} \), but not necessarily equal to it (i.e. the lattice does not have to be an exact hypercube).

The standard way to simulate persistence uses four data structures:

- A bit (or, for implementation simplicity, byte) array of size \( N \), representing the activity pattern (\( s_i = 1 \) if site \( i \) is active, \( s_i = 0 \) otherwise), which is replaced at each time step by a new empty array. It is used for checking whether a site to be activated is already active or not.
- A list of indices of all active sites during the previous time step. This list is used to activate neighbors in the next time step.
- A similar list containing the active sites during the present time step, which originally is also empty and which will replace, after the time step is finished, the previous list.
- A bit array of size \( N \) representing the history of all sites: \( t_i = 1 \), if site \( i \) had been active during any previous time step, and \( t_i = 0 \) otherwise. This array is updated continuously, but erased only at the start of a new run.

The simulation proceeds then in the usual way, starting with the initial list of active sites (which can be a single site or a finite fraction of all sites) and simulating time step after time step, until either a maximal time is reached, all activity has died out, or until all sites have been activated at least once. For runs which start with a single active site, only a tiny fraction of the lattice will actually be activated when \( d \) is large. In that case a direct implementation of the bit arrays is wasteful of memory and is replaced by hashing. Details are discussed e.g. in [9].

While single-site starts are most efficient for locating the critical point [10], and were used for this also in the present work, they cannot so easily be used for measuring
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persistence. For the latter, starts with a finite density of active sites (say $\rho(0) = 1/2$) are most straightforward, but they require enormous memory in high dimensions, since hashing is of no use. If we want to have no finite-size effects, we have to use lattices whose linear size is larger than $t^{1/z}$, where $t$ is the simulation time and $z$ is the dynamic critical exponent which for DP is $z = \nu_\parallel/\nu_\perp < 2$. Even if we use multispin coding (i.e. 1 bit per site), we can only simulate rather short times on present-day workstations.

A way out of this dilemma is to use the time reversed process discussed in [4, 5]. The persistence probability $P(t)$ is defined as the probability that none of the space–time points $(i, t')$ for fixed $i$ and $0 \leq t' < t$ is activated by any of the active sites on the initial hypersurface $(i', 0)$. This means that if site $i$ is still persistent at time $t$, there cannot be any path of active sites (an analogue argument holds also for bond percolation) connecting any of the sites $(i, t')$ to any $(i', 0)$. But such paths, if they did exist, could also be followed in the opposite direction. Thus $P(t)$ is also equal to the probability that the cluster of sites activated by ‘sources’ on the line interval $\{(i, t'); -t \leq t' < 0\}$ does not survive to time 0.

This is implemented in the following recursive way (see figure 1). Let us denote by $C_t$ the cluster activated by the sites (‘seed’) $\{(i, t'); -t \leq t' < 0\}$, and by $H_0$ the hyperplane $\{(i', 0); 0 \leq i' < N\}$. We start with $t = 1$, in which case $C_t$ is just the site $(i, -1)$ plus all sites with $t' \geq 0$ connected to it. If $C_t \cap H_0$ is not empty, i.e. if the seed activates at least one site in $H_0$, we discard $C_t$ and start a new run. Otherwise, we add the site $(i, -t - 1)$ to the seed and activate all sites connected to it which are not already in $C_t$. The new cluster, which will be at least as large as $C_t$ but in general not much larger, is $C_{t+1}$ (or rather, due to the particularities of the lattices used in this paper, $C_{t+2}$; see the discussion at the end of this section). This is iterated until either the cluster intersects $H_0$ or until $t = t_{\text{max}}$ is reached.

It might seem at first that this is much more storage demanding than direct simulation, since we have to store now the entire space–time bit pattern, not only the spatial pattern at a fixed time. What saves us, however, is that the clusters are fractal with spatial fractal dimension of $\leq 2$, whence hashing will be very efficient.

