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LETTER TO THE EDITOR

Scaling of overhangs in $(1 + 1)$ -dimensional directed processes in a gradient

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Abstract. When a gradient is imposed in the control parameter of a directed process in a $(1 + 1)$ -dimensional directed process, a front may occur. The position of this front evolves in steps of size one in the direction opposite to the gradient, and in steps of size equal to or larger than one in the other direction. The larger steps are due to overhangs. There is a critical value for the control parameter only if the first moment of the step size distribution in the direction of the gradient is *not* singular—i.e. it takes on a finite value in the ‘thermodynamic’ limit. If there is a critical point, this step-size distribution is a power law at this point, with an exponent larger than two, and which we conjecture to be equal to $3 - \beta/\nu_{\perp}$. β is the order parameter exponent, and ν_{\perp} is the spatial correlation length exponent. In a finite gradient there is a second exponent governing the upper cut-off in the step-size distribution. This exponent is equal to $\nu_{\perp}/(1 + \nu_{\perp})$. These two exponents govern the convergence of the position of the front towards the critical value of the control parameter. We exemplify our discussion with directed site percolation, and with two versions of a model originally designed to study catalytic reactions.

Cellular automata [1]—or more generally directed processes—possessing a critical point for a certain value of some control parameter are abundant. They are appealing in that besides being easy to study on a computer, their dynamics may be complicated enough to encapsulate all the intricacies of non-equilibrium phase transitions. Examples of such models include, apart from directed percolation [2], inhomogeneous deterministic cellular automata such as the Kauffman model [3]. In these models the critical point separates a chaotic phase sensitive to the initial conditions—known as the damage-spreading phase—from a non-chaotic one [3]. Other examples are models constructed to study catalytic chemical reactions [4, 5], or fully developed hydrodynamic turbulence [6]. In these models the critical point separates an active—or turbulent—phase from a ‘poisoned’—or laminar—phase.

The gradient method, originally invented by Sapoval *et al* [7], has been used for two of the above-mentioned systems besides percolation [8] to determine the critical value of the control parameter, namely directed percolation [9] and damage spreading [10]. In this method the control parameter varies linearly in some direction along the network of nodes. In $(1 + 1)$ dimensions—i.e. one spatial and one temporal dimension—this direction is along the chain of nodes. If there exists a critical point for some value of the control parameter, a front will appear separating the two phases somewhere along the chain. The mean position of this front defines an effective critical value of the control parameter and, in the limit of zero gradient, this effective threshold value will converge to the critical value of the control parameter. If p_{eff} is the effective

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threshold, and p_c is the critical value of the control parameter p , we expect the convergence

$$p_{\text{eff}}(g) = p_c - Bg^x + \text{corrections} \quad (1)$$

when g , the gradient in p , becomes small.

In practice, this means that *three* parameters have to be determined: p_c , A and the exponent x . Since one has no control over the expected corrections to scaling, some of the potential accuracy of the method is lost. The exponent x has been found for two-dimensional percolation [11]. One aim of this letter is to provide a method to identify not only the exponent of the leading correction term, ag^x , but also the exponents governing the terms of higher order for a general $(1+1)$ -dimensional directed process. As will be apparent from our numerical results, the second correction to scaling term is *larger* in magnitude than the leading term ag^x for the system sizes we work with.

For concreteness, let us in the following discuss the special case of directed (site) percolation [2]. Suppose we have a square lattice placed at 45° compared with its lower boundary. The nodes in this lattice are then 'filled' with probability p or 'empty' with probability $1-p$. We define an X axis parallel to the lower boundary, and a 'time' axis perpendicular to it. The lattice is in a percolating state at a 'time' T if there is at least one node connected to the lower boundary through a continuous path only touching filled nodes. This particular node is said to be percolating. In the thermodynamic limit, there is a critical p_c such that for $p > p_c$, there will always be percolating nodes for any T . For $p < p_c$ there will be no percolating nodes in the limit $T \rightarrow \infty$. Numerically [12], and by series expansion [13], the percolation threshold has been determined to be $p_c = 0.7055$ (1). Domany and Kinzel [14] recognised that directed percolation is equivalent to a cellular automaton of the following type. For each node choose a random number between 0 and 1. If this number is less than the parameter p , and at least one of the neighbours of this node is 1 at the previous time step, set this node to 1. Otherwise, set it to 0. This updating is done simultaneously for all the nodes in the chain. The initial state of the cellular automaton is chosen to be all nodes in state 1. We will discuss directed percolation in this language.

