Exact Fractal Dimension of the Loop-Erased Self-Avoiding Walk in Two Dimensions

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The fractal dimension of the loop-erased self-avoiding walk is shown to be identical to that of the chemical path on equally likely spanning trees. This result is valid for arbitrary lattices and in all dimensions. In particular, in two dimensions, using the spanning tree correspondence and the known results for the Potts model from conformal field theory, the fractal dimension is shown to be exactly $\frac{5}{4}$ as conjectured by Guttmann and Bursill.

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The self-avoiding walk (SAW) on lattices has been studied extensively for many years as a model which captures the self-excluded volume effect in real linear polymers. In the simplest model, all possible n-step SAWs are assigned equal statistical weights. However, several other SAW models, such as the true self-avoiding walk [1], kinetically growing walk [2], and infinitely growing self-avoiding walk [3], have also been studied. An interesting variation is the one-parameter (η) family of random walks called Laplacian random walks (LRW) introduced by Lyklema and Evertsz [4]. For $\eta=1$, LRW corresponds to the loop-erased self-avoiding walk (LESAW) introduced by Lawler [5]. An LESAW is obtained by erasing loops from the path of a simple random walker as soon as they are formed. The average end-to-end distance r of LESAW scales with the number of steps n of the walk as $r\sim n^{\nu_{\rm LESAW}}$ for large n, where $1/\nu_{\rm LESAW}$ is the fractal dimension of the walk. While $\nu_{\rm LESAW}$ is rigorously known [5] to be $\frac{1}{2}$ for dimensions $d\geq 4$ with logarithmic corrections in $d=4$, no exact results are available for $d=2$ and 3. Lawler has shown [6] that $\nu_{\rm LESAW}$ is bounded below by the Flory exponent $\nu_F=3/(d+2)$ of the usual SAW for $d=2$ and 3. Based on numerical estimates, Guttmann and Bursill have recently conjectured [7] that $\nu_{\rm LESAW}$ is $\frac{4}{5}$ in two dimensions.

In this Letter, we study a model of growing trees introduced by Broder [8]. We show that the chemical paths on these trees (the chemical path between two vertices of a tree being the unique path connecting them along the edges of the tree) correspond to LESAWs. If these trees are space filling, they form spanning trees with equal probability. In fact, we show that the fractal dimension of LESAWs is identical to that of the chemical path of random spanning trees and this result is valid for arbitrary lattices in all dimensions. In particular, in two dimensions, using this correspondence and known results for the Potts model from conformal field theory, we prove the conjecture of Guttmann and Bursill.

Consider a t-step ordinary random walk W starting at an arbitrary site O of a d-dimensional hypercubic lattice. We first collect the set of edges corresponding to the last exit of W from every site except the last visited site. This set forms a tree $T_B(W)$ which Broder called the backward tree at time t [8]. Similarly, the collection of the edges corresponding to the first entry of W to every site, except the starting site O, forms another tree called the forward tree $T_F(W)$ at time t. For example, in Fig. 1, we show a 20-step random walk from O to R on a two-dimensional square lattice. The numbers beside the bonds indicate the step numbers and the arrows indicate the directions of the steps. The corresponding backward and the forward trees, at $t=20$, are shown in Figs. 2 and 3, respectively.

As the walk W grows with time t, the corresponding trees $T_B(W)$ and $T_F(W)$ also grow. The forward tree $T_F(W)$ has a frozen structure in the sense that any part of the tree, once formed, remains unchanged for all subsequent times. In other words, the bonds of the lattice that are present in the tree at time t continue to remain

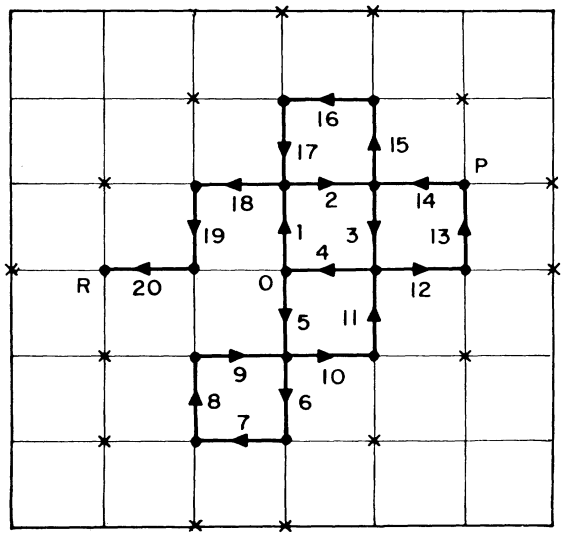

FIG. 1. A 20-step ordinary random walk W on a square lattice from O to R. The numbers beside the bonds indicate the step numbers and the arrows specify the directions of these steps. P is an arbitrary site visited by the walker. The sites marked by crosses are the yet unvisited nearest neighbors of the visited sites.