While $P(t)$ is the chance that $C_t$ survives up to times that are $\geq t$, and thus $\theta$ describes its survival probability, the new critical exponent $\zeta$ describes the growth of its mass. There are several ways to describe this growth. The first, and maybe most natural would be to use the ansatz

$$M(t) \equiv \langle \#C_t \rangle \sim t^{\zeta_1}, \quad (3)$$

where $M(t)$ is the average mass of the still surviving clusters. Its main disadvantage is that contributions to $M(t)$ from early times might not scale, but decrease only slowly in importance as $t$ grows.

Alternatively we can define critical exponents via the increase of integrated quantities like $M(t)$, as this depends less on these non-scaling contributions. Thus in the following we will define $\zeta$ via the average number $m(t)$ of activated sites (except for the site at the tip of the cluster) during the step $C_{t-2} \rightarrow C_t$,

$$m(t) \sim t^{\zeta}. \quad (4)$$
Figure 1. Typical cluster of the time reversed process, where a segment of a line \( i = 0, -t \leq t' < 0 \) is the active seed. The growth is upward but in epochs, where each epoch corresponds to the downward extension of the seed by one site. The sites activated during the last epoch are given a different color. Notice that only every second site (arranged in a checkerboard pattern) is used for the process. Notice also that a straightforward growth of the cluster, without breaking it up into epochs, would be much less efficient. Typical clusters would be very fat, before applying the conditioning of not cutting constant-\( t \) hyperplanes, and most clusters would not meet the condition. The main virtue of the present algorithm is that such clusters are eliminated already at a very early stage.

If there were no correlation between the cluster mass and its survival probability, we would have obviously

\[
\zeta_1 = \zeta + 1.
\]

The same should still hold if there is exact scaling. Our numerics suggests that equation (5) is correct, but with large finite-\( t \) corrections. Apparent deviations from equation (5) will dominate our error estimates.
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In addition to its mass we can also measure other characteristics of the cluster, such as its spatial extension. As usual in time-dependent critical phenomena we can define \( z' \) as

\[
R(t) \sim t^{1/z'}.
\]

(6)

The same definition can also be used for ordinary DP clusters, where \( z = \nu_\parallel/\nu_\perp \) [8].

We measured \( z' \) for \( d = 1 \) and \( d = 2 \) and found \( z' = z \) within rather small error bars (\( z' = 1.5803(9) \) for \( d = 1 \), \( z' = 1.770(9) \) for \( d = 2 \); the corresponding values of \( z \) are 1.5807 [11] and 1.767 [12]). Thus we conjecture that \( z' = z \) exactly. The fact that critical exponents describing geometric aspects are more robust than others is also well known from standard critical phenomena, where entropic boundary exponents are different from bulk exponents, while correlation length exponents do not change near boundaries [13].

The relative efficiencies of direct simulations of half active lattices, on the one hand, and the simulation of single time reversed clusters, on the other hand, can be obtained by estimating the number of sites that have to be tested/activated to establish that one site persists up to time \( t \). In the direct approach this is

\[
n_{\text{tested}}^{\text{direct}} \approx \sum_{t'=0}^{t} \rho(t)/P(t) \sim t^{\theta+1-\delta},
\]

(7)

where \( \delta \) is the exponent for the decay of the density of active sites. For the time reversed cluster growth it is

\[
n_{\text{tested}}^{\text{reverse}} \sim t^{\zeta+1}.
\]

(8)

The ratio is

\[
n_{\text{tested}}^{\text{reverse}}/n_{\text{tested}}^{\text{direct}} \sim t^{\zeta+\delta-\theta}.
\]

(9)

If the exponent in this formula is negative, the time reversed cluster growth has less time complexity than the direct simulation.