Suppose now that the chain of nodes has a length L . Furthermore, choose a constant gradient $g = 1/L$ so that $p = 0$ for the leftmost node, and $p = 1$ for the rightmost node. Thus, at node X , $p = X/L$. As the directed-percolation cellular automaton is run, a front develops if there is a critical $p = p_c$. The mean position—averaged over time—of this front defines an *effective* threshold $p_{\text{eff}}(g) \rightarrow p_c$ as $g \rightarrow 0$, as described through (1).

At a time T , the front is situated at node X_T (measured from the leftmost one). At the next time step, $T+1$, the front can either move one step to the left with probability $p = X_T/L$ or one step to the right with probability $p(1-p)$. In addition, the front may also make jumps of j steps to the right, where $j \geq 2$. These larger jumps are due to the appearance of 'overhang', caused by the merging of clusters of non-percolating nodes along the front, as shown in figure 1.

We define $N(j, g)$ to be the probability of having a jump of size j . Here $j = -1$ denotes a step to the left, $j = 1$ a step of size one to the right, and $j \geq 2$ a jump to the right due to an overhang.

The mean position of the front, which defines $p_{\text{eff}}(g)$, is constant if the mean step size is zero:

$$\sum_{j=-1}^{1/g} jN(j, g) = 0. \quad (2)$$

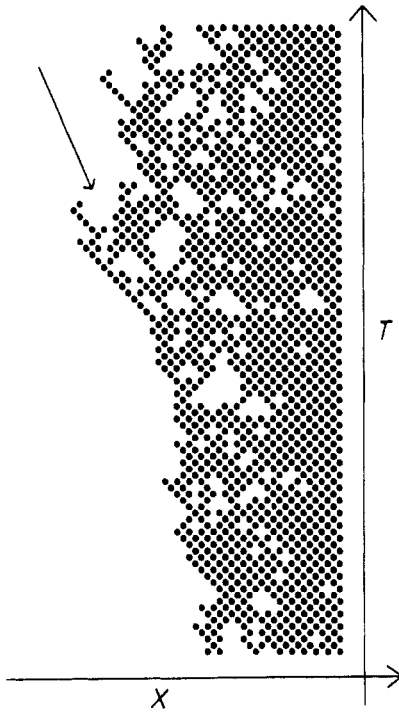


Figure 1. The appearance of an overhang leads to a jump in the position of the front from one time step to the next one.

We also have that

$$N(-1, g) = p_{\text{eff}}(g). \quad (3)$$

This is so since the probability of jumping to the left from a position $X_f = pL$ is p . The average probability of jumping to the left must then be equal to $\langle X_f \rangle / L = p_{\text{eff}}$. This probability is of course nothing but $N(-1, g)$, and (3) follows. Combining (2) and (3) we get

$$p_{\text{eff}}(g) = \sum_{j=1}^{1/g} jN(j, g) = \langle j(g) \rangle \quad (4)$$

where $\langle j(g) \rangle$ denotes the average step size *to the right*.

We are now at the very heart of the analysis we are presenting: Through (4) we see that whatever scaling behaviour for small gradients we find for p_{eff} , it will be the same for the average jump size to the right, $\langle j(g) \rangle$. Equation (1) was written down for directed site percolation, but the arguments leading to (2), are general and valid for all directed (1+1)-dimensional processes. Equation (3) is, however, not generally valid. An example is the Browne-Kleban process [5] in the Monte Carlo update version, to be discussed below. In this case $N(-1, g)$ is a more complicated function of p_{eff} than (3). However, if this function is analytic, the conclusions we draw in this letter concerning (1) are still valid.

The model of Browne and Kleban describes a one-component catalytic reaction occurring on a surface. The model is updated as follows: each node along the chain may be in a state either 'covered' (1) or 'uncovered' (0). At random we choose a node

for updating. If the state is 'covered', we do nothing to the node and go on to choose another one. If the node is 'uncovered', and it has no neighbours that are 'covered', we set the node to 'covered'. If one neighbour is 'covered' we set the node to 'covered' with probability p , or with probability $1-p$ we leave the node 'uncovered' and set the neighbouring 'covered' node also to 'uncovered'. If both neighbouring nodes are 'covered', we set the node to 'covered' with probability p and with probability $1-p$ leave the node 'uncovered' and set one of the neighbours—which one is chosen at random—to 'uncovered'. There is a critical p_c such that for $p > p_c$, all the nodes will end up in the state 'covered' in a finite time, and for $p < p_c$ there will always be 'uncovered' nodes for an infinite system. p_c has been determined to be 0.2762 (5) previously [5, 15].

