FIRST PASSAGE PERCOLATION IN MANY DIMENSIONS

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We consider first passage percolation on a d-dimensional hypercubical lattice. The passage time for each bond is an independent exponentially distributed random variable with mean l. For large separations, the limiting ratio of expected minimum passage time between two points along an axis and their separation is a constant μ_d, and we show that $\lim_{d\to\infty} \mu_d d/\ln d = 1/2$.

The first passage percolation problem was defined by Hammersley and Welsh in 1965 to model the spread of fluid in a random medium [1]. Our understanding of this problem has increased much more slowly than of Bernoulli percolation, a detailed scaling theory for which exists, and in the special case of two dimensions, several critical exponents and critical probabilities are known exactly. For the first passage problem, no exact results are known in more than one dimension. For the asymptotic rate of fluid spread, only upper and lower bounds are known. For the variance of first passage times, arguments of universality predict some exponents in two dimensions conjectured to be exact [2]. On the Bethe lattice the exact value of the asymptotic rate has been obtained by Derrida and Spohn [3]. The present status of this subject is well described in some recent review articles [4–6].

In this paper we consider the first passage percolation on a d-dimensional hypercubical lattice. Each site of the lattice is characterized by a d-dimensional integer vector $x \equiv (x_1, x_2, ..., x_d)$. To each pair of nearest neighbour sites x and y, we assign a non-negative random variable t_{xy}, called the passage time of the step from x to y. The passage time of a path is defined as the sum of passage times of steps constituting the path. The first passage time from the origin to a hyperplane is defined as the minimum of the passage time of all path from the origin to some site in the hyperplane.

For simplicity, we restrict ourselves to the case all

t_{xy} are independent random variables, the probability that any chosen step has a passage time lying between t and $t+dt$ being $e^{-t} dt$. Let $\mathbb{P}_m$ denote the hyperplane $x_1 = m$, and let τ_m be first passage time from origin to $\mathbb{P}_m$. Hammersley and Welsh [1] showed that as m tends to infinity τ_m/m tends to constant μ_d with probability 1. This constant is lattice dependent and is called the time constant for the lattice. The precise value of μ_d is not known for any $d > 1$. In the limit of large d, the effect of loops is less important and some simplifications occur [7,8]. Kesten [5] showed that there exist constants C_1 and C_2 such that for all $d > 1$

$$C_1 \frac{\ln d}{d} \leqslant \mu_d \leqslant C_2 \frac{\ln d}{d}. \tag{1}$$

In this paper we derive an improved upper bound on μ_d for arbitrary d. In the limit of large d, our bound coincides with the already known lower bound on μ_d to leading order in d, and we show that

$$\lim_{d\to\infty} d\mu_d/\ln d = \tfrac{1}{2}. \tag{2}$$

For the exponential distribution of $\{t_{xy}\}$, the first passage percolation problem is equivalent to the Eden model [9] defined as follows: At time $t=0$, all sites of the lattice are "healthy", except the origin which is "infected". A healthy site having k infected neighbours at any time t has a probability $k\,dt$ of catching infection in a subsequent small interval dt. An infected site never recovers. As time increases, more

and more sites get infected, and the boundary separating the infected sites from the healthy sites moves outwards. The time constant μ_d is the inverse of the velocity of the infection front along the x_1-axis.

To derive an upper bound on μ_d, we consider a modified infection process in which the infection of sites in $\mathbb{P}_m$ by neighbouring infected sites in $\mathbb{P}_{m+1}$ is not allowed. All other infection rates are the same as in the original process. The time constant for the modified process is not less than that in the original, and an upper bound on time constant in the modified process is also a bound on μ_d.

