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LETTER TO THE EDITOR

Large-cell renormalisation group for the backbone problem in percolation†

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Abstract. We give a position-space renormalisation group treatment of percolation backbones. Introducing a ghost field which couples only to backbone bonds, we put this problem on the same conceptual footing as pure percolation. This framework allows us to apply scaling arguments to obtain all the exponents from the scaling powers $\tilde{y}_p$ and $\tilde{y}_h$; these in turn are calculated from the renormalisation group using large cells.

1. Introduction

Percolation as a model of disordered systems has seen numerous applications in recent years (Stauffer 1979 and references therein). One such example is conduction through a lattice in which conducting and non-conducting bonds are randomly distributed with probabilities p and $(1-p)$ respectively (see, e.g., Kirkpatrick 1973). If one applies a potential across a cluster of conducting bonds (figure 1(a)), the bonds fall into two classes: '*backbone*' bonds, which carry current (figure 1(b)), and 'dangling ends', through which no current flows. Previous work on the problem has been limited to a Monte Carlo calculation of the order parameter exponent by Kirkpatrick (1978) using finite-size scaling arguments.

Here we put the backbone problem on the same conceptual footing as pure percolation. In analogy to pure percolation, we take the 'free energy' $\bar{G}(p, \bar{h})$ as the

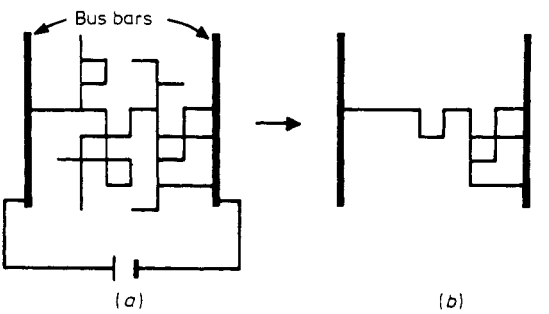

Figure 1. Bus bars are attached to the extremities of a cluster and a potential difference applied (a). Current flows in the backbone bonds (b), but not through 'dangling ends' which are attached to the backbone at only one vertex.

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mean number of finite backbones per lattice bond, where $\bar{h}$ is a 'ghost' field *which couples only to backbone bonds.* We assume $\bar{G}(p, h)$ to be, asymptotically, a generalised homogeneous function of the parameters $(p-\bar{p}_c)$ and $\bar{h}$, with scaling powers $\bar{y}_p$ and $\bar{y}_h$ respectively. The exponents of interest are then derived from the scaling powers. We show that $\bar{y}_p = y_p$, the scaling power for pure percolation, and $\bar{p}_c = p_c$. Furthermore we calculate $\bar{y}_h$ from a large-cell transformation.

We choose the order parameter

$$\bar{P}(p) \sim (p-p_c)^{\bar{\beta}} \tag{1a}$$

to be the fraction of occupied bonds in the backbone of the infinite cluster, in analogy with $P(p) \sim (p-p_c)^{\beta}$, the fraction of occupied bonds in the *entire* infinite cluster (figure 2(*a*)). Similarly, the exponent $\bar{\gamma}$ describes the divergence of the mean size of finite backbones $\bar{S}(p)$

$$\bar{S}(p) \sim |p-p_c|^{-\bar{\gamma}} \tag{1b}$$

in analogy with $S(p) \sim |p-p_c|^{-\gamma}$, the mean size of finite clusters (figure 2(*b*)).

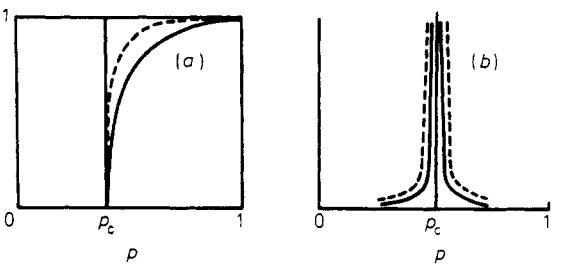

Figure 2. Schematic behaviour of backbone quantities (full curves) as a function of pure percolation quantities (broken curves). (*a*) shows the order parameters P and $\bar{P}$, while in (*b*) we sketch the mean size functions S and $\bar{S}$.

