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LETTER TO THE EDITOR

Percolation and motion in a simple random environment

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Abstract. We present a particularly simple model of deterministic classical motion in a two-dimensional random environment. As the parameters of the model are varied, a transition occurs from all trajectories being localised to some being extended. We construct a mean-field theory for this transition, and relate the model exactly to percolation models in particular parameter ranges. We point out that it is a member of a new class of site percolation analogues of directed bond percolation.

Recently, there has been a lot of interest in random walks in a random environment (RWRE) (e.g., Sinai 1982, Gates and Westcott 1982, Fisher 1984, Fisher *et al* 1985). In this letter we discuss a particularly simple model of *deterministic* classical dynamics in a random environment, which we relate to a generalised form of percolation. The model shows a transition from all trajectories being localised to some being extended, as parameters are varied. The model is defined on a 2D lattice, with the velocity of the 'particle' being allowed to change direction, but not magnitude, the change being determined by a quenched random rotation matrix on each lattice site. As might be expected, the physical origin of this discrete model was a charged particle moving in a random magnetic field, which may have astrophysical applications (e.g., short time dynamics of particles in a turbulent magnetised plasma). Of the RWRE models, the closest relative is Gates and Westcott (1982). In this letter, we restrict ourselves to establishing some exact results and constructing a mean-field theory of the transition.

The model consists of an underlying lattice with 'instructions' defined at each site; trajectories are defined by following the instructions. To be more precise: a particular realisation of the model is a square lattice of sites, with a two-dimensional rotation matrix, $\mathbf{R}(\boldsymbol{n})$, associated with each site, $\boldsymbol{n}$. The magnitude, θ, of the rotations may be 0, $\pm\pi/2$ or π, sites with these values being called forwards, left, right (or generically turning) and backwards sites respectively. In figure 1, which shows a typical realisation, the symbols on the sites indicate the magnitudes in an obvious manner. The magnitudes are picked at random, with no correlation between different sites. A particular realisation (or configuration) may be characterised by the set of probabilities $\{P(\theta)\}$ that a randomly picked site will have magnitude θ. This set of parameters contains the important information.

A trajectory is denoted by the set $\{\boldsymbol{r}(L)\}$, where $\boldsymbol{r}(L)$ is the position of the 'particle' or the front of the trajectory at time step L. Alternatively, we may use the set of steps $\{\boldsymbol{l}(L)\}$ defined by

$$\boldsymbol{r}(L) \equiv \boldsymbol{r}(L-1) + \boldsymbol{l}(L). \tag{1}$$

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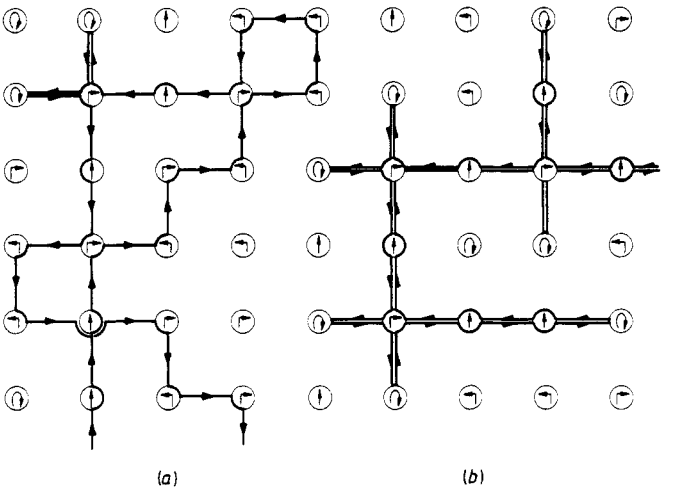

Figure 1. A realisation of the model. (*a*) A typical trajectory is indicated. (*b*) A trajectory to illustrate the 'sausage' percolation idea is illustrated on the right.

The steps are generated by

$$\boldsymbol{l}(L+1) = \mathbf{R}(\boldsymbol{r}(L)) \cdot \boldsymbol{l}(L). \tag{2}$$

Thus, the rotation matrix on a site rotates incoming directions into outgoing ones. Note that this is a one to one relationship, so the trajectory cannot branch, merge or end. It is also important to note that the $\mathbf{R}(\boldsymbol{n})$ do not depend on the time step—they are quenched. A consequence of these two points is that all trajectories must either be infinite or cyclic, and moreover, that any trajectory which is contained in a finite area of the lattice must be cyclic.

