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COMMENT

Mean field renormalisation group calculations for directed percolation on the square lattice

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Abstract. A simple extrapolation technique for mean field renormalisation group calculations is described. Application of this method to large cell calculations for percolation on the directed square lattice yields $p_c = 0.7067 \pm 0.0001$ (site problem) and $p_c = 0.6454 \pm 0.0002$ (bond problem).

It has previously been shown that the mean field renormalisation group (MFRG) method of Indekeu *et al* (1982) may be directly applied to percolation problems (De'Bell 1983). In this comment, extensions of the calculations for site and bond percolation on the directed square lattice to larger cells are reported and estimates of the critical probability p_c obtained by extrapolation to the large cell limit are presented.

In the variant of the MFRG described by De'Bell (1983) the percolation probability P at the origin is calculated for a cell of l^d sites, and sites neighbouring the cell are connected to a ghost site with probability b. Scaling requirements then lead to

$$bP'(b') = b'P(b) \tag{1}$$

where primed and unprimed quantities refer to cells (symmetric about the origin) of different sizes. Solving (1) to leading order in b and b' yields recursion relations which are valid in the region of the critical point. De'Bell obtained the recursion relations for the bond and site percolation problems on the directed square lattice (with all parallel bonds directed in the same sense) for square cells with axes parallel to the lattice bonds and $l \leqslant 11$. The fixed points p^* of these relations were consistent with the assumption that they should approach the critical probability p_c smoothly as the rescaling factor l/l' approached 1, in agreement with the results of Indekeu *et al* (1982) for the Ising model. However, the correlation length exponent $\nu_\parallel$ showed an initial tendency to move away from the expected value, this tendency reversing only for the largest cell considered. (Kinzel and Yeomans (1981) have shown that both a longitudinal and a transverse correlation length may be defined for directed percolation; however, only the longitudinal exponent $\nu_\parallel$ is relevant to our present analysis, cf Redner (1982).)

The 'transfer matrix' method of Blease (1977) has been used to calculate the coefficient of b in $P(b)$ for fixed values of p, the site (bond) occupation probability. By plotting these data as a function of p, the fixed point value $p = p^* = p'$ which satisfied (1) to leading order in $b(b')$ was determined for various pairs of cells. (This technique

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leads to small statistical errors in the data but is necessary to minimise the computer memory used.) Two classes of square cells were considered: class (a)—those with axes parallel to the lattice bonds, and class (b)—those with axes at 45° to the lattice bonds. In all cases considered here, l and l' in (1) refer to pairs of cells in the same class such that l immediately follows l' in order of size and $l/l' \to 1$ as $l \to \infty$.

Typical values of p^* and the corresponding estimate of

$$\nu_{\parallel} = \ln(l/l')/\ln(\partial p'/\partial p | p^*)$$

for the site problem are shown in table 1; similar results were obtained for the bond problem. The values of p^* continue to approach the expected values of p_c smoothly as $l/l' \to 1$. The values of $\nu_{\parallel}$ also show an upward trend consistent with the assumption that they should approach the expected value; however, the variation in $\nu_{\parallel}$ with l/l' is rather slow. Moreover, the last ten values of $\nu_{\parallel}$ obtained for cells in class (b) ($l/l' \simeq 1.07$–1.04) are scattered in the range 1.39 ± 0.01 and no clear upward trend can be distinguished. We assume this is because the statistical errors in the estimates of $\ln(\partial p'/\partial p | p^*)$ for $\partial p'/\partial p \sim 1$ are of the same order of magnitude as the overall upward trend. As a result of these features it is not possible to make any reliable extrapolation of $\nu_{\parallel}$ to $l/l' = 1$ from the data for $\partial p'/\partial p$.

Table 1. Sample values of the fixed point p^* and correlation length exponent $\nu_{\parallel}$ for the site problem for cells with axes (*a*) parallel to and (*b*) at 45° to the lattice bonds.

(*a*)			(*b*)		
l/l'	p^*	$\nu_{\parallel}$	l/l'	p^*	$\nu_{\parallel}$
1.286	0.6385[a]	1.261[a]	1.105	0.6589	1.373
1.222	0.6471[a]	1.267[a]	1.074	0.6673	1.379
1.182	0.6533	1.272	1.061	0.6713	1.389
1.133	0.6618	1.287	1.051	0.6745	1.388
1.105	0.6675	1.293	1.046	0.6761	1.395
1.087	0.6717	1.298	1.043	0.6776	1.398

[a] From exact recursion relations (De'Bell 1983).

De'Bell (1983) has previously pointed out that the low values of $\nu_{\parallel}$ obtained may be associated with the highly anisotropic nature of large clusters for directed percolation close to p_c, and several authors have argued that anisotropic transformations should be employed to treat directed problems (Herrmann *et al* 1983, Redner and Mueller 1982 and references therein). (Cells in class (b) contain all sites that can be reached from the origin and are less than a given distance along the longitudinal ('preferred') direction. Thus the width of the cone of fluid flow (or sites connected to the origin) is independent of the edges of the cell. In this sense, cells in class (b) satisfy the criteria of Herrmann *et al* (1983).) Therefore, in the application of the finite size scaling analysis described below, we have adopted the central estimate of $\nu_{\parallel} = 1.73$ obtained from series expansions (De'Bell and Essam 1983).

