COMMENT

Further comments on the one-dimensional percolation problem with multineighbour bonds

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Abstract. One-dimensional site and bond percolation problems with bonds connecting Lth nearest neighbours are solved exactly by using an infinite cell to cell renormalisation group transformation. Both 'thermal' and magnetic critical exponents are obtained through the scaling relations. Although universality breaks down for site and bond percolation when $L \geq 2$, Suzuki's weaker universality still holds.

One-dimensional site percolation with bonds connecting Lth nearest neighbours has been solved exactly by using the generating function method (Klein *et al* 1978). Although p_c is always equal to one, the critical behaviour is found to be L dependent. The critical exponents are $2 - \alpha = L$, $\beta = 0$, $\nu = \gamma = L$, $\delta = \infty$ and $\eta = 1$. Recently, the transfer-matrix method has been used to find the correlation length exponent ν for both site and bond percolation in one dimension with further neighbour bonds. The results are $\nu = L$ for the site percolation and $\nu = L(L+1)/2$ for the bond percolation (Zhang and Shen 1982, Zhang *et al* 1983).

In this comment we present a renormalisation group approach to the same problem. In the limit of infinite cell to cell transformation, both 'thermal' and magnetic scaling powers are obtained exactly. All the critical exponents can then be obtained by using scaling relations.

It is well known that the one-dimensional ($d = 1$) percolation problem with nearest neighbour bonds can be solved exactly by choosing any scaling factor b of the cell (Reynolds *et al* 1977). This is not true when $d \geq 2$. For a finite cell, renormalisation introduces various complications into the renormalised system. To overcome these complications, one can either introduce more parameters into the system, such as next nearest neighbour bond, correlations etc, or alternatively, one can let the cell become larger and larger. It is believed that the infinitely large cell limit will yield the correct critical behaviour. By taking the latter approach, Reynolds *et al* (1980) studied both site percolation on the square lattice and one-dimensional site percolation with multineighbour bonds. In the latter case, a closed-form recursion relation is found and the correct correlation length exponent $\nu = L$ is indeed obtained in the infinite cell limit. Here, we will extend this method in two ways. Firstly, we include the 'ghost site' so that the magnetic exponents can also be obtained. Secondly, we apply this method to the bond percolation case with some modifications of the cells.

We consider the site percolation first. For a system with Lth nearest neighbour bonds, a cell to cell renormalisation must be used and the renormalised cell must contain at least L sites. The reasons for such an adoption are explained in great detail

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in Reynolds *et al* (1980). In the case of $L = 2$, we show in figure 1 both the original cell with size $l = 3$ and the renormalised cell with size $L = 2$. Every site in the original cell is occupied with probability p and every occupied site is joined to the 'ghost site' with probability h. Similar definitions of $\tilde{p}$ and $\tilde{h}$ are used in the renormalised cell. For a renormalised cell of size L, the probability of traversing this cell is just

$$p'(L) = 1 - \tilde{q}^{L} \tag{1}$$

where $\tilde{q} = 1 - \tilde{p}$. This is because all the L sites must be missing in order to prevent us from traversing, and here the presence of the ghost site is irrelevant. For an original cell of size l, the probability of traversing this cell is

$$p'(l) = p^{l} + \binom{l}{1}p^{l-1}q + \ldots + \binom{l}{L-1}p^{l-L+1}q^{L-1} + \left[\binom{l}{L} - (l-L+1)\right]p^{l-L}q^{L}$$