In order to be able explicitly to write down a balance equation for this type of model, we have devised a simultaneous-update version of the Browne-Kleban model. The updating of *neighbouring* nodes to the one chosen in the Monte Carlo procedure, translates in this model to nearest and *next-nearest* interactions. There is, however, no unique way of transcribing the Browne-Kleban model. The problem is that a node is simultaneously neighbour to two other nodes, besides having two neighbours. Thus, during one update, conflicting values to a given node may be assigned. This problem is solved by choosing an 'order of importance' to the various possibilities. Our choice was to let a site stay 'covered' in such a conflict. The resulting behaviour of this cellular automaton is rather surprising. It turns out that uncovered nodes always move *in pairs*. The equation corresponding to (4) in this model reads

$$1 - p_{\text{eff}}(g) = \langle j(g) \rangle. \quad (5)$$

The asymptotic behaviour of the effective threshold is thus, in light of this discussion, closely related to that of the step-size distribution. We make the following scaling *ansatz* for this distribution:

$$N(j, g) = j^{-a} f(jg^b) \quad (6)$$

where a and b are two scaling exponents, and the function f has the limiting behaviours $f(z) \rightarrow \text{constant}$ for $z \rightarrow 0$ and $f(z) \rightarrow 0$ faster than a power law for $z \rightarrow \infty$. The existence of a finite threshold p_c leads to a lower bound on the exponent $a \geq 2$, since the sum $\langle j(g) \rangle = \sum_{j \geq 1} j N(j, g)$ must be dominated by the small values of j .

In order to determine the two exponents a and b in the step-size distribution, we calculate two moments, $\langle j^k(g) \rangle = \sum_{j \geq 1} j^k N(j, g)$, for large enough k so that the sums are dominated by the large j . These sums may then be approximated by the integrals, $\langle j^k(g) \rangle \approx \int_1^\infty j^k N(j, g) dj$. These integrals behave as

$$\langle j^k(g) \rangle = A_k g^{b(a-k-1)} \quad (7)$$

where A_k is a constant independent of the gradient g . In figure 2 we demonstrate the scaling of the third, fourth and fifth moments in the case of directed site percolation. Table 1 shows deduced exponents a and b for the three models we have studied. This table indicates that these three models belong to the same universality class. This result is consistent with the findings of Aukrust *et al* for the Monte Carlo update version [15].

We now turn to the question of relating the exponents a and b to more familiar exponents. The exponent b governing the cut-off length in the jump size distribution is the easiest to recognise: it must be the same as the one governing the width of the front $W(g) = \langle (X_f - \langle X_f \rangle)^2 \rangle^{1/2} \sim g^{-\gamma}$, since there is only one length scale governing the

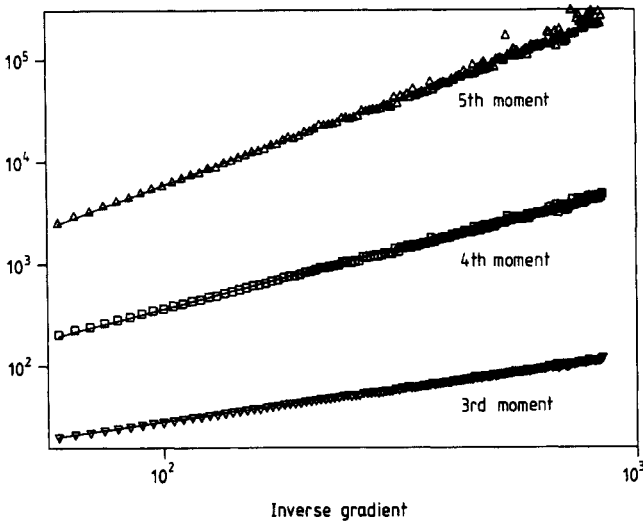


Figure 2. The third, fourth and fifth moments of the jump size distribution for directed percolation as a function of the inverse of the gradient g . Also shown are the predicted curves from (4).

Table 1. The exponents a and b governing the jump size distribution for directed site percolation (DP), the Browne-Kleban model with Monte Carlo updating rules (MBK), and the Browne-Kleban model with simultaneous updating (SBK). These data are based on simulating these directed processes on lattices with L varying from 10 to 250, and 10^6 time steps in the case of the DP and SBK models. For the MBK model 5×10^5 Monte Carlo updates were done. One sample for each model was generated.

	DP	MBK	SBK
a	2.75(2)	2.65(10)	2.80(10)
b	0.53(1)	0.51(5)	0.51(5)

development of the front. The exponent y has been determined by Sapoval *et al* [7] to be

$$y = \frac{\nu_{\perp}}{1 + \nu_{\perp}} \tag{8}$$

where ν_{\perp} is the spatial correlation length exponent.