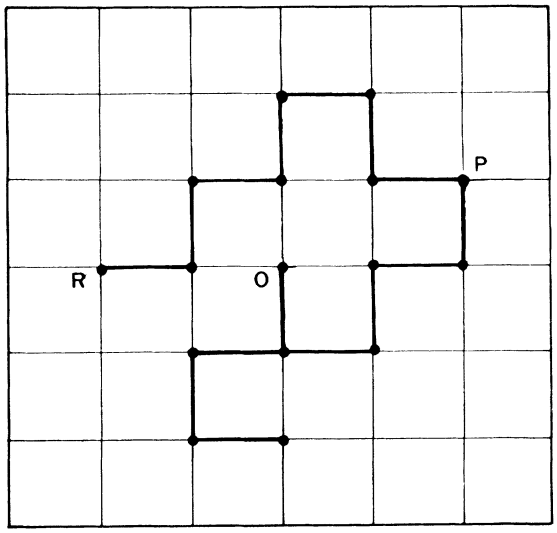

FIG. 2. The backward tree $T_B(W)$ corresponding to the walk W in Fig. 1. It is the collection of edges corresponding to the last exit of W from every visited site except the last site R.

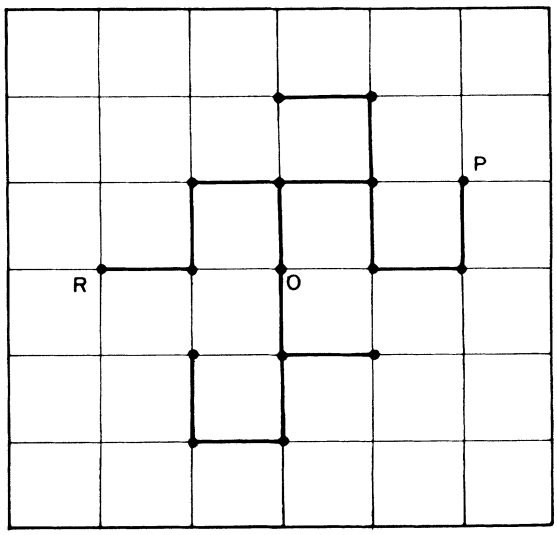

FIG. 3. The forward tree $T_F(W)$ corresponding to the walk W in Fig. 1. It consists of edges corresponding to the first entry of W to every visited site except the starting site O.

so at all later times. This is because the edges corresponding to the first entry of the walk to the visited sites do not change with time. The backward tree $T_B(W)$, however, does not have this property as the last exit from a visited site may change when the walker comes back there at some subsequent time. Because of this frozen structure of the forward tree $T_F(W)$, its time evolution can be viewed as a growth model in which new bonds add to the tree as the walk proceeds. At a given time t, the number of edges in the tree is equal to $S_t - 1$, where S_t is the number of distinct sites visited by W within t.

The growth of the tree is governed by the following rule. Let R be the last site visited by the t-step walk W (see Fig. 1). The tree can grow next along any of the bonds that connect the already visited sites to their yet unvisited nearest neighbors. Denote this set of bonds by B_t and the set of the nearest neighbors by G_t. For the walk W shown in Fig. 1 at $t=20$, the set G_t consists of sites marked by crosses. Then the probability P_i that the tree will grow next along the bond i is given by the probability that the walker, starting at R, will traverse the bond i before traversing the set $\{B_t - i\}$. If X and Y denote, respectively, the visited and the yet unvisited ends of the bond i, then from the general theory of random walks [9] P_i equals the component of $-\nabla\phi$ at X in the direction from X to Y along the bond i, i.e., $P_i = \phi_X - \phi_Y$, where ϕ satisfies the equation

$$\nabla^2\phi(\mathbf{r}) = \delta_{\mathbf{r},\mathbf{R}} ,$$

with $\delta_{\mathbf{r},\mathbf{R}}$ the Kronecker delta function and $\mathbf{R}$ the position vector of the last visited site R. The boundary conditions are given by $\phi(\mathbf{r})=0$ for all $\mathbf{r} \in G_t$. Because of this Laplacian nature of the growth rule, the forward tree $T_F(W)$ may be called the Laplacian tree.