$$+ p^{l-L}q^{L}[(1-t)(1-t^{l-L-1}) + (1-t^{2})(1-t^{l-L-2}) + \ldots$$

$$+ (1-t^{l-L-1})(1-t)] + O(q^{L+1}) \tag{2}$$

where $q = 1 - p$ and $t = 1 - h$. The term $-(l-L+1)p^{l-L}q^{L}$ in (2) comes from the following reason. If all the L missing sites form a row, the connectivity of the cell breaks. There are $(l-L+1)$ ways to do it. When all the L missing sites do form a row, there is still a possibility of traversing the cell if the occupied sites on both sides of the 'missing row' are connected though the 'ghost site'. This probability is given in the last term of (2). By equating (1) and (2) we have the first recursion relation.
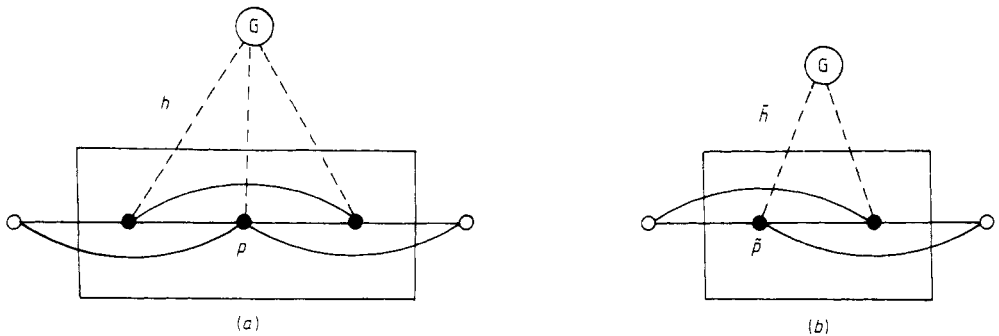

Figure 1. Site percolation with $L = 2$. (*a*) Original cell with size $l = 3$. (*b*) Renormalised cell with size $L = 2$.

To find the second recursion relation, we require the probability of reaching the 'ghost site' from either end of the cell to be equal for the original and renormalised cells. For the renormalised cell this probability is

$$p'(L)h'(L) = \tilde{p}^{L}(1-\tilde{t}^{L}) + \binom{L}{1}\tilde{p}^{L-1}\tilde{q}(1-\tilde{t}^{L-1}) + \ldots + \binom{L}{L-1}\tilde{p}\tilde{q}^{L-1}(1-\tilde{t})$$

$$= 1 - (1-\tilde{p}\tilde{h})^{L} \tag{3}$$

where $\tilde{t} = 1 - \tilde{h}$. For the original cell this probability is

$$p'(l)h'(l) = p^l(1-t^l) + \binom{l}{1}p^{l-1}q(1-t^{l-1}) + \ldots + \left[\binom{l}{L} - (l-L+1)\right]p^{l-L}q^L(1-t^{l-L})$$

$$+ p^{l-L}q^L[(1-t)(1-t^{l-L-1}) + \ldots + (1-t^{l-L-1})(1-t)] + O(q^{L+1}h). \tag{4}$$

By equating (3) and (4), we find the second recursion relation. From both recursion relations the critical point is found at $p^* = 1$, $h^* = 0$. Taking the differentiations on both sides of the recursion relations and evaluating at the fixed point (p^*, h^*), we find

$$[(\tilde{q}/q)^{L-1}\,\partial\tilde{p}/\partial p]_* = l - L + 1, \tag{5}$$

$$\partial\tilde{h}/\partial h|_* = l/L, \tag{6}$$

$$\partial\tilde{p}/\partial h|_* = 0, \qquad \partial\tilde{h}/\partial p|_* = 0, \tag{7}$$

where '*' means that we evaluate the function at the fixed point (p^*, h^*). Since in the limit of $q \to 0$ we have

$$\lim_{q \to 0} \frac{\tilde{q}}{q} = \lim_{p \to 1} \frac{1-\tilde{p}}{1-p} = \lim_{p \to 1} \frac{\tilde{p}-p^*}{p-p^*} = \frac{\partial\tilde{p}}{\partial p}\bigg|_*, \tag{8}$$

from (5) and (8), we find

$$\partial\tilde{p}/\partial p|_* = (l-L+1)^{1/L}. \tag{9}$$

The scaling powers y_p and y_h are defined by

$$\partial\tilde{p}/\partial p|_* = b^{y_p}, \qquad \partial\tilde{h}/\partial h|_* = b^{y_h}. \tag{10}$$

Since $b = l/L$, using (6), (9) and (10), we find $\lim_{l \to \infty} y_p = 1/L$ and $y_h = 1$. From the following scaling relations (Reynolds *et al* 1980)

$$\begin{aligned}
2 - \alpha = y_p^{-1}, \qquad \beta = (1-y_h)/y_p, \qquad \delta = y_h/(1-y_h), \\
\gamma = (2y_h - 1)/y_p, \qquad \nu = y_p^{-1}, \qquad \eta = 3 - 2y_h,
\end{aligned} \tag{11}$$

we find $2 - \alpha = L$, $\gamma = \nu = L$, $\eta = 1$, $\beta = 0$ and $\delta = \infty$. These results agree with the results obtained by the generating function method (Klein *et al* 1978).

