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LETTER TO THE EDITOR

Diffusion on lattice animals and percolation clusters: a renormalisation group approach

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Abstract. A position space renormalisation group method is developed to study the scaling properties of random walks on fractals. Calculations in two dimensions for site lattice animals and site percolation clusters yield numerical results for the critical exponent defined by the asymptotic behaviour of the root-mean-square displacement of the walker. The renormalisation group results are consistent with recent Monte Carlo calculations.

The problem of random walks on random networks was proposed by de Gennes (1976) in the context of an 'ant in the labyrinth'. Much of our present understanding of this problem has been the result of computer simulations and scaling arguments. The goal of this paper is to develop a position space renormalisation group method applicable to random walks on self-similar geometrical structures. Examples of such 'fractals' are percolation clusters at threshold and random lattice animals.

Fractals are characterised in part by the fractal dimension d_f defined by (Mandelbrot 1982)

$$s \sim (R_s)^{d_f} \qquad (s \text{ large}), \tag{1}$$

where s is the number of particles, and R_s is a linear dimension of the cluster. The root-mean-square displacement R_N of the random walker from the origin defines a second length scale (Mitescu and Roussenq 1983). The 'fractal dimension of the walk' d_w on the fractal aggregate is defined by the asymptotic behaviour

$$N \sim (R_N)^{d_w} \qquad (N \text{ large}), \tag{2}$$

where N is the number of steps in the walk. For the special case $d_f = d$, we have $d_w = 2$ independent of the spatial dimension d of the lattice and the relative values of R_N and R_s. Our interest is in the 'self-similar' limit (Gefen *et al* 1983) for which $1 \ll R_N \ll R_s$. Although in this limit d_w depends on d, Alexander and Orbach (1983) have conjectured that the ratio $2d_f/d_w = \frac{4}{3}$, independent of d, for random walks on percolation clusters. Arguments have been made (Leyvraz and Stanley 1983, Meakin and Stanley 1983, Rammal and Toulouse 1982) to support the more general conjecture that $2d_f/d_w = \frac{4}{3}$ for all homogeneous fractals of which percolation clusters and lattice animals are examples.

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A position space renormalisation group (PSRG) treatment of random walks on lattice animals and percolation clusters requires the determination of the recursion relations for both the random walk and the cluster. In order to determine the latter for both clusters in a unified formalism, we adopt the two-parameter approach of Family and Coniglio (1980) in which a weight K is identified with an occupied site, and an independent parameter q is associated with an empty site. Since the cluster configurations to be included in the recursion relations for K and q depend on the random walk renormalisation transformation, we first discuss the latter.

To determine the recursion relation for the random walk, we interpret the random walk as a kinetic process (Nakanishi and Family 1983), and introduce a weight w to describe the walk and its behaviour under rescaling. The weight associated with a particular step at site a is w/z_a, where z_a is the coordination number at site a. Since there are z_a possible directions, the total weight of all possible steps from a particular site is w. This kinetic interpretation of the random walk problem differs from the more common 'static' interpretation (see for example Family and Gould 1984) for which all walks with an equal number of steps are given equal weight. (There is no difference in the two interpretations on the perfect lattice since the coordination numbers for every site are identical.)

The requirement, that a step of the random walk be allowed only between occupied sites of the original lattice and between renormalised sites on the rescaled lattice, implies that a minimum of two cells is necessary for a consistent determination of the random walk renormalisation transformation. In addition, since the weight associated with a particular step depends on the coordination number of the initial site, the occupancy of all the nearest-neighbour sites of the initial site is relevant. Therefore for the square lattice we adopt a five-cell geometry (see figure 1) and consider all walks originating from the central cell. In order that walks be allowed to each of the four nearest-neighbour cells (labelled N, S, E and W in figure 1), we assume the existence of a connected path between the central cell (cell C) and each adjacent cell,

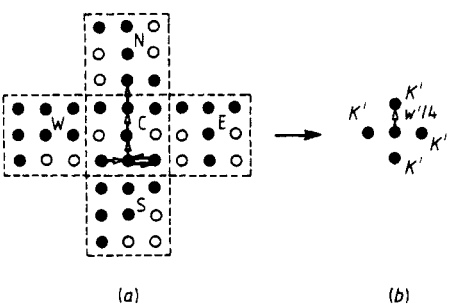

Figure 1. The five-cell geometry necessary on the square lattice for a consistent determination of the random walk renormalisation transformation. We assume the existence of a connected path between the central cell C and each of its neighbours N, S, E and W. In addition, a connected spanning path exists in each of the five cells. The starting point for each walk is the lower-left corner of cell C; a walk spans if it reaches the bottom row of cell N. The example shown (for cells of linear dimension $b = 3$) corresponds to one term in the generating function $R_w(K, q, w)$ containing all spanning walks on all spanning clusters. (a) A spanning walk of weight $(w^6/512)K^{30}q^{15}$. There are 30 occupied sites (full circles) with weight K and 15 empty sites (open circles) with probability q; the weight of a step is w/z_a, where z_a is the coordination number at site a. (b) The corresponding walk on the renormalised lattice.