We introduce the 'magnetic' field mentioned above using the ghost site concept (Griffiths 1967, Kasteleyn and Fortuin 1969). This extra site, off the lattice, connects with every backbone bond on the lattice with probability $\bar{h}$. Thus $\bar{G}(p, \bar{h})$, the mean number of finite backbones, includes only those clusters in which none of the backbone bonds has a connection to the ghost site. For this interpretation in pure percolation see, e.g., Reynolds *et al* (1977).

Due to the existence of a diverging length, standard renormalisation group techniques should apply. These lead to a scaling form for the singular part of $\bar{G}$,

$$\bar{G}_{\text{sing}}[L^{\bar{y}_p}(p-\bar{p}^*), L^{\bar{y}_h}(\bar{h}-\bar{h}^*)] = L^d \bar{G}_{\text{sing}}[(p-\bar{p}^*), (\bar{h}-\bar{h}^*)], \tag{2}$$

in the vicinity of the fixed point $(\bar{p}^*, \bar{h}^*)$. Here L is the length rescaling factor in the transformation, and d is the spatial dimension. The scaling powers $\bar{y}_p$ and $\bar{y}_h$ are defined in the neighbourhood of the fixed point in terms of the renormalised probabilities p' and h' through

$$(p'-\bar{p}^*) = L^{\bar{y}_p}(p-\bar{p}^*) \tag{3a}$$

and

$$(\bar{h}'-\bar{h}^*) = L^{\bar{y}_h}(\bar{h}-\bar{h}^*). \tag{3b}$$

The critical exponents $\bar{\beta}$ and $\bar{\gamma}$, in terms of the scaling powers, are

$$\bar{\beta} = (d - \bar{y}_h)/\bar{y}_p \tag{4a}$$

and

$$\bar{\gamma} = (2\bar{y}_h - d)/\bar{y}_p. \tag{4b}$$

These relations hold if $\bar{P}$ and $\bar{S}$ have the singular nature of the first and second ghost field derivatives of $\bar{G}$ respectively. This is true in pure percolation (Reynolds *et al* 1977), and for the backbone problem as well (cf §4 below). Having the scaling powers we can, in like manner, define all the usual critical exponents.

2. Renormalisation group transformation

We transform from a cell of side L, including ghost bond connections to backbone bonds, to a single lattice bond and a single ghost bond (cf figure 3). The renormalised lattice bond is occupied if the cell is spanned in one direction (Reynolds *et al* 1978). At $\bar{h} = 0$, this renormalisation group transformation for p' reduces to that of pure percolation. Therefore $\bar{y}_p = y_p$ and $\bar{p}^* = p^*$, where y_p and p^* pertain to pure percolation. On the square bond lattice treated here, $p^* = \frac{1}{2}$ exactly for all lattice rescalings where spanning is in one direction with non-periodic boundary conditions (Bernasconi 1978).

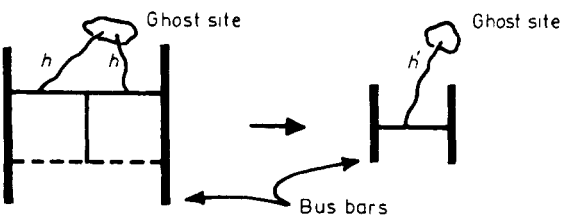

Figure 3. An example of the renormalisation group transformation for the $L = 2$ cell. Two lattice bonds are unoccupied (broken lines) in this particular configuration. Only backbone bonds have possible connections to the ghost site, as shown.