Let P be any arbitrary site visited by the t-step walk W (see Fig. 1) and let W_{OP} denote the part of W between the starting point O at $t=0$ and the last entry to P. For example, in Fig. 1, W_{OP} is a 13-step walk from O to P and is represented by the sequence $(1,2,3,\ldots,13)$. We now retrace this path W_{OP} starting from O and erase the loops from the path as soon as they are formed, until we reach P. To be precise, we move along the path W_{OP}, check at every site on this path whether there is a sequence of steps from there leading to the recurrence of the walk at that site, and, if so, remove that sequence. For example, in Fig. 1 the two sequences of steps in W_{OP}, namely $(1,2,3,4)$ and $(6,7,8,9)$, form loops. Once we remove these two sequences from W_{OP}, $(1,2,3,\ldots,13)$, we are left with a LESAW that connects O and P and consists of steps $(5,10,11,12,13)$. But, these edges clearly correspond to the last exit of W_{OP} from every site except P, and hence form the chemical path between O and P on the backward tree $T_B(W)$ (see Fig. 2). Thus the chemical paths on the backward tree $T_B(W)$ consist of LESAWs.

In a similar way, we now reverse the path W_{OP}, $(1,2,3,\ldots,13)$, in Fig. 1, i.e., consider the sequence $(13,12,11,\ldots,3,2,1)$, and erase loops while retracing this reversed path from P to O. In Fig. 1, the sequence $(11,10,9,8,7,6,5,4)$ forms a loop on this reversed path and hence is removed. This leaves us with the steps $(13,12,3,2,1)$ which form a self-avoiding path between O and P. We call this path the loop-erased reversed walk (LERW). Clearly from Fig. 1 the LERW between O and P consists of edges corresponding to the first entry of W_{OP} to every site except O and hence forms the chemical

path on the forward tree $T_F(W)$ between O and P (see Fig. 3).

Now, suppose the trees are growing on a finite lattice of L^d sites. Consider the forward tree $T_F(W)$ corresponding to the t-step walk W. Because of the frozen structure of $T_F(W)$, the chemical distance, i.e., the length of the chemical path, between two vertices separated by Euclidean distance r remains unchanged while the tree grows. Also the chemical path is identical to the LERW. Hence, the average chemical distance n scales with r as $n \sim r^{1/\nu_{\mathrm{LERW}}}$ and this remains unchanged for all subsequent times while the walk W keeps growing. Now, in the limit when the walk W covers the full lattice, i.e., no site remains unvisited, the corresponding $T_F(W)$ forms a spanning tree on the lattice and the LERWs become the chemical paths on the spanning trees. Broder has shown [8] that these forward spanning trees, generated from all possible lattice covering walks, occur with equal probability. If the average chemical distance n on equally likely spanning trees scales with r as $n \sim r^{1/\nu_{\mathrm{chem}}}$, we immediately get $\nu_{\mathrm{chem}} = \nu_{\mathrm{LERW}}$. By simple time-reversal symmetry, the backward spanning trees $T_B(W)$'s are also generated with equal probability and the LESAWs are identical to the chemical paths on these random spanning trees. Thus we get $\nu_{\mathrm{LESAW}} = \nu_{\mathrm{LERW}} = \nu_{\mathrm{chem}}$ and this result is clearly valid for arbitrary lattices in arbitrary dimensions.

Several results regarding random spanning trees are known because of its connection to some other models of statistical mechanics such as the random resistor network [10], the q-state Potts model in the limit $q \to 0$ [10], and the Abelian sandpile model [11] of self-organized criticality. In fact, it can be shown that the bonds forming the chemical paths on random spanning trees are identical to the red bonds of the q-state Potts clusters, defined by Coniglio [12], in the limit $q \to 0$. In particular, in two dimensions, by mapping the Potts cluster problem onto a Coulomb gas problem and using conformal field theory, Coniglio has shown [12] exactly that the fractal dimension $D_R(q)$ of the red bonds, for all $q \in [0,4]$, is given by

$$D_R(q) = (8g - 3g^2 + 16)/8g ,$$

where

$$q = 2 + 2\cos(\pi g/2) .$$

Thus, for $q = 0$, the fractal dimension of the red bonds and hence that of the chemical path of random spanning trees, $d_f = 1/\nu_{\mathrm{chem}}$, is $\frac{5}{4}$. This, together with $\nu_{\mathrm{LESAW}} = \nu_{\mathrm{chem}}$, proves the conjecture that $\nu_{\mathrm{LESAW}} = \frac{4}{5}$ in two dimensions.

If the walk W continues even after covering the lattice, the corresponding spanning tree $T_F(W)$ does not change. However, $T_B(W)$ keeps changing as the walk proceeds each step after covering the lattice. As noted by Broder [8], this generates a sequence of equally likely spanning trees on the lattice. We note that this, in fact, is a very fast Monte Carlo algorithm for generating an unbiased sequence of spanning trees as it requires, at each step, only local updating of the edges corresponding to the last exit of the walk. This is faster than the previously suggested algorithms [11]. This sequence generates two mutually uncorrelated trees at an interval of $O(t_c)$ steps, where t_c is the covering time of the random walk and varies as L^d with logarithmic corrections for all $d \geq 2$ [13]. Numerical results for statistics of spanning trees generated by this algorithm will be published elsewhere.

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