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COMMENT

Position space renormalisation group approach to fractal dimensions of an infinite cluster, its backbone and cutting bonds for percolation

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Abstract. A position space renormalisation group method is presented to study the cluster structure of an infinite cluster at the percolation threshold. Fractal dimensions of an infinite cluster, its backbone and cutting bonds are determined by the small-cell method for two-dimensional bond percolation. It is shown that the fractal dimension of its cutting bonds agrees with the inverse of the connectedness length exponent at the fixed point.

Recently, there has been increasing interest in fractals (Mandelbrot 1982, Stanley and Ostrowsky 1986). The percolating infinite cluster is one of the most intensively studied random fractals (Kirkpatrick 1979, Stauffer 1979, 1985, Deutscher *et al* 1983, Stanley and Coniglio 1983, Kapitulnik and Deutscher 1984). Much of our understanding of the structure of clusters for percolation has been obtained by computer simulation. Although such a procedure can yield accurate results and many insights into the structure of such clusters, it nevertheless is not easy in comparison with the renormalisation group approach. Here we develop a renormalisation group method applicable to the cluster structure of percolation. One measure of the structure of an infinite cluster for percolation is the manner in which N, the total number of bonds in the infinite cluster, scales with the linear dimension L of the cluster, $N \sim L^D$ where D is the fractal dimension of the infinite cluster. The infinite cluster is composed of a backbone through which electrical current flows and dangling bonds hanging on to it. The number N_b of bonds within the backbone also scales with a different fractal dimension D_b: $N_b \sim L^{D_b}$. Furthermore, there are two kinds of bonds in the backbone: (a) cutting (singly connected) bonds, which have the property that if they are cut, the backbone ceases to conduct and (b) multiply connected bonds, which have the property that they can be cut without interrupting the flow (Stanley 1977). The number N_c of cutting bonds in the infinite cluster scales with $N_c \sim L^{D_c}$. Coniglio (1981, 1982) provided a rigorous argument that for all d, $D_c = 1/\nu$ where the ν represents the connectedness length exponent. We shall calculate the fractal dimensions D, D_b and D_c by using a position space renormalisation group (PSRG) method (Burkhardt and van Leeuwen 1982). We restrict ourselves to the bond percolation problem on the square lattice. The lattice is divided into cells of linear dimension b, a probability p is associated with each occupied site in the cell and the cells are rescaled to a single bond or a smaller cell. We first note that our PSRG method is different from the original PSRG in respect of the scale fractor b. Let us consider the division of the lattice into cells. The simplest example is indicated in figure 1(a). Each cell, divided by the broken lines, is renormalised to

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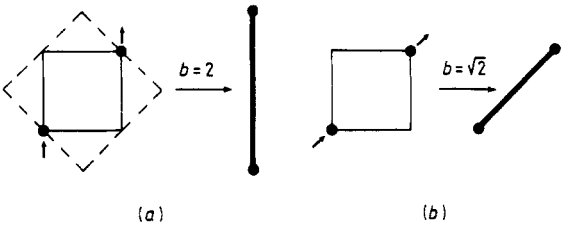

Figure 1. Illustration of the dividing and rescaling of a $b=2$ cell for bond percolation on the square lattice. The rescaled bonds are indicated by bold lines. Arrows indicate the entries and exits of current. (a) A $b=2$ cell. Broken lines indicate boundaries divising the square lattice into the cells. (b) A $b=\sqrt{2}$ cell, presented by Young and Stincombe (1975).

a single bond of linear dimension $b=2$. In comparison with the original decimation transformation (Young and Stinchcombe 1975), the scale factor is different by a factor $\sqrt{2}$ (see figure 1(b)). The bonds into the cell are doubly counted in the decimation transformation by Young and Stinchcombe. The entries and exits of current are indicated by arrows. By making the choice of figure 1(a), at the Nth renormalisation with $p=1$, the total number of bonds is 4^N, while the total length is 2^N. The perfect lattice has therefore a dimension D equal to 2. When one divides the lattice into cells, it is necessary to satisfy the following relation between the number of bonds n_t and the scale factor b:

$$n_t = b^2 \tag{1}$$

where the n_t indicates the total (occupied and unoccupied) number of bonds within the cell. To the cell (size b_1)-to-cell (size b_2) transformation, the following relation must be satisfied:

$$n_{t,1}/n_{t,2} = (b_1/b_2)^2 \tag{2}$$

where the $n_{t,1}$ (or $n_{t,2}$) represents the total number of bonds in the cell with the length scale factor b_1 (or b_2).