Before leaving this section, let us make three remarks:

- For the estimates of \( p_c \) we used the variance reduction method described in [14, 15]. This gave particularly big improvements for \( d > 4 \).
- As noticed already in [4, 5], the regions left and right of the site at which persistence is measured are decoupled and can be treated independently. Thus the sites \( i' > 0 \) and \( i' < 0 \) in figure 1 can be simulated independently. The two sides contribute the same to \( M(t) \) and to \( \log P(t) \), so decay is much slowed down when only one half of the cluster is simulated and accuracy is substantially improved.
- For any \( d \) we use lattices where each bond changes only one of the spatial coordinates and, of course, time (more precisely, an active site can activate nearest neighbors in a simple hypercubic lattice at exactly one unit later time). Thus the lattices separate naturally into two checkerboard type sublattices. If activation is at the start restricted to one of them, it stays on it forever. Thus we can, without loss of generality, start with active sites restricted to one of the sublattices (for \( d = 1 \) this is clearly seen in figure 1). Again this divides the exponent \( \theta \) by a factor 2 as compared to simulations where both sublattices are active, and makes simulations easier. The values of \( \theta \) quoted below refer to activation restricted to one sublattice.

1 Unfortunately, in DP also \( 2/z \) is sometimes called \( z \).
Table 1. Main results. All values of \( p_c \) are new estimates, except the value for \( d = 1 \) which is from [11]. \( t_{\text{max}} \) is the maximum time over which clusters of the time reversed process are grown, and \( N_{cT} \) is the number of clusters grown in this way, including those which died before reaching \( t_{\text{max}} \). For \( d = 2 \) a large number of direct simulations were made, typically up to the same \( t_{\text{max}} \), and their results are also taken into account in the estimate of \( \theta \). The question mark for \( \theta(d = 3) \) indicates that the data are also compatible with some other relation (e.g. a stretched exponential) instead of a power law. The last column uses values from [8].

| \( d \) | \( p_c \) | \( \theta \) | \( \zeta \) | \( t_{\text{max}} \) | \( N_{cT}/10^9 \) | \( \eta + \delta \) |
|---|---|---|---|---|---|---|
| 1 | 0.705 485 22(4) | 1.5167(7) | 0.472(1) | 195 000 | 19.5 | 0.473 15 |
| 2 | 0.344 573 6(3) | 1.611(7) | 0.689(6) | 19 360 | 85.0 | 0.685(6) |
| 3 | 0.208 104 0(4) | 1.57(2) | 0.85(1) | 6 250 | 11.7 | 0.85(2) |
| 4 | 0.146 159 3(2) | 1.37(2) | 0.97(2) | 4 230 | 1.4 | 1.0 |
| 5 | 0.112 337 3(2) | 1.216(12) | 0.998(7) | 3 130 | 1.0 | 1.0 |
| 6 | 0.091 308 7(2) | 1.175(11) | 1.002(6) | 2 610 | 0.42 | 1.0 |
| 7 | 0.076 993 36(7) | 1.115(7) | 1.002(4) | 1 370 | 0.40 | 1.0 |

3. Results

Our main results are summarized in table 1. Except for \( d = 1 \), where extremely precise estimates of \( p_c \) are available from series expansions [11], we first made standard spreading simulations [10] where we measured the mass, survival probability, and r.m.s. radius of clusters grown from single-site seeds. For \( d = 4 \) we took into account the logarithmic corrections calculated in [16] in the same way as in [14]. Otherwise, we estimated the value of \( p_c \) by demanding that the total number of all active sites is a pure power law for large \( t \), up to possible corrections to scaling. Virtual lattice sizes were in each case \( 2^{64} \), which allowed for \( t \) values at least twice as long as those used for measuring persistence. The results are given in the second column of table 1.

Results for \( P(t) \) are shown in figure 2. The curves for \( d = 2 \)–7 show the raw data (multiplied by \( t^{1.5} \)), while the curve for \( d = 1 \) shows the square of the actually measured survival probability (see section 2). The data for \( d = 1 \) show by far the smallest corrections to scaling—they are well represented by a power law for \( t > 100 \). In contrast, for \( d = 2 \) and 3 we see the extremely strong deviations from scaling noticed already in [4]. A priori, the strongest deviations would have been expected for \( d = 4 \) since this is the upper critical dimension for DP, and we must expect logarithmic corrections there as for all other observables. It is completely unclear why the corrections to scaling are largest for \( d = 3 \) instead, and why they also seem to decrease most slowly with \( t \) (they seem more compatible with logarithmic corrections than with power-law terms). Indeed, the data for \( d = 3 \) taken by themselves might suggest a different relation between \( \theta \) and \( t \) than a power law, e.g. a stretched exponential. Although it is extremely unlikely from a theoretical point of view, we cannot really exclude this possibility. For \( d > 4 \) the corrections to scaling are still large, but exponents defined for them via

\[
P(t) \sim t^{-\theta} \left(1 + \frac{a}{t^\Delta}\right)
\]