For current to reach the ghost site, the renormalised lattice bond and ghost bond must both be occupied. On the original 'site level', current must be able to enter the cell, flow through a backbone, and reach the ghost. The recursion relation involving $\bar{h}$ is then (cf Reynolds' PhD thesis (unpublished) and also Reynolds *et al* to be published)

$$p'\bar{h}' = 1 - \langle (1 - \bar{h})^{N_B(p)} \rangle. \tag{5}$$

Here N_B is the number of backbone bonds which can be reached from one edge of the cell for a particular configuration, and $\langle \ldots \rangle$ denotes the configurational average. For small $\bar{h}$, equation (5) becomes

$$p'\bar{h}' = \bar{h}\langle N_B(p) \rangle. \tag{6}$$

By inspection, the fixed-point value of the ghost field is $\bar{h}^* = 0$. The eigenvalue associated with the ghost field is

$$\bar{\lambda} = (\partial\bar{h}'/\partial\bar{h})\big|_{\substack{\bar{h}=\bar{h}^* \\ p=p^*}} = p^{*-1}\langle N_B(p^*) \rangle \tag{7a}$$

from which (cf equation (3*b*))

$$\bar{y}_h = \ln(p^{*-1}\langle N_B(p^*)\rangle)/\ln L. \tag{7b}$$

3. Large-cell calculation

We expect that the value of $\bar{y}_h$ should improve with increasing cell size, and that an accurate numerical estimate may be obtained by extrapolation (Reynolds *et al* 1978). To this end we have generated Monte Carlo data on $N_B(p^* = \frac{1}{2})$ for a sequence of cell sizes of up to 500×500 sites in two dimensions. We have used a depth-first-search algorithm, following Tarjan (1972)†.

By plotting $\ln \bar{\lambda}_h(L)$ for this sequence of successively larger cell sizes against $\ln L$ (figure 4(*a*)), we find the slope $\bar{y}_h = 1{\cdot}63 \pm 0{\cdot}01$. Furthermore, $\bar{y}_h$ may also be extrapolated as the intercept of a plot of $\bar{y}_h(L)$ against $1/\ln L$ (figure 4(*b*)). The result $\bar{y}_h = 1{\cdot}63 \pm 0{\cdot}01$ agrees with the $\ln \bar{\lambda}_h$ extrapolation. Using $y_p^{-1} = 1{\cdot}356 \pm 0{\cdot}015$ (Reynolds *et al* 1978), we obtain $\bar{\beta} = 0{\cdot}50 \pm 0{\cdot}02$ and $\bar{\gamma} = 1{\cdot}71 \pm 0{\cdot}04$ (cf equations (4*a*, *b*)). Our value for $\bar{\beta}$ is consistent with that of Kirkpatrick (1978), who finds $\bar{\beta} = 0{\cdot}5$–$0{\cdot}6$ using finite-size scaling arguments and Monte Carlo data on the square site lattice. The operational procedure for determining $\bar{\beta}$ by this renormalisation group in the limit of large cells coincides with the finite-size scaling calculation. In this limit, the dominant