as well as the existence of a spanning path within each of the five cells. These assumptions allow us to determine the weight of all walks from the central cell to its nearest neighbours. An example of the rules for weighting the walks is given in figure 1. We consider only one spanning rule for the random walks: the starting point of the walk is fixed at the lower-left corner of cell C, and a walk spans if the walk traverses vertically to cell N. The form of the recursion relation is

$$(w'/4)K'^5 = R_w(K, q, w) \tag{3}$$

where the generating function R_w is the weighted sum of all spanning walks on all possible clusters. The renormalised weight w' is the generating function of a single step on the rescaled lattice. The factor of $\frac{1}{4}$ in (3) is unambiguous and necessary to ensure that the recursion relation reduces to the correct form for the perfect lattice. The fractal dimension d_w defined in (2) is given by $d_w = \ln(b)/\ln(\lambda_w)$, where $\lambda_w = \partial w'/\partial w$ is evaluated at the critical fixed point parameters of the cluster K^*, q^* and at the critical fixed point w^* of (3) (cf Stanley *et al* 1982).

A consistent evaluation of (3) for d_w requires the determination of the renormalisation transformations for K and q with the same five-cell geometry. The complications due to the requirement of a connected path between cell C and cells N, S, E and W can be minimised by noting that the existence of such a path depends only on the 'surface' sites of cell C and the configurations of the surface row or column adjacent to cell C of the nearest-neighbour cells. Our procedure is to generate all connected clusters which span a cell of linear dimension b, and classify these clusters according to their various possible row or column configurations. The total weight of each possible row or column configuration is determined by summing the weights of all spanning clusters with the same row or column configuration. We obtain the recursion relation for K'^5 by determining the weight of each spanning cluster of cell C and multiplying it by the total weight of each adjacent row or column which yields a connected path. In order to maintain symmetry between the weights of the row and column configurations, we define a cell to be occupied only if a connected path exists in both the horizontal and vertical directions. (The results for d_w are insensitive to this spanning rule.) Since we are interested in the statistics of percolation clusters, we generate all spanning clusters rather than all spanning configurations. Family and Reynolds (1981) discuss the relation of these two approaches and show that they are equivalent for percolation clusters at threshold. For the lattice animal problem we follow Family (1983) and consider only clusters originating at the lower-left corner of the centre cell. No such restriction is made for the percolation clusters.

The results of the five-cell calculation of d_f and K^* for site lattice animals and site percolation clusters on the square lattice are shown in table 1 for $b = 2$, 3 and 4. Note that $q^* = 1$ for lattice animals and $q^* = 1 - K^*$ for percolation clusters. If we assume (cf Family and Reynolds 1981) that $d_f(b)$ behaves as $d_f(b) = d_f + a_1(\ln\ b)^{-1} + a_2(\ln b)^{-2}$, we find the extrapolated values $d_f = 1.50$ and $d_f = 1.76$ for lattice animals and percolation clusters respectively (see table 3). These values are consistent with the extrapolated one-cell results of $d_f = 1.48$ for lattice animals (Family 1983) and $d_f = 1.85$ for percolation clusters (Family and Reynolds 1981) using the same spanning rule.

The enumeration of the spanning cluster configurations and the calculation of K^* makes it possible to proceed with the determination of d_w. The existence of two length scales in the present problem requires that the maximum number of steps in a walk be limited such that $R_N \ll R_s$. We know that at the critical weight w^* corresponding

Table 1. Results of the five-cell calculation of the fractal dimension d_f and the fixed point K^* of site lattice animals and site percolation clusters on the square lattice. The geometry of the five-cell configurations is shown in figure 1; the linear dimension of each cell is b.

	Lattice animals		Percolation clusters	
b	d_f	K^*	d_f	K^*
2	1.6521	0.5035	1.8189	0.8016
3	1.5958	0.4104	1.8068	0.7593
4	1.5760	0.3672	1.7995	0.7308

to the limit $N \to \infty$, only random walks of length $R_N \sim N^{1/d_f}$ are important. Hence we adopt the rule that spanning walks whose number of steps is greater than b^2 are not included in R_w. For the same reason we omit walks which return from sites in the neighbouring cells to sites in cell C. Note that these rules and our other reasonable assumptions for determining R_w become exact in the large cell limit.