In practice, we may initiate a trajectory by picking a site and direction and working forwards and backwards using (1) and (2). In general the trajectory (constructed as above) will not visit every site from all four directions (it is not space filling, in a general sense), so any realisation of the model will have many distinct trajectories associated with it. These trajectories will not overlap (in the sense of steps being parallel and between the same two sites). This is again because they cannot merge or branch.

It is natural to compare the trajectories with random walks. The most closely related type is the true self-avoiding walk (TSAW) of Amit *et al* (1983). In our case, we can regard the rotations at each step as independent random variables until a site is visited twice, when the rotation is uniquely determined. This is similar to the bias in picking the next step in the TSAW when on a neighbour of a previously visited site. The difference is in the peculiarity of the nature of the unique determination. This will be discussed more formally elsewhere.

Having defined the model, the interesting question is: does the nature of the trajectories vary as realisations are picked with differing $\{P(\theta)\}$? By considering extreme cases of all forwards sites ($P(0)=1$) and all backwards sites ($P(\pi)=1$) we see that it must: for $P(0)=1$ all trajectories are straight lines which extend across the whole lattice, whereas for $P(\pi)=1$ each trajectory is localised on two sites, being

reflected between them. As $P(\pi)$ is decreased away from unity one might expect a transition to occur, when extended trajectories appear, with an associated phase diagram in the three-dimensional space of the $\{P(\theta)\}$ (3D as the $P(\theta)$ must add to unity). Some interesting quantities to investigate are: the probability of a site having an infinite trajectory passing through it (reminiscent of the probability of belonging to the infinite cluster in percolation); the index γ in $\langle r^2(L)\rangle \sim L^\gamma$ for extended trajectories where $\langle\ \rangle$ indicates an average over initial sites on a given configuration; the distribution of localisation lengths for localised trajectories defined (for a particular trajectory) by

$$\lambda^2 = \lim_{\sigma\to\infty} \frac{1}{\sigma} \sum_{\tau=0}^{\sigma} (r(\tau) - r(0))^2 \tag{3}$$

for fixed $\{P(\theta)\}$, and how the average localisation length diverges as $\{P(\theta)\}$ approaches a delocalisation transition.

We will now consider some regions of the 'phase diagram' where, by exact or approximate mapping onto percolation problems, we bound or estimate the domains in which extended trajectories exist, constructing a mean-field theory of the transition.

A connection with percolation is obvious at an intuitive level—extended trajectories percolate across the sample—however, the exact connection is more subtle and depends on the region being studied, as will be shown. Firstly, we introduce a new variable, $\Delta = P(\pi/2) - P(-\pi/2)$, and use $P(0)$, $P(\pi)$ and Δ as the variables to label the axes of the phase diagram—see figure 2(*a*). The allowed region is inside the tetrahedron. For $\Delta = 0$ (i.e. no left or right bias), it reduces to the triangle in figure 2(*b*). Initially we consider this restricted region.

Unless a connected cluster of non-backwards sites (i.e. $\theta \neq \pi$) exists across the sample, no extended trajectory can exist. This is because a backwards site merely reflects a trajectory back onto the site from whence it came, thus being unable to connect two sites. Thus the critical probability for site percolation, $P_c \simeq 0.6$, yields a bound that extended trajectories cannot exist for $(1 - P(\pi)) \leqslant P_c$. This bound is shown by the vertical line in figure 2(*b*). We can also get an exact answer for the diagonal boundary line in figure 2(*b*), $P(0) + P(\pi) = 1$. Here the trajectories are 'sausages' confined between backwards sites. The average length of the sausages is $P(\pi)^{-1}$, showing an expected divergence as $P(0)$ tends to unity. The model is equivalent to one-dimensional site percolation, with the backwards sites being analogous to the unoccupied sites.

We may use this picture, with the addition of turning sites, as the basis for an approximate analysis of the whole of the parameter space. This treatment constitutes a mean-field theory of the transition to extended trajectories. On the right-hand side of figure 1, we see that the addition of turning sites connects intersecting sausages to form clusters. This naturally implies a percolation approach to estimating when an extended trajectory will appear. Consider a backwards site and move along a sausage away from it; what is the probability, σ, of not percolating? The first contribution is from the smallest non-percolating sausage, where the next site is a backwards one; this obviously has weight $P(\pi)$. The next shortest has an intermediate site which may be straight on, or a turning site, leading to a non-percolating sausage section (each with probability σ) to each side. These have weights $P(0)$ and $\sigma^2 P(T)$ respectively, where $P(T) = P(\pi/2) + P(-\pi/2)$. We may continue to build up the non-percolating sausage, site by site, leading to a geometric series which self-consistently defines σ.

