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LETTER TO THE EDITOR

On the spreading of two-dimensional percolation

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Abstract. New high statistics measurements of the spreading dimension $\hat{d}$ for two-dimensional percolation are presented. The value $\hat{d} = 1.675 \pm 0.005$ excludes, in particular, a recent conjecture of Havlin and Nossal.

Some time ago, Middlemiss *et al* (1980, see also Alexandrowicz 1980, Pike and Stanley 1981) introduced several new critical exponents for percolation. They measure essentially how the infinite cluster is unveiled if one starts at an arbitrary initial point on it, and constructs the cluster by adding layer by layer in discrete time steps. In each step, all sites are added which are on the boundary of the part already constructed, and which are occupied (resp., in bond percolation, which are connected to the already constructed part by unbroken bonds). These latter sites are called 'growth sites'.

Interesting aspects are e.g. the increase of the cluster mass M_t unveiled at time t, given at $p = p_{cr}$ by a scaling law

$$M_t \sim t^{\hat{d}}, \tag{1}$$

and the growth of its average radius R_t, given by

$$R_t \sim t^{\nu/\nu_\parallel}. \tag{2}$$

The same exponents were later studied independently by Grassberger (1983) (called I in the following), and were computed for $d = 2$ by Monte Carlo simulations. The accuracy was comparable to that of Pike and Stanley (which was much higher than that of Alexandrowicz and of Middlemiss *et al*) but the results were not in agreement.

In I, this kind of cluster growth was interpreted as the spreading of an epidemic with short infectious period (one time step) and with permanent immunisation. The exponent $\nu/\nu_\parallel$ measures then the increase of affected area ($\nu_\parallel$ was called τ in Alexandrowicz (1980) and in I), while the exponent $\hat{d}$ measures the increase of the number of affected individuals (the 'size' of the epidemic (Bailey 1975)). We shall follow Vannimenus *et al* (1984) and call $\hat{d}$ the spreading dimension.

Paper I contained also a detailed formulation of hyperscaling relations (see also Havlin and Nossal 1984), showing that there is indeed only one exponent in addition to the exponents known previously. The spreading dimension, although not considered explicitly there, is found from these scaling relations to be

$$\hat{d} = (2\nu - \beta)/\nu_\parallel. \tag{3}$$

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More recently, several authors (Hong and Stanley 1983a, b, Havlin and Nossal 1984, Herrmann *et al* 1984, Vannimenus *et al* 1984, Angles d'Auriac *et al* 1984, Rammal *et al* 1984, Stanley 1984) have again taken up this problem. Monte Carlo calculation of supposedly comparable statistics to that of I and of Pike and Stanley (1981) have been presented, again with mutually exclusive results. In addition, Havlin and Nossal conjectured an exact relation which can be written as

$$\nu_{\parallel} = 2\nu - 1 - \beta \qquad \text{(Havlin-Nossal conjecture)}. \tag{4}$$

Inserting here the values (Nienhuis 1984) $\nu = \frac{4}{3}$ and $\beta = \frac{5}{36}$ for $d = 2$, we would obtain $\nu_{\parallel} = 1.5278$.

Although the above conjecture can be shown to be wrong in the $\varepsilon \equiv (6-d)$ expansion (Cardy and Grassberger 1985), we found the situation sufficiently confused to justify a new precise Monte Carlo measurement in two dimensions, the details of which will be described below.

The results for $\hat{d}$ and $\nu_{\parallel}$ are shown in table 1, together with previous estimates. We see that the Havlin-Nossal conjecture is violated by 3 standard deviations. Also, several of the Monte Carlo estimates mentioned above are incompatible with our values.

Table 1. Spreading dimension and exponent $\nu_{\parallel}$ for two-dimensional percolation. Values obtained by using as constraints the scaling relations of I are marked by an asterisk.

Reference	$\hat{d}$	$\nu_{\parallel}$
Alexandrowicz (1980)	1.69 ± 0.05	1.57 ± 0.10
Pike and Stanley (1981)	1.64 ± 0.02	1.49 ± 0.02
Grassberger (1983)	1.69 ± 0.02*	1.494 ± 0.015*
Hong and Stanley (1983a)	—	1.38 ± 0.1
Hong and Stanley (1983b)	—	~ 1.55
Havlin and Nossal (1984)	1.64 ± 0.02	1.54 ± 0.05
Rammal *et al* (1984)	1.72 ± 0.02	—
Herrmann *et al* (1984)	—	1.46 ± 0.07
This work	1.675 ± 0.005*	1.509 ± 0.004*

The method employed in the present paper is essentially the same as in I. In particular, we study bond percolation on a square lattice, in order to use the fact that the percolation probability is known rigorously (Kesten 1980) as $p_{cr} = \frac{1}{2}$. Also, we do not build the infinite cluster by starting from a single centre point. Instead, we start from a whole line of wetted sites, and unveil layer by layer the points connected to that line. Boundary conditions are chosen periodic, i.e. we actually consider a cylinder, starting with a wetted circumference and watching the spread parallel to the axis. A typical pattern formed in this way is shown in figure 1. The growth sites are indicated by heavy dots; the sites whose connection to the line $x = 0$ is already established are shown as light dots.