In order to motivate this analysis, we note that if $\xi_{\parallel} \ll l$ the probability that there is a pathway from the origin to a site adjacent to the cell, and hence the coefficient of b in $P(b)$, is small. As P is increased, $\xi_{\parallel}$ approaches the distance of the sites connected to the ghost site from the origin and there is a rapid increase in the coefficient of b.

Since it is this rapid increase in the coefficient of b which results in the fixed point we expect

$$\xi_{\parallel}(p^*) \propto \tilde{l} \tag{2}$$

where $\tilde{l}$ is the linear dimension of the cell if sites directly connected to the ghost site are included. Hence, for p^* sufficiently close to p_c,

$$\tilde{l}^{-1/\nu_{\parallel}} \propto (p_c - p^*). \tag{3}$$

(Similar finite scaling analysis has been applied to Monte Carlo renormalisation group calculations for undirected percolation by Reynolds *et al* (1978, 1980).)

The values of p^* for the ten largest cells in class (b) were plotted against $\tilde{l}^{-1/\nu_{\parallel}}$ by a least squares routine for both the site and bond problems (figure 1). The resulting estimates of p_c are shown in table 2.

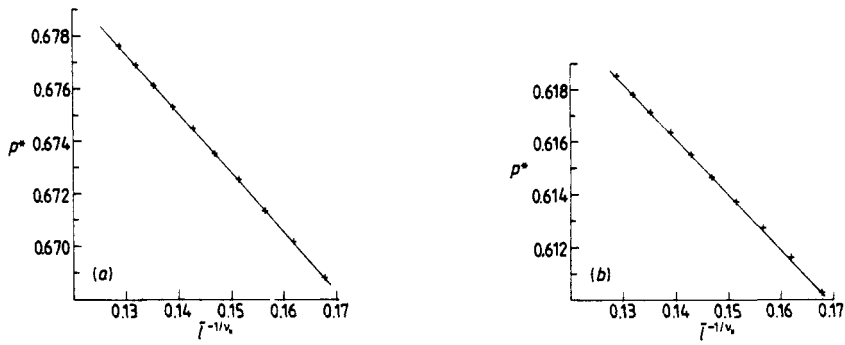

Figure 1. p^* against $\tilde{l}^{-1/\nu_{\parallel}}$ with $\nu_{\parallel} = 1.73$ for the site (a) and bond (b) problems.

Table 2. Estimates of p_c based on the ten data points closest to p_c and variation of the central estimate with the number of data points (N) considered.

N	Bond problem p_c	Site problem p_c
10	0.6454 ± 0.0002	0.7067 ± 0.0001
9	0.6453(5)	0.7066
8	0.6454(5)	0.7065(5)
7	0.6455	0.7063
6	0.6457	0.7065
5	0.6457	0.7065
Series† expansions	0.6446 ± 0.0002	0.7061 ± 0.0001

† De'Bell and Essam 1983.

For both problems considered the estimate of p_c obtained by our present method is slightly too high to be consistent with the estimate obtained from series expansions. However, it must be recalled that equation (3) is valid only for p^* 'sufficiently close' to p_c. In the case of our present data the difference between p^* for the largest cell considered and p_c is still large compared with the range of p spanned by our data

points and, in principle, equation (3) should be written in the form

$$\tilde{l}^{-1/\nu_\parallel} \propto (p_c - p^*)[1 + A(p_c - p^*) + B(p_c - p^*)^{\Delta_1} + \ldots] \tag{4}$$

where A and B are constants and $\Delta_1 = 1.02 \pm 0.02$ (e.g. Adler *et al* 1983, cf also De'Bell *et al* 1984).

In an attempt to determine the effects of the correction terms in (4) we have performed a range of fit analysis by successively removing the data points farthest from p_c and fitting the remaining points to (3) (De'Bell *et al* 1984) (table 2). Although the site problem results show a slight initial downward trend, both sets of results tend to vary about the value obtained with ten points, indicating that the statistical errors are of the same order as the overall curvature. Similarly attempts to include correction terms of the type indicated in (4) in our least squares fitting procedure were unable to obtain consistent results. As remarked previously, the range of p over which data points were available is small compared with the range over which we must extrapolate, and therefore the curvature due to the correction terms in the range of the available data may be expected to be small.

In summary, extrapolations of data obtained from extended mean field renormalisation group calculations for directed percolation on the square lattice, result in values of the critical probability which are slightly too high to be consistent with series expansion results. However, the inconsistency is small ($\leqslant 0.1\%$) and, since the transfer matrix method yields values of p^* relatively distant from p_c, may probably be attributed to the neglect of correction terms of the type indicated in (4). In view of our above comments, the extension of the MFRG method to large cells by Monte Carlo techniques would be of considerable interest and we hope that this report might stimulate interest in such an extension.

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