(10)

doi:10.1088/1742-5468/2009/08/P08021
Values of $\theta$, with subjective error bars dominated by the uncertainties of parameterizing the scaling corrections, are shown in Table 1. While our estimates of $\theta$ are typically larger than those of [6], they agree with those of [4] with one minor exception: while $\theta > 1.62$ is quoted in [4] for the contact process for $d = 2$ (and extrapolating the corresponding curve in figure 3 of their paper would suggest indeed a value substantially larger than 1.62), we obtain 1.611(1) for $d = 2$. We believe that this is most likely due to an inaccurate value of the critical rate $\lambda_c$ used in [4].

Table 1 suggests that $\theta \to 1$ in the limit $d \to \infty$, as predicted analytically in [4]. But the agreement is not quantitative, as our values are much larger than those given by equation (14) of [4]. It might be that this is because the latter was derived for bond percolation, but this seems unlikely in view of the good agreement between exponents obtained for (site) DP and for the contact process. This agreement strongly suggests universality.

Log–log plots of the size $M(t)$ of inverse dynamics clusters $C_t$ against $t$ are shown in figure 3. To stress that $\zeta_1 = 2$ within statistical errors for $d > 4$, and to reduce the plotting range on the $y$-axis, we plotted actually $M(t)/t^2$. Notice also that points on the central line (which belong to $C_t$ trivially) are excluded from $M(t)$. We see strong deviations from pure power laws for all dimensions that are $\neq 2$, but the data are in all cases compatible with asymptotic power laws. Similarly large deviations from pure power laws are also seen in log–log plots of $m(t)$ versus $t$ (see figure 4), but the correction to scaling exponents $\Delta$, defined via equation (10), are systematically larger there. Thus extracting asymptotic power laws from figure 4 is easier than extracting them from figure 3, in spite of the larger statistical fluctuations. The asymptotic exponents extracted from figures 3 and 4 should be related by equation (5). For all dimensions this relation is roughly fulfilled, with the
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Figure 3. Estimates of $M(t)/t^2$ against $t$, for $d = 1$ (bottom) to $d = 7$ (top). Here $M(t)$ is the number of active space–time sites (excluding the centerline) in inverse dynamics clusters $C_t$.

Figure 4. Estimates of $m(t)/t$ against $t$, for $d = 1$ (bottom) to $d = 7$ (top). Here $m(t)$ is the number of active sites (excluding the centerline which is always active) added to the inverse dynamics clusters $C_t$ during the step $(t-2) \rightarrow t$. To reduce statistical fluctuations, data have been binned with $\Delta t/t \approx 0.03$.

resulting estimates quoted in table 1. The errors quoted there are mostly reflecting the discrepancies between the estimates based on figures 3 and 4.

After submission of this paper, it was pointed out to me by Hinrichsen [7] that $\zeta$ can be related to standard exponents. If we assume that the density in the time reversed cluster decays radially, from a value near unity, as $r^{-z\delta}$ with a radial cutoff at $r_c \sim t^{1/z}$,
then
\[ \zeta = d/z - \delta. \]  \hfill (11)

Using the hyperscaling relation \( d/z = 2\delta + \mu \) for \( d \leq 4 \), where \( \eta \) describes the average number of active sites in single-site seeded DP clusters [8], this can be written as
\[ \zeta = \eta + \delta. \]  \hfill (12)

While equation (11) can only hold for \( d \leq 4 \) (for \( d > 4 \) the assumption of a power-law radial density decay from a value of order unity must fail), equation (12) seems to hold for all dimensions. To demonstrate this, we quote in the last column of table 1 the values of \( \eta + \delta \) from [8]. In all cases, agreement holds to better than two standard deviations. Notice that equation (12) is very surprising. It says that two cluster growth mechanisms which seem to have no close relationship, and for which the cluster survival probabilities scale with different critical exponents, have nevertheless the same growth exponents after conditioning on survival.