Let $\langle \tau_n \rangle$ denote the expected value of τ_n. Then the bounds on μ_d are derived using the well-known subadditivity result [1]

$$\mu_d \leqslant \langle \tau_n \rangle / n, \quad \text{for all } n = 1, 2 \ldots . \tag{3}$$

We first derive a bound on $\langle \tau_1 \rangle$. Consider the evolution of the infection process starting from a state in which infected sites are subset C of $\mathbb{P}_0$, and all other sites are healthy. Let $T(C)$ be the expected waiting time before the infection reaches $\mathbb{P}_1$. If C_0 is the configuration with a single infected site, then clearly $T(C_0) = \langle \tau_1 \rangle$.

Let the number of sites in C be i, and the number of perimeter bonds of C lying in $\mathbb{P}_0$ be S. Since for each site in C, there is a bond to a healthy neighbour in $\mathbb{P}_1$, the total number of perimeter bonds of C is $S+i$. The average waiting time before the next infection is $1/(S+i)$. With probability $i/(i+S)$ the new perimeter site is in $\mathbb{P}_1$, and with probability $1/(i+S)$ each, it will be the end point of a perimeter bond of C, giving rise to a new cluster C′ having $i+1$ sites. Then clearly

$$T(C) = \frac{1}{i+S}\left(1 + \sum_{C'} T(C')\right), \tag{4}$$

where the summation over C′ extends over all clusters obtained by additing the end site of a perimeter bond to C.

Let T_{i+1} be the maximum value of $T(C)$, taken over all possible cluster C′ having $i+1$ sites, i.e.

$$T_{i+1} = \max_{|C'| = i+1} T(C') . \tag{5}$$

Then eq. (4) gives

$$T(C) \leqslant [(1+S)T_{i+1}]/S + i . \tag{6}$$

For a $(d-1)$-dimensional hypercubical lattice for any cluster C having i sites, we have

$$S \geqslant \lceil 2(d-1)i^{(d-2)/(d-1)} \rceil \stackrel{\text{def}}{=} s_i , \tag{7}$$

where $\lceil x \rceil$ is the smallest integer not less than x. Since $T_{i+1} \leqslant 1/(i+1)$, the right-hand side of eq. (6) is a monotonically decreasing function of S. Using eq. (7), we get

$$T(C) \leqslant [1/(s_i+i) + s_i/(i+s_i)]T_{i+1} . \tag{8}$$

This holds for all configurations C having i sites, and hence, in particular,

$$T_i \leqslant [1/(s_i+i) + s_i/(i+s_i)]T_{i+1} . \tag{9}$$

Iteration of this equation gives

$$\langle \tau_1 \rangle \leqslant (1+s_1)^{-1}[1+s_1(2+s_2)^{-1}[1$$
$$+s_2(3+s_3)^{-1}[1+s_3(4+s_4)^{-1}[\ldots . \tag{10}$$

For any d, eq. (10) with the s_i defined by (7) gives an upper bound on $\langle \tau_1 \rangle$ as a convergent series, which may be summed numerically. The result for some selected law values of d are given in table 1.

This bound using a slightly different argument was reported earlier at a Cargese school [10]. This preliminary report, unfortunately, has some errors. Its eq. (13), and hence the results are true for the bond-Eden problem, and not for the site-Eden problem as claimed. Secondly, due to an extra approximation used an incorrect behaviour $\mu_d \sim d^{1/d-1}$, for large d was obtained.

For large d and $n \ll d$, in eq. (10), $S_n/(n+s_n)$ may be replaced by $e^{-1/2d}$, and we get to leading order in d

Table 1

Upper bounds to the time constant μ_d, using the bounds on $\langle \tau_1 \rangle$ and $\langle \tau_2 \rangle$. For easy comparison with the asymptotic results, we list the values of $2\langle \tau_1 \rangle d/\ln(2d)$ and $\langle \tau_2 \rangle d/\ln(2d)$ for some selected values of d.

d	$2\langle \tau_1 \rangle d/\ln(2d)$	$\langle \tau_2 \rangle d/\ln(2d)$
2	1.7233	1.6042
3	1.4735	1.3433
4	1.3568	1.2223
5	1.2924	1.1559
7	1.2204	1.0815
10	1.1632	1.0227
20	1.0918	0.9504
40	1.0521	0.9116

$$\langle \tau_1 \rangle \approx \sum_{n=1}^{\infty} e^{-n/2d} \frac{1}{2nd} \approx \frac{\ln(2d)}{2d} . \tag{11}$$

This compares well with the existing bound (1) due to Kesten with $C_2 = 11$.