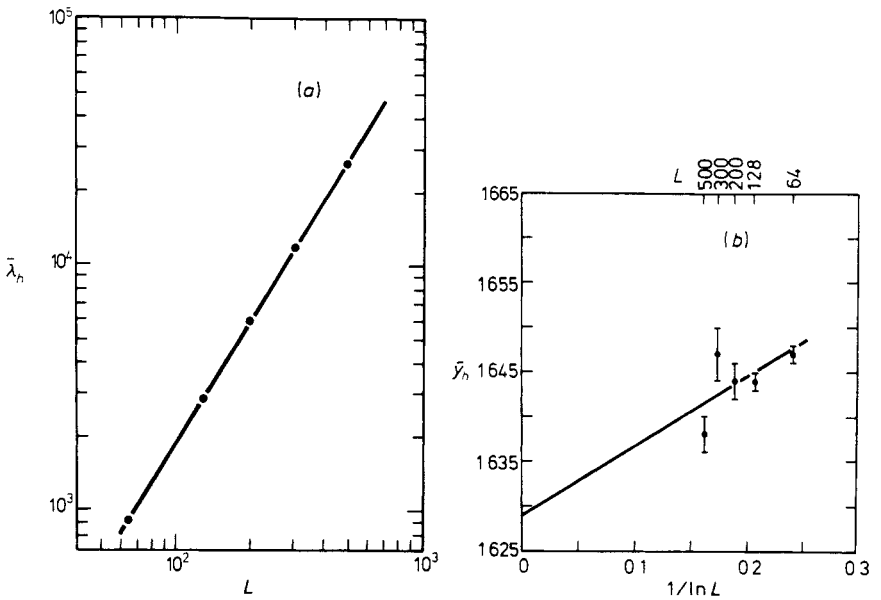

Figure 4. Renormalisation group data are extrapolated to the limit of infinite cell size to obtain an estimate of the true value of $\bar{y}_n$. (*a*) $\ln \lambda_h(L)$ against $\ln L$, where L is the rescaling length. The slope is $\bar{y}_h = 1{\cdot}63 \pm 0{\cdot}01$. (*b*) $\bar{y}_h(L)$ against $1/\ln L$. The intercept is $\bar{y}_h = 1{\cdot}63 \pm 0{\cdot}01$. The straight lines shown are least-squares fits to the data. The error bars in (*a*) are too small to be shown. The number of Monte Carlo trials ranges from 2000 at $L = 500$ to 6000 at $L = 64$.

† We note that the search algorithm mentioned above includes 'bridge' bonds in the backbone. These are bonds which connect two equipotential vertices of the electrical backbone and do not actually carry current.

contribution to $\bar{\lambda}_h$ comes from realisations with a spanning backbone. In our calculation we have, in fact, ignored 'edge' contributions (which vanish as the surface to volume ratio of the cell) for computational convenience.

4. Generating function for the backbone problem

In equations (4*a*, *b*) we have taken the usual relation between the exponents and the scaling powers. This may be justified as follows. The mean number of finite backbones per lattice bond, $\bar{G}(p, \bar{h})$, is a generating function for moments of the backbone size distribution $\bar{n}_b(p, \bar{h}) = \bar{n}_b(p)(1-\bar{h})^b$. This is in analogy to pure percolation. Here $\bar{n}_b(p)$ is the average number of finite backbones of size b, per lattice bond, in the absence of a ghost field. For non-zero $\bar{h}$,

$$\bar{G}(p, \bar{h}) = \sum_{b=0}^{\infty} \bar{n}_b(p, \bar{h}). \tag{8}$$

The first moment of $\bar{G}(p, \bar{h})$ is the fraction of lattice bonds in finite backbones. It is also proportional to the first derivative with respect to $\bar{h}$ of the generating function:

$$\bar{G}^{(1)}(p, \bar{h}) = \sum_{b=1}^{\infty} b\bar{n}_b(p, \bar{h}) = -(1-\bar{h})\,\partial\bar{G}(p, \bar{h})/\partial\bar{h}. \tag{9}$$

Defining $f_B(p)$ as the fraction of lattice bonds in backbones both finite and infinite,

$$p\bar{P}(p, \bar{h}) = f_B(p) - \bar{G}^{(1)}(p, \bar{h}). \tag{10}$$

Assuming $f_B(p)$ is regular, $\bar{P}$ must be asymptotically equal to the singular part of $\bar{G}^{(1)}$.

In the same manner, $\bar{S}(p, \bar{h})$, the weight-averaged mean backbone size is given by

$$\bar{S}(p, \bar{h}) \equiv \bar{G}^{(2)}(p, \bar{h}) = \sum_{b=1}^{\infty} b^2\bar{n}_b(p, \bar{h}) \sim \partial^2\bar{G}/\partial\bar{h}^2. \tag{11}$$

5. Summary

We have introduced a ghost field $\bar{h}$ which couples only to backbone bonds. By doing so we have put the backbone problem on the same footing as pure percolation. We have defined a large-cell renormalisation group transformation for this problem, and calculated the associated scaling powers $\bar{y}_h$ and $\bar{y}_p = y_p$. The average number of finite backbones is shown to be a generating function for the quantities of interest (e.g. $\bar{P}$ and $\bar{S}$).

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