We should point out that in this way we do not obtain the infinite cluster only. Instead, we obtain all sites connected to the original line, even if they belong to finite clusters. This is however no problem, since the relevant scaling laws were already formulated in I. In particular, the number of wetted sites in the tth layer (i.e., the number of growth sites at time t) decreases like

$$N_t \sim t^{(\nu-\beta)/\nu_{\parallel}-1}, \tag{5}$$

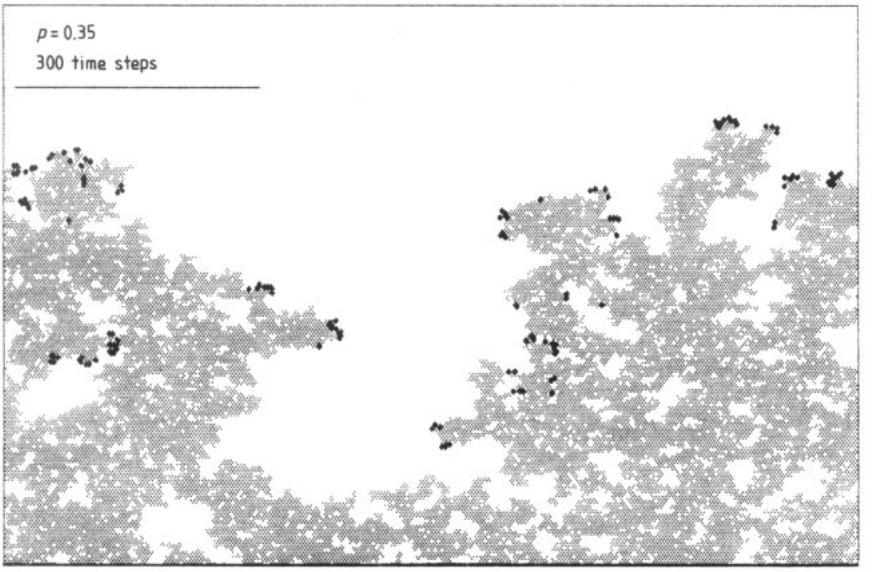

Figure 1. Sites connected to the line $x = 0$ by <300 links in a typical run at $p = p_{cr}$. The cluster spreads in each time step $t \to t+1$ by adding the next layer, consisting of sites connected by exactly t links. These latter sites, called 'growth sites', are denoted by heavy dots. For technical reasons, a triangular lattice is shown (all numerical results quoted are for square lattices).

and the mean distance of these growth sites from the starting line $x = 0$ increases like

$$\langle x_t \rangle \sim t^{\nu/\nu_\parallel}. \tag{6}$$

The main differences to I concern the algorithm used to find the wetted sites, and the method used to extract critical exponents from the data.

In contrast to I, we now stored, in one big matrix of bit maps, whether each lattice site is already wetted or not. This requires only one bit per site, thus allowing lattices of 3840×600 sites to be used on a rather small computer. In another array were stored the coordinates of all growth sites. For each time step, the new growth sites (i.e. sites not yet wetted and adjacent to old growth sites, connected to them by unbroken bonds) were written on a new array, and the bit maps were continuously updated to include all new growth sites as wetted sites. At the end, the old array of growth sites was replaced by the new one, and the next time step started. This method, in addition to needing modest storage, is rather fast. This is essentially due to the fact that the infinite cluster need not be known before it is uncovered layer by layer. Thus, each wetted site is tested only about two times during the whole process, while non-wetted regions are never tested at all.

Due to the efficiency of the algorithm, we could make 1600 runs of 1035 time steps (=layers), with all sites on a line of 3840 sites originally wetted in each run. This took about 35 hours of CPU time on a CYBER 170/720, corresponding to $\sim$4 hours on a CYBER 76. The total number of wetted sites was $\sim 1.1 \times 10^9$, to be compared e.g. with a total of $\sim 5 \times 10^7$ in Havlin and Nossal (1984), and with $\sim 2 \times 10^7$ in Rammal *et al* (1984).

The main advantage of growing from a whole line instead of a single site is that one avoids the large fluctuations during the first time steps when the number of growth sites is very small. These fluctuations of course affect all observables at all later times.

The other improvement over I concerns the estimation of critical exponents. In I, straight lines were simply fitted to plots of $\log N_t$ resp. $\log\langle x_t\rangle$ against t. In view of the danger of overlooking corrections to scaling in this way (Lyklema and Kremer 1984), we used a different method in the present paper. In figures 2 and 3 we show the quantities

$$A_t = \frac{t\langle x_t\rangle}{\frac{1}{2}\langle x_t\rangle + \sum_{t'=1}^{t-1}\langle x_{t'}\rangle} - 1, \tag{7}$$

$$B_t = \frac{tN_t}{\frac{1}{2}N_t + \sum_{t'=1}^{t-1} N_{t'}}, \tag{8}$$

plotted against $1/t$. It is easily seen that

$$\frac{\nu}{\nu_\parallel} = \lim_{t\to\infty} A_t, \qquad \frac{\nu-\beta}{\nu_\parallel} = \lim_{t\to\infty} B_t, \tag{9}$$