Next, we consider the bond percolation case. For the same reasons as in the site percolation case, a renormalised cell must contain at least L sites for a system with Lth nearest neighbour bonds. In the case of $L = 3$, we show in figure 2 both the original cell with $l = 5$ and renormalised cell with $L = 3$. Here p and $\tilde{p}$ denote respectively the bond occupation probability in the original and renormalised cells. In the case of bond percolation, the bonds belonging to a cell are not all well defined. For instance, in figure 2(a) the bonds 1 to 6 connect both sites inside and outside the cell. If we want to count the total number of bonds belonging to the cell correctly, only half of the six bonds can be included. If we include, for instance, bonds 1 to 3 and neglect 4 to 6, then the definition of the cell is still ambiguous. One way to overcome this difficulty is to split all the inter-cell bonds into two parts; one part has occupation probability 1 and the other part has probability p. By doing so, the connectivity of the system remains unchanged; however, the cells can now be defined unambiguously. In figure 2(a), we let the parts of the bonds 1 to 3 belonging to the cell have occupation probability p, while the parts of the bonds 4 to 6 belonging to the cell have occupation probability 1, and are indicated by bold lines. The probability
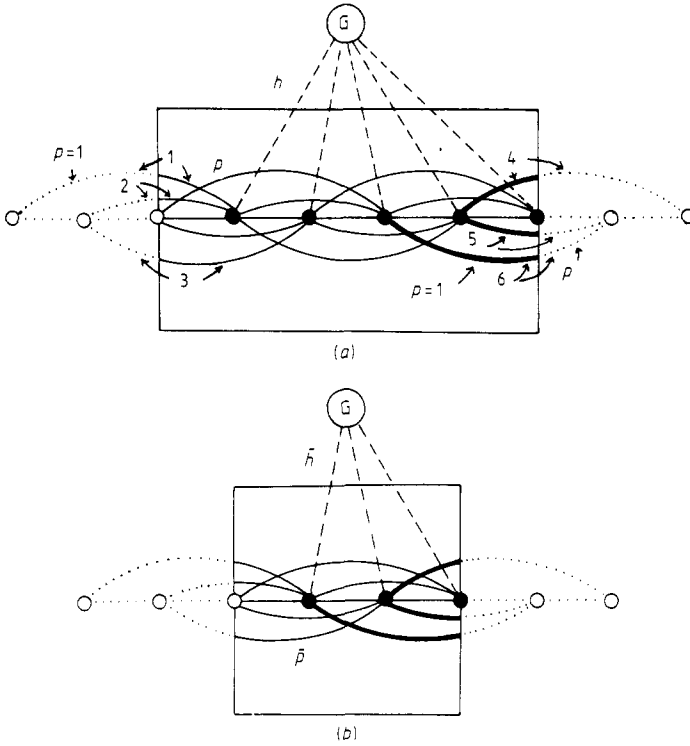
Figure 2. Bond percolation with $L = 3$. (a) Original cell with size $l = 5$. (b) Renormalised cell with size $L = 3$.

of traversing the cell is defined as the probability of traversing from one side of the cell to the other side of the cell. Since all the sites connected by bonds with probability 1 are definitely connected, as far as the connectivity is concerned, we can shrink all these sites into one site while preserving the total number of bonds connecting to the 'ghost site'. Figure 2 can be drawn schematically in figure 3.

Considering the case of general L, in the renormalised cell, there are $L(L + 1)/2$ bonds connecting only two ends and there are L bonds connecting to the 'ghost site' from the right end. The probability of traversing the cell is
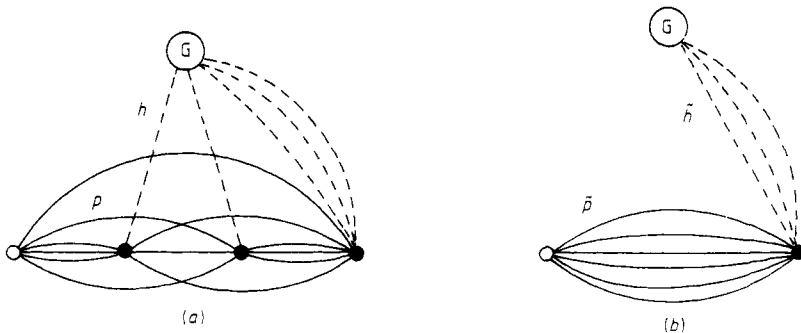
$$p'(L) = 1 - \tilde{q}^{L(L+1)/2}. \tag{12}$$

Figure 3. (a) and (b) are schematical diagrams for figures ($2a$) and ($2b$) respectively.