From the viewpoint of fractal geometry, it is found that the lattice formed by the repeated transformations in figure 1(a) corresponds to the bond-disordered system on the diamond hierarchical lattice (Luck 1985). In general, we find that the geometric textures, formed by the repeated PSRG transformations, correspond to the 'regular random fractals' proposed by Martin and Keefer (1985). Let us calculate the fractal dimensions of an infinite cluster, its backbone and its cutting bonds, with the use of the definition of fractal dimension for the regular random fractal. First, we derive the fractal dimension of an infinite cluster at criticality. The number of bonds within a spanning cluster between entries and exits in a spanning configuration α is represented by $n_{i,\alpha}$. Then the mean value of $n_{i,\alpha}$ is

$$\langle n_i \rangle = \sum_\alpha n_{i,\alpha} f_\alpha \tag{3}$$

where the f_α is the probability of a particular configuration α. The probability $R(p)$ that a cell of size b is connected between the entries and the exits is given by

$$R(p) = \sum_\alpha f_\alpha. \tag{4}$$

At the fixed point $p^* = R(p^*)$, an incipient infinite cluster appears. The fractal dimension D of the infinite cluster is given by

$$D = \ln\langle\langle n_i \rangle\rangle^* / \ln b \tag{5}$$

where the asterisk indicates the value at the fixed point and the $\langle\langle n_i\rangle\rangle$ is the average number of bonds within spanning cluster if the cell is connected: $\langle\langle n_i\rangle\rangle = \langle n_i\rangle / R(p)$.

Similarly, we derive the fractal dimensions of the backbone and its cutting bonds:

$$D_b = \ln\langle\langle n_b\rangle\rangle^* / \ln b \tag{6}$$

and

$$D_c = \ln\langle\langle n_c\rangle\rangle^* / \ln b \tag{7}$$

where the n_b and the n_c represent respectively the number of bonds through which electrical current flows in the spanning cluster and the number of bonds such that if one is cut the entries are no longer connected to the exits in the cell.

We calculate the fractal dimensions D, D_b and D_c for the simplest case (figure 1(a)) by way of example. Figure 2 shows spanning configurations for a $b = 2$ cell. $\langle\langle n_i\rangle\rangle$, $\langle\langle n_b\rangle\rangle$ and $\langle\langle n_c\rangle\rangle$ are respectively given by

$$\langle\langle n_i\rangle\rangle = (4p^4 + 3\times 4p^3q + 2\times 2p^2q^2)/R(p) \tag{8}$$

$$\langle\langle n_b\rangle\rangle = (4p^4 + 2\times 4p^3q + 2\times 2p^2q^2)/R(p) \tag{9}$$

$$\langle\langle n_c\rangle\rangle = (2\times 4p^3q + 2\times 2p^2q^2)/R(p) \tag{10}$$

where $R(p) = 2p^2 - p^4$. At the fixed point $p^* = R(p^*)$, we obtain the following relation:

$$\mathrm{d}R/\mathrm{d}p|_{p^*} = \langle\langle n_c\rangle\rangle^*. \tag{11}$$

The rigorous relation $D_c = 1/\nu$ derived by Coniglio (1982) holds for this case. In table 1, the first line shows estimated fractal dimensions for the case shown by figure 1(a).

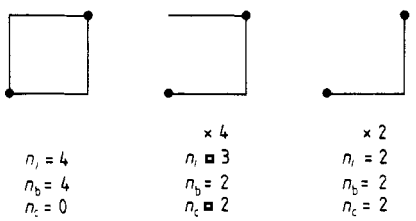

Figure 2. Spanning configurations that arise in the position space renormalisation group for bond percolation on the square lattice using a $b = 2$ cell. For each spanning configuration, the number of bonds within a spanning cluster (n_i), the number of bonds through which current flows (n_b) and the number of bonds such that if one is cut the entries is no longer connected to the exits (n_c) are given just below each figure.

Table 1. List of the fractal dimensions by the PSRG approach for the cases shown in figures 1(a), 3(a) and (b), 3 (cell (b)-to-cell (a) transformation) and figure 4, compared with other sources.