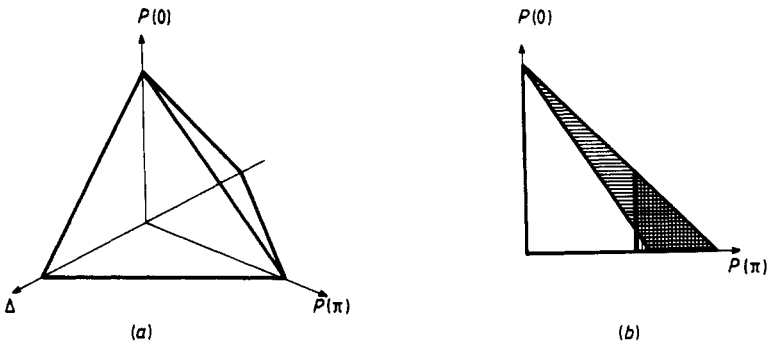

Figure 2. (*a*) The general parameter space. (*b*) For $\Delta = 0$, with bound on region of extended trajectories (vertical line) and estimate of transition line (diagonal line). Any extended trajectories are expected to be outside the union of the two shaded regions.

After a little rearrangement we find

$$\sigma = (P(\pi) + P(T)\sigma^3)/(1 - P(0)), \tag{4}$$

a result also obtained by Chalker (1985) in the equivalent problem of solving the model on a four-fold coordinated Cayley tree. If we define $\sigma \equiv 1 - \rho$, then for small ρ we may determine the growth in percolating probability, that is

$$\rho \simeq [2 - (P(\pi)/P(T))]/3. \tag{5}$$

Therefore, $P(\pi)/P(T) = 2$ or $3P(\pi) + 2P(0) = 2$ is the boundary of extended trajectories, and is shown in figure 2(*b*).

The above treatment constitutes a 'mean-field theory' for the transition, the approximation being the neglect of loops in the sausage percolation cluster: if there are no loops, then there is only one trajectory per sausage cluster, visiting all sites. Thus we may identify sausage and trajectory percolation. With loops, this is not generally true. The approximate treatment should be best near $P(0) = 1$, where loops are improbable, and worst when $P(\pi)$ tends to unity, as we will see later. Another point to stress is that a conventional mean-field theory—where only the single sites were considered (rather than using the sausages as building blocks)—would neglect the strong correlations of the sausage structure, particularly near $P(0) = 1$.

We next examine the effect of left-right bias, by considering the line $P(\pi/2) + P(-\pi/2) = 1$. Consider a cluster of lefts surrounded by rights. It is easy to see that inside the cluster, the trajectories will be cyclic on groups of four squares, and that there will be two longer trajectories running around the boundary. The readers may convince themselves that this is the general structure by drawing a few pictures. Since the longer trajectories will mainly exist on the outside of clusters of lefts or rights, one expects that the existence of extended trajectories will be related to percolation. In fact the problem can be mapped onto *bond* percolation, as we will show. The argument is lengthy and we only give the main steps and their intuitive content.

In figure 3 we show a typical trajectory. It is clear that the trajectory can be generated by the barriers shown in the figure, which we will define and construct below. Locally, it is possible to define the barriers because any given trajectory may only enter

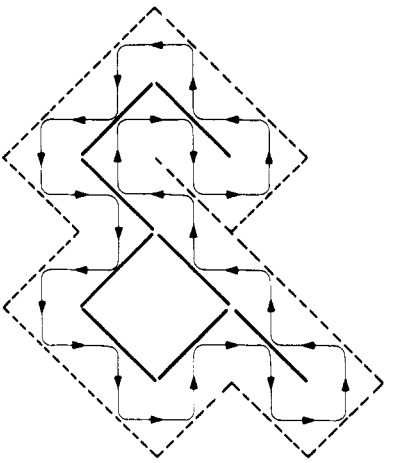

Figure 3. Interior and exterior barriers of a typical trajectory for a sample with only $\pm\pi/2$ sites.

a given site via opposite edges and not neighbouring ones. The barrier may be drawn diagonally across the site, as shown in figure 3. The constraint of entering via opposite edges is a consequence of the trajectory being unable to run between two sites in both directions: this can be proved for random walks (where each step is perpendicular to the previous one), of which our trajectories are a subset. This also implies that the trajectories do not cross themselves, although they may touch a barrier at the same place from both sides—a situation which occurs in figure 3.