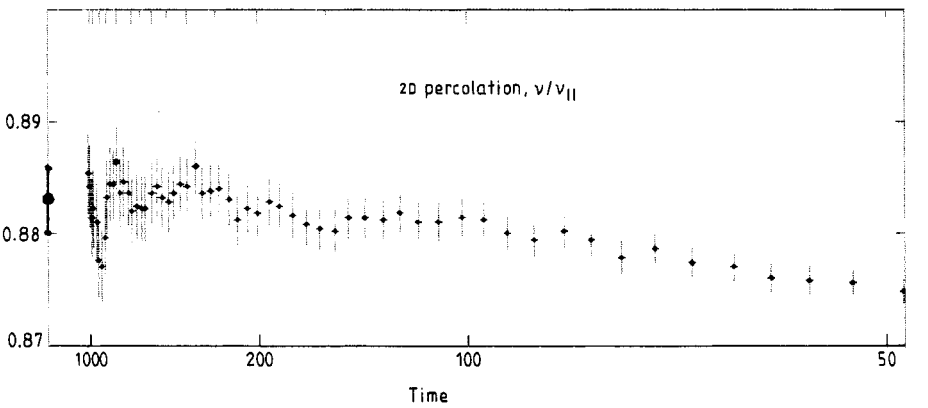

Figure 2. Quantity A_t against $1/t$. The limit of A_t for $t\to\infty$, indicated by the bold dot, is equal to $\omega/\omega_\parallel$.

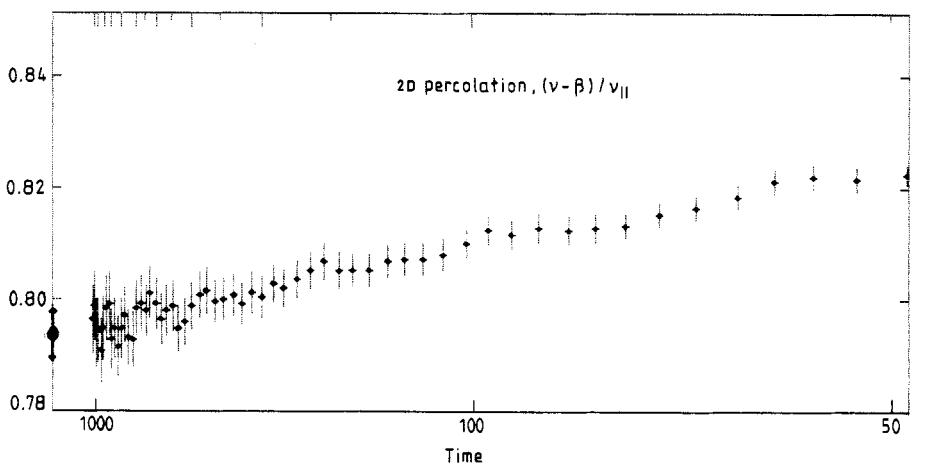

Figure 3. Quantity B_t against $1/t$.

with corrections proportional to $1/t$ if all corrections to scaling have exponents >1, and with corrections $\sim t^{\Delta}$, $0<\Delta<1$, otherwise. From figures 2 and 3 one sees that the latter corrections are not needed. One also sees that straight lines in log-log plots, corresponding to fitting horizontal lines in figures 2 and 3, would produce spuriously small errors.

From figures 2 and 3 we can read the estimates

$$\frac{\nu}{\nu_{\parallel}} = 0.883 \pm 0.003, \qquad \frac{\nu-\beta}{\nu_{\parallel}} = 0.793 \pm 0.004.$$

This leads first to $\beta/\nu = 0.102 \pm 0.007$, in perfect agreement with the exact value $\beta/\nu = 5/48 = 0.1042$. Using this latter value, we finally obtain the results quoted in table 1.

Other exponents derived from these are the 'minimal path exponent' (Stanley 1984) $\nu_{\parallel}/\nu = 1.132 \pm 0.003$ and the exponent $\nu_{\parallel} - \nu = 0.176 \pm 0.006$ governing the velocity of the spread in the supercritical case: for $p > p_{cr}$, one has $\langle x_t \rangle \sim |p - p_{cr}|^{\nu_{\parallel}-\nu} t$.

Finally, we want to use the opportunity to clarify a confusing statement made in I. There, it was said that the solitary wave of growth sites has a time-independent finite width and a shape as shown in figure 3 of that paper. In this form, this might not be true since the wave was defined there as an ensemble average, and the position of the wave might fluctuate from realisation to realisation, with a variance $\propto t$. This would then lead to a symmetric shape of the wave with a width $\propto \sqrt{t}$. The results of that paper should however describe the average shape of the wave after shifting the centre of each section of length $L \gg |p - p_{cr}|^{\nu-\nu_{\parallel}-\beta}$ to the origin (such sections contain $\gg 1$ growth sites, allowing a shape and width to be defined).

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