The explicit enumeration of the spanning random walks on the many possible five-cell clusters is done using the counting method described in Family and Gould (1984). For a given central cell configuration, we group together all neighbour cell configurations which yield the same coordination numbers of the occupied surface sites of the central cell. Such a grouping, which we refer to as 'method E', reduces computer time and allows us to calculate the coordination numbers exactly within the five-cell geometry. The results for d_f and w^* are given in table 2 for $b = 2$, 3 and 4. If we assume that d_w behaves as $d_w(b) = d_w + c_1(\ln b)^{-1} + c_2(\ln b)^{-2}$, we find that $d_w = 2.18$ for lattice animals and $d_w = 2.76$ for percolation clusters (see table 3). (For comparison our result for a random walk on a perfect lattice is $d_w = 2.05$ rather than the exact

Table 2. PSRG results of a five-cell calculation of the fractal dimension d_w and fixed point w^* of random walks on the perfect lattice, site lattice animals and site percolation clusters on the square lattice. Method E corresponds to the exact calculation of the coordination numbers of the occupied surface sites of the central cell and is expected to give more reliable results for small cells than Method A in which the coordination numbers are obtained by an average over all possible adjacent configurations.

	b	2	3	4
Perfect	w^*	1.6211	1.3443	1.2311
Lattice	d_w	1.5165	1.6570	1.7229
Lattice animals				
Method E	w^*	1.7018	1.3203	1.1347
	d_w	1.5232	1.6603	1.7382
Method A	w^*	1.7228	1.4309	1.2633
	d_w	1.5316	1.6912	1.7680
Percolation clusters				
Method E	w^*	1.7517	1.4251	1.4129
	d_w	1.5470	1.7039	1.8409
Method A	w^*	1.7593	1.4981	1.3163
	d_w	1.5470	1.7197	1.7895

Table 3. The extrapolated values of d_f, the fractal dimension of the cluster, and d_w, the fractal dimension of the random walker on the cluster substrate, obtained for lattice animals and percolation clusters from the present five-cell PSRG calculation. The coordination numbers were obtained using method E as explained in the text. The calculated values of the ratio $2d_f/d_w$ are also shown and found to be consistent with the conjectured value $\frac{4}{3}$ for homogeneous clusters (Leyvraz and Stanley 1983, Rammal and Toulouse 1983, Alexander and Orbach 1982).

	Lattice animals	Percolation clusters
d_f	1.50	1.76
d_w	2.18	2.76
$2d_f/d_w$	1.38	1.28

value $d_w = 2$.) Although the numerical value of d_w differs considerably for lattice animals and percolation clusters, we note that the ratio $2d_f/d_w$ obtained in our five-cell PSRG calculation is close to $\frac{4}{3}$ for both clusters (see table 3); this numerical result is consistent with the generalised Alexander–Orbach conjecture (Leyvraz and Stanley 1983, Meakin and Stanley 1983, Rammal and Toulouse 1982).

In the limit where the size of the cluster is restricted to be larger than the span of the walk, Monte Carlo results for $d = 2$ give $d_w = 2.6 \pm 0.3$ for lattice animals (Wilke *et al* 1983) and $d_w = 2.84 \pm 0.05$ for percolation clusters (Havlin and Ben-Avraham 1983). The small cell PSRG values for d_w are consistent with these results. However, if we determine the coordination number of each surface site of the central cell by averaging over all possible configurations of adjacent cells E, S and W, we find that the extrapolated value of d_w is inconsistent with the Monte Carlo result for percolation clusters. We refer to this modification as 'method A'. Since a walk to a site of cell N is not possible unless the site is occupied, the average is made for given configurations of cells C and N. The most consistent results for w^* and d_w are found by averaging z rather than $1/z$. From the results shown in table 2, we find the extrapolated values $d_w = 2.16$ for lattice animals and $d_w = 2.10$ for percolation clusters.

Sahimi and Jerauld (1983) have developed a one-cell PSRG approach and found $d_w = 2.81$ for $d = 2$ percolation clusters. They adopt a static interpretation of the random walk, an interpretation which is inconsistent with the Monte Carlo experiments. Moreover, their one-cell calculation is not consistent with the requirement that a step be allowed only between occupied sites. Keyes (1983) has developed a two-cell PSRG method which in detail is different from ours and obtains $d_w = 2.47$ on the triangular lattice.

If we use the extrapolated values of d_w shown in table 3 and finite size scaling considerations, we obtain $w^* = 1.00$ for lattice animals and $w^* = 1.32$ for percolation clusters. Since the same considerations yield $w^* = 1.11$ for the perfect lattice rather than the exact result $w^* = 1.00$, we conjecture that w^* for lattice animals is less than unity. These relative values of w^* are indicative of the fact that w^* as well as d_w are not monotonic functions of the fractal dimension d_f of the cluster. The physical significance of w^* can be understood by noting that w' can be interpreted as being proportional to the probability of a step to an occupied nearest-neighbour site on the renormalised lattice; its inverse is proportional to the mean time for waiting at a site before a step. Since w^* represents an unstable fixed point, we see that the flow from the value $w = 1$ on the original lattice is toward the stable fixed point $w^* = 0$ for

percolation clusters. For lattice animals the flow appears to be towards the stable fixed point $w^* = \infty$. Hence the renormalised waiting time on long length scales is found to be short for lattice animals and long for percolation clusters. An intuitive explanation of this conjectured qualitatively different behaviour would be of interest.

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