The value of ν_{\perp} is 1.097 2(4) for directed percolation [16], leading to $y = 0.523$ 2(5). This value should be compared with those found for b quoted in table 1.

The exponent a reflects the structure of the clusters of *non-percolating* or ‘covered’ nodes, and we conjecture that it is related to the order parameter exponent β in the following way:

$$a = 3 - \beta / \nu_{\perp}. \tag{9}$$

Our argument runs as follows. The size distribution of clusters of non-percolating nodes—or ‘covered’ nodes—along the X axis is given by [6] $H(h) \sim h^{-(2-\beta/\nu_{\perp})}$. This exponent is the fractal dimension of the self-affine set that the percolating nodes form.

The next step in this argument is to assume that the jumps sample an undistorted cluster size distribution. The jump measures the width of a cluster at the point where the barrier of percolating nodes separating it from the front disappears. When constructing the histogram $H(h)$ the clusters of non-percolating nodes (measured along the X axis) is sampled at every time step. However, the sampling of the cluster sizes in terms of the jumps are sampled *once per merging cluster in the T direction*. Thus, in order to take this bias into account the histogram $H(h)$ must be divided by h to be compared with the jump size distribution $N(j)$: $N(j) = H(j)/j$. This leads to (9). For directed percolation [6] $\beta = 0.280(4)$ leading to $a = 2.745(4)$ by using (9). Again, this value should be compared with those listed in table 1.

We now return to the question of the scaling exponent x appearing in (1). Through the balance equation (2), this scaling exponent must also appear in the scaling of the first moment of the jump size distribution. If we expand the first moment of the jump size distribution in g assuming $f(z)$ is analytic in z as $z \rightarrow 0$, we find

$$\langle j(g) \rangle = \sum_{j=1}^{1/g} jN(j, g) = A - Bg^{b(a-2)} + Cg^b + \dots \tag{10}$$

The second term in this equation comes from the upper limit of this sum, while the third term comes from the lower limit.

Thus, we recognise A as p_c , the exponent $b(a-2)$ as the exponent x , and the exponent b as the first correction to scaling exponent. We show a plot of p_{eff} as a function of g , with the predicted behaviour from (10) for directed site percolation superposed in figure 3: $p_{\text{eff}} = 0.7055 - 0.0912g^{0.390} - 1.11g^{0.5232}$. It is interesting to note that the prefactor of the leading term in this expression is much smaller than the correction to scaling term. Thus, without knowing the correction to scaling exponents $b(a-2)$, b, \dots one would identify x with b . A least squares fit *assuming* $p_c = 0.7055$ gives $x = 0.51$, which is very close to $b = 0.5232$ rather than $b(a-2) = 0.390$. We also note that higher-order corrections to scaling in the effective threshold may also be

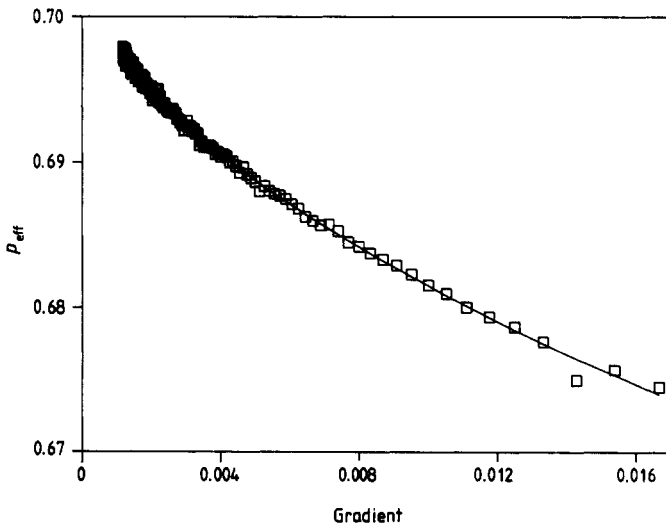


Figure 3. The effective threshold p_{eff} for directed percolation as a function of g measured directly (\square) and as predicted from (10) (full curve).

calculated from (10). A similar fit for the Browne-Kleban model gives $p_{\text{eff}} = 0.276 - 0.100g^{0.390} - 0.792g^{0.532}$.

We have through this method a way to find the exponent β if it is not known beforehand, independently of any knowledge of the critical value of the control parameter p . Our present work on these ideas has been restricted to (1 + 1)-dimensional directed processes. However, it would be natural to generalise them to other dimensions, and to *non-directed* processes.

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