An improvement over eq. (10) is obtained by using eq. (13) with $n = 2$, and estimating $\langle \tau_2 \rangle$. The method is a straightforward generalization of above. Let $T(C_1, C_2)$ be the expected waiting time before the infection reaches $\mathbb{P}_2$, if we start with a configuration C_1 of infected sites in $\mathbb{P}_0$, and configuration C_2 of infected sites in $\mathbb{P}_1$, and all other sites healthy. Let the number of sites in C_1 and C_2 be i and j respectively, and the number of perimeter bonds C_1 and C_2 lying in the same hyperplane be S_1 and S_2. Let B be the number of bonds from C_1 to *healthy* sites in $\mathbb{P}_1$. Then the total number of bonds that can cause infection is $S_1 + S_2 + B + j$. Arguing as before, we get

$$T(C_1, C_2) = (S_1 + S_2 + B + j)^{-1}$$

$$\times \left(1 + \sum_{C_1'} T(C_1' C_2) + \sum_{C_2'} T(C_1 C_2') \right), \tag{12}$$

where the summations over C_1 and C_2 are over configurations obtained by adding an infected site to C_1' and C_2' respectively. We define

$$T_{i,j} = \max_{C_1, C_2} T(C_1, C_2) \tag{13}$$

the maximum being taken over all configurations C_1 and C_2 with i and j sites respectively. We use the inequalities

$$S_1 \geqslant s_i , \tag{14}$$

$$S_2 \geqslant s_j \tag{15}$$

and

$$B \geqslant |i - j|_+ , \tag{16}$$

where $|x|_+$ is equal to x for positive x, and zero otherwise. As argued earlier, S_1, S_2 and B in (12) can be replaced by their lower bounds, and $T(C_1 C_2)$, $T(C_1', C_2)$ and $T(C_1, C_2')$ by upper bounds giving

$$T_{i,j} \leqslant \frac{1 + s_i T_{i+1, j} + (s_j + |i - j|_+) T_{i, j+1}}{s_i + s_j + j + |i - j|_+} . \tag{17}$$

Also, from the definition it is clear that

$$\langle \tau_2 \rangle = T_{1, 0} . \tag{18}$$

Using (17), $T_{1, 0}$ can be expressed in terms of $T_{2, 0}$ and $T_{1, 1}$, which in turn can be expressed in terms of $T_{3, 0}$, $T_{2, 1}$, and $T_{1, 2}$, and so on. After many such recursions, when the coefficiens of T's have become very small, we can truncate the hierarchy using

$$T_{i, j} \leqslant 1/j . \tag{19}$$

The numerical values of the bounds thus derived are also listed in table 1. It is easy to derive similar bounds for $\langle \tau_3 \rangle$ but the calculation becomes numerical very time consuming for large d.

It is easy to derive a lower bound for μ_d, using a variant of the original Hammersley and Welsh argument [4]. One gets

$$(2d - 3)\mu_d + \sqrt{1 + 4\mu_d^2}$$

$$+ \ln[(\sqrt{1 + 4\mu_d^2} - 1)/2\mu_d] \leqslant 0 . \tag{20}$$

This implies, in particular, that the lower bound on μ_d is to leading order in d given by $\ln(d)/2d$. Since our upper bound to μ_d (eq. (11)) and the lower bound eq. (20) agree with each other to leading order in d, we get

$$\lim_{d \to \infty} d\mu_d / \ln(2d) = \tfrac{1}{2} , \tag{21}$$

which is the result claimed. It is interesting to note from table 1 that this limit is approached from below.

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References

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