Type	p^*	D	D_b	D_c
Figure 1(a)	0.618	1.610	1.305	0.610
Figure 3(a)	0.5	1.488	1.339	0.603
Figure 3(b)	0.5	1.547	1.310	0.606
Figure 3	0.5	1.713	1.230	0.613
Figure 4	0.5	1.734	1.444	0.700
Other sources	0.5[a]	1.90[b]	1.62[c]	0.75[a]

[a] Stauffer (1979, 1985).
[b] Kapitulnik and Deutscher (1984).
[c] Hermann and Stanley (1984).

We also calculate the fractal dimensions for another cases. We partition the square lattice into cells (see figure 3(a) and (b)) which will be renormalised into a single bond. The total number of bonds in a cell equals to the square of the scale factor for each case shown by figure 3(a) and (b). We estimate the fractal dimensions by the use of equations (5), (6) and (7). The estimated fractal dimensions for the cases of figure 3(a) and (b) are respectively shown by the second and third lines in table 1. For these cases the Coniglio relation (11) holds.

Until now, we have considered the conventional PSRG approach of transforming from a system of cells to a new system of bonds. However, one can consider a transformation in which one passes from a system of cells of size b_1 to a system of cells of size b_2. Such a 'cell-to-cell' transformation enables one to have a rescaling length b_1/b_2. Then the fractal dimensions are given by

$$D = \ln(\langle\langle n_i\rangle\rangle_1^*/\langle\langle n_i\rangle\rangle_2^*)/\ln(b_1/b_2) \tag{12}$$

$$D_b = \ln(\langle\langle n_b\rangle\rangle_1^*/\langle\langle n_b\rangle\rangle_2^*)/\ln(b_1/b_2) \tag{13}$$

$$D_c = \ln(\langle\langle n_c\rangle\rangle_1^*/\langle\langle n_c\rangle\rangle_2^*)/\ln(b_1/b_2). \tag{14}$$

We calculate the fractal dimensions for the cell (shown by figure 3(b))-to-cell (shown by figure 3(a)) transformation. The estimated values are given by the fourth line in table 1. We also consider the other case indicated by figure 4. This case is presented by Reynolds *et al* (1977) and Bernasconi (1978). Though they treat it as a cell-to-bond transformation, we consider it as a cell-to-cell transformation. The total number of bonds in the cell (shown by figure 4) is not satisfied with equation (1) but with equation (2). By using equations (12), (13) and (14), the fractal dimensions are estimated and shown by the fifth line in table 1. In these cell-to-cell transformations, the Coniglio's relation is also satisfied.

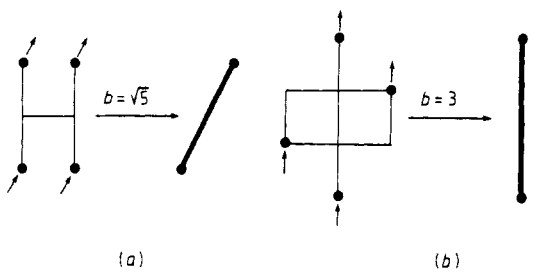

Figure 3. Illustration of the rescalings of a $b=\sqrt{5}$ cell (a) and a $b=3$ cell (b) for bond percolation on the square lattice.

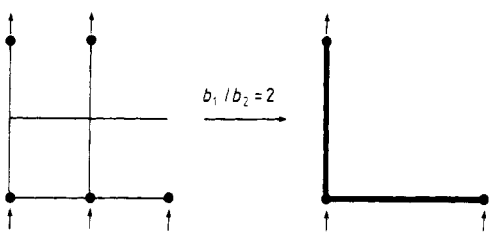

Figure 4. One example of a cell-to-cell transformation. The cell with eight bonds scales to the cell with two bonds. To this cell-to-cell transformation, the relationsip (2) is satisfied.

In summary, we present the PSRG method to derive the three fractal dimensions (of an infinite cluster, its backbone and cutting bonds) in relation to the cluster structure of an infinite cluster at the percolation threshold. It is shown that our PSRG method is satisfied with Coniglio's relation: $D_c = 1/\nu$. Our renormalisation group approach for the fractal dimensions of the cluster structure in percolation is completely general and is not limited to the particular models considered here. To have better values for the fractal dimensions, it will be necessary that one perform large-cell calculations by a Monte Carlo renormalisation method.

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