In the original cell, there are m bonds connecting $l-L+2$ sites, where $m = lL-[(L-1)+(L-2)+\ldots+2+1]=L[l-(L-1)/2]$. At the right end, there are L bonds connecting to the 'ghost site', and all other $l-L$ sites except the left end have one bond connecting to the 'ghost site'. The number of bonds crossing a vertical line between any two nearest neighbour sites is $L(L+1)/2$. This is the least number of missing bonds required to break the connectivity of the cell and there are $(l-L+1)$ ways to do it.

The probability of traversing the cell is

$$p'(l) = p^m + \binom{m}{1}p^{m-1}q + \ldots + \left[\binom{m}{L(L+1)/2} - (l-L+1)\right]p^{m-L(L+1)/2}q^{L(L+1)/2}$$
$$+ p^{m-L(L+1)/2}q^{L(L+1)/2}[(1-t)(1-t^{l-1}) + (1-t^2)(1-t^{l-2}) + \ldots$$
$$+ (1-t^{l-L})(1-t^L)] + O(q^{L(L+1)/2+1}). \tag{13}$$

The last term in (13) is the probability of traversing the cell through the 'ghost site' when all the bonds crossing a vertical line between two nearest neighbour sites are missing.

The probability of reaching the 'ghost site' from either end of the renormalised cell is

$$p'(L)h'(L) = (1 - \tilde{q}^{L(L+1)/2})(1 - \tilde{t}^L). \tag{14}$$

For the original cell, we have

$$p'(l)h'(l) = (1-t^l)\left[p^m + \binom{m}{1}p^{m-1}q + \binom{m}{2}p^{m-2}q^2 + \ldots + \binom{m}{2L-1}p^{m-2L+1}q^{2L-1}\right]$$
$$+ p^{m-2L}q^{2L}[N_{l-L+2}(2L)(1-t^l) + N_{l-L+1}(2L)(1-t^{l-1})] + O(q^{2L+1}h) \tag{15}$$

where $N_J(2L)$ is the number of ways that $2L$ missing bonds can be arranged such that there are J sites in the cell (including both ends) being connected. The value of $N_J(2L)$ is irrelevant to the critical behaviour. As we will find at the critical point $p^* = 1$, $h^* = 0$ the scaling power y_h is determined by the term $(-t^l p^m)$ only.

Recursion relations are obtained by equating (12) to (13) and (14) to (15). The following results are easily found. The critical (fixed) point is at $p^* = 1$, $h^* = 0$, and

$$\partial \tilde{p}/\partial p|_* = (l-L+1)^{2/L(L+1)}, \tag{16}$$

$$\partial \tilde{h}/\partial h|_* = l/L, \tag{17}$$

$$\partial \tilde{p}/\partial h|_* = 0, \qquad \partial \tilde{h}/\partial p|_* = 0 \tag{18}$$

where (8) has been used to obtain (16). Since $b = l/L$, from (10), we find $\lim_{l\to\infty} y_p = 2/L(L+1)$ and $y_h = 1$. Using the scaling relations (11), we obtain the following exponents: $2 - \alpha = L(L+1)/2$, $\gamma = \nu = L(L+1)/2$, $\eta = 1$, $\beta = 0$ and $\delta = \infty$. The 'thermal' exponents obtained here are consistent with the results obtained by using the transfer-matrix method (Zhang *et al* 1983). The magnetic exponents obtained here are new results.

Although the site and bond percolations do not belong to the same universality when $L \geq 2$, however, Suzuki's weaker universality still holds (Suzuki 1974). The renormalised exponents ($\hat{\gamma} = \gamma/\nu = 1$, $\hat{\beta} = \beta/\nu = 0$, $\hat{\eta} = \eta = 1$, $\hat{\delta} = \delta = \infty$ and $(2-\alpha)/\nu = 1$) are both independent of L and independent of site or bond percolation.

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