Having defined the barriers locally, they may be connected to form a network by using two rules. Starting from a barrier on one site: if a neighbour is of the same type of site, then its barrier must be perpendicular to the first one, thus joining it at a vertex of the site; if, on the other hand, the neighbouring site is of the opposite type, then the barrier should be parallel to the first, leaving a gap through which the trajectory runs. Then repeat on the next site visited, etc. Note how these rules have been implemented in figure 3. Each finite trajectory, which visits more than four sites, is formed by reflection from an inner and outer set of barriers which reside on sites of opposite types (there is no ambiguity about 'inner' and 'outer', as the trajectories do not cross themselves). Conversely, any cluster of barriers constructed by these rules (not following the trajectory but working away from an initial site in all directions) will be surrounded by a trajectory. One should note that on any site there is a second barrier separating the other two sections of trajectory. The same rules of determination apply to this second set of barriers. The set of all trajectories on a given realisation of the model is divided into two groups, which are determined by the two networks of barriers.

If we take one of the two networks of barriers and moreover pick the barriers residing on one of the two types of sites, then the clusters of barriers may be thought of as bond percolation clusters (the sections of barrier are the bonds). The trajectory encloses the perimeter of the cluster and the trajectory length is proportional to the perimeter length. The probability of a bond existing is the probability of the type of site it is associated with. The trajectories become longer as the difference between the probabilities of lefts and rights decreases, some trajectories becoming extended when

$P(\pi/2) = P(-\pi/2)$. We note that the mean-field theory does not predict this transition, as it makes no distinction between left and right sites. In fact, a percolation argument can also be used on the line $P(\pi) + P(\pi/2) = 1$ (or $-\pi/2$), yielding a site percolation transition at $P(\pi/2) = P_c$. A bound can be placed on extended trajectories not existing for $P(\pi/2) \geqslant P_c$ on the line $P(0) + P(\pi/2) = 1$, again using a site argument.

Finally, we should mention a more fundamental connection of this model to percolation, which does not depend on any particular parameter range. There are fundamentally two types of percolation—site and bond. In the case of bond percolation there is a directed variant (e.g., Kinzel 1983). Our model seems to be an example of a site analogue of directed bond percolation, where the direction on the bond is analogous to the matrix on each site. In our case all bonds are present, but the connections between the bonds (the matrices) are the random variables. In directed bond percolation all *sites* are present, however, the *bonds* are random variables. Our model becomes more similar to general directed bond percolation (where both, either or neither bond may be present), when a more general matrix, connecting incoming bonds to outgoing bonds, that a pure rotation is allowed—for instance no connection at all (site absent)—or a many-to-one relation between incoming and outgoing bonds.

Lattice versions of the Lorentz gas and Ehrenfest's wind-tree model are also variants of this (e.g. Spohn (1980) and references therein, particularly Gates (1972a, b)), and our model may be thought of as a rotational analogue of them.

An application of our model is in the generation of closed random curves, in particular, the excluded volume properties of the line $P(\pi/2) + P(-\pi/2) = 1$ could be useful. This might be used in studies of ring polymers, either in solution or in the melt (by considering the entire set of trajectories).

A number of interesting questions are still open. What is the accuracy of the mean-field theory? By analogy with the special properties of random walks in two dimensions, it is possible that all trajectories (except at $P(0) = 1$, $P(\pi/2) = P(-\pi/2) = 1$ and $P(\pi/2) = P_c$, $P(\pi) = 1 - P_c$) are localised. If there are extended trajectories, what is γ in $\langle R^2 \rangle \sim S^\gamma$? There is no obvious Flory argument, as the effect of a trajectory on itself is not just 'repulsion'. To what extent are trajectories correlated with each other? One might wonder about 'screening'. What happens in higher dimensions? There are several possible generalisations, simple arguments leading to upper critical dimensions of four or two. Is a renormalisation group treatment possible? Is the transition first order? We are currently studying real space treatments, which seem sensitive to the weight function employed. We are also performing Monte Carlo calculations. What is the relation to the continuum problem? It is interesting to note that in the continuum problem, percolation occurs in the 'adiabatic' limit of the correlation length of the magnetic field being large compared to the RMS cyclotron radius—then the trajectories follow the contours of constant B, on a larger scale than the cyclotron radius (see, for example, Alfvén and Fälthammer 1963). Thus all trajectories except the one corresponding to the extended B-contour are localised, within the adiabatic approximation. Finally, can this lattice model be formulated in a Hamiltonian or Lagrangian manner? One problem is with the definition of a conjugate momentum.

To conclude, we have presented a new simple model of ballistic motion in a random environment. It shows a transition between all trajectories being localised to having extended ones. We have constructed a mean-field theory of this transition, and related the model to various particular percolation models. Finally, it was argued that it is a special case of a new class of percolation processes.

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