Finally, let us discuss the relative time complexities of direct and time reversed (single-cluster) simulations using equation (9) and the critical exponents given in table 1 and in [8]. For \( d = 1 \) we find that the time reversed simulation is much more efficient, by a factor \( \sim t^{0.9} \). Thus one gains several orders or magnitude in CPU time. The same is qualitatively true for \( d = 2 \), although the difference is much less: only a factor \( \sim t^{0.4} \). For \( d = 3 \) the two methods have the same time complexity, and for \( d > 3 \) the ranking is reversed—quite substantially \( (t^{-0.9}) \) for \( d = 7 \). Thus direct simulations would be much faster in high dimensions, if we could solve the space complexity (memory limitation) problem. The other advantage of time reversed simulations is of course that they offer the unique possibility to measure the exponent \( \zeta \).

4. Discussion

We presented in this paper numerical estimates for the local persistency exponent \( \theta \) in DP. These estimates are more precise than previous ones for spatial dimensions \( d \leq 4 \), and are the first published ones for \( d > 4 \). The latter were made possible by a combination of hashing (virtual memory) and a novel way to simulate the growth of the time reversed clusters discussed in [4,5]. The latter algorithm suggested also very naturally another new critical exponent, \( \zeta \). It seems that \( \theta \) and \( \zeta \) are not trivially related, but that \( \zeta \), which describes the cluster growth of an artificial time reversed evolution with modified dynamics, is the same as the usual DP exponent describing mass growth of active clusters. While this is supported both by an indirect heuristic argument and by numerics, it seems very surprising and not well understood intuitively.

We verified the very large corrections to scaling seen in previous analyses of local persistency in DP, in particular for two and three spatial dimensions. Indeed, these corrections seem to be larger for \( d = 3 \) than for \( d = 4 \), where we would have expected \textit{a priori} that logarithmic corrections should give the strongest deviations from a pure power law. Although we see no theoretically appealing scenario for it, the data alone would suggest that the asymptotic behavior of \( P(t) \) in three dimensions is not described by a power law at all, but rather by a stretched exponential or something similar.
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In the present paper we dealt only with directed percolation, but very similar problems can also be studied for ordinary (undirected) percolation. The situation is maybe best described in two dimensions (analogous to one spatial plus one temporal dimension in DP). Let us consider a wedge cut out from a square lattice, with edges $W_1$ and $W_2$ meeting in point $P$ and extending to infinity away from $P$. The angle between $W_1$ and $W_2$ is $\alpha$. Let us furthermore consider intervals $I_1$ and $I_2$ on $W_1$ and $W_2$, respectively, with lengths $\ell_1$ and $\ell_2$. We can then ask for the probability $P(I_1, I_2, \alpha)$ that there is no path from any point on $I_1$ to any point on $I_2$. This is complementary to the probability that there is a path from $I_1$ to $I_2$. Probabilities of the latter type (called ‘crossing probabilities’) were studied extensively [17]–[19], but it seems that neither $P(I_1, I_2, \alpha)$ nor its generalizations to higher dimensions were studied previously.

Acknowledgments

I am indebted to Purusattam Ray for introducing me to this subject and for pointing out [4]. Without his encouragement and insistence I would not have started this work. I also want to thank the Chennai Institute of Mathematical Sciences, where this work was begun, for its hospitality and stimulating atmosphere. But most of all I am indebted to Haye Hinrichsen for pointing out to me equation (11), and for allowing me to use this unpublished result in the present paper.

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doi:10.1088/1742-5468/2009/08/P08021