PHYSICAL REVIEW 8 VOLUME 30, NUMBER ¹ ¹ JULY 1984

New method for growing branched polymers and large percolation clusters below p_c

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We propose a new Monte Carlo method for generating large branched polymers; it is based on enrichment of percolation clusters below p_c . We find that one must take care to distinguish two different ensemble averages: one at constant mass s and the other at constant chemical distance *l*. For constant s, we obtain clusters belonging to the universality class of lattice animals, while for constant l we get topologically one-dimensional structures for all d.

The structural properties of percolation clusters and lattice animals are currently a subject of intensive study.^{$1-13$} Whereas percolation clusters are used to model gels,¹ lattice animals represent the principal model for branched polymers in dilute solutions.² For all concentrations p below the percolation threshold p_c the large clusters seem to have the critical exponents of lattice animals, i.e., of the $p \rightarrow 0$ limit. Thus we denote here as "animals" all clusters with radius much greater than correlation length ξ .¹ Since the probability of generating such a cluster using Monte Carlo methods is very small' (decays exponentially with size) there has not been much study of their structure compared to percola- $\frac{1}{2}$ tion.^{3-7, 10}

Here, we propose a new method for generating statistical ensembles of large lattice animals ("branched polymers").³ The method is analogous to the enrichment method s successfully used to generate self-avoiding walks ("linear polymers").⁹

METHOD

First we use the conventional cluster growth method¹⁰ to generate a percolation cluster of s_0 sites, say $s_0 = 20$, using a value of p so small that the probability of obtaining a 20-site cluster π is typically about 0.01 (i.e., 100 trials may be necessary to succeed in growing the 20-site cluster). After finally obtaining a cluster of size s_0 , we make a fixed number A of attempts to increase it to size $2s_0$, where A is chosen to satisfy $A \ll 1/\pi^{8.9}$ If we "fail" (i.e., the cluster chosen to satisfy $A \ll 1/\pi^{8.9}$ If we "fail" (i.e., the cluster terminates for all A attempts), then we discard the *entire* cluster and return to the beginning. If we succeed, then we make A new attempts to increase our cluster from size $2s_0$ to size $3s_0$ and so on. Being interested in "universal" quantities only we did not make the difficult extrapolation $p \rightarrow 0$, since already at finite p animal exponents are expected.

RESULTS

Using this procedure, we typically generated lattice animals of size 300 on a square lattice with $p=0.4$ and $p=0.22$ for a cubic lattice. In order to confirm that they had the critical exponents of lattice animals, we measured the mean-square radius of gyration R_g^2 as a function of the number of sites (Fig. 1); from the slope we find d_f $n=1.55\pm 0.05$ for $d=2$ and $d_f=2.0\pm 0.05$ for $d=3$, consistent with independent estimates of the fractal dimensistent with independent estimates of the fractal dimension.¹¹ We found that different values of s_0 and p give the same values of d_f if we maintain the condition $A\pi \ll 1$.

In general, a cluster is characterized not only by its geometric structure (parametrized by the fractal dimension d_f) but also by its topological structure (parametrized, for example, by the chemical dimension d_i).¹² First we define example, by the chemical dimension d_l).¹² First we define the chemical distance l as follows.¹² We choose a site to call the origin. The occupied neighbors of this site form the first "shell"; its chemical distance *l* from the origin is one. The next-nearest neighbors of the origin form the second shell with $1=2$ and so on. The total number of sites or "mass" at a chemical distance less than or equal to *l* scales as

$$
s(l) \sim l^{d_l} \tag{1}
$$

There are two possible ways to form the ensemble averages in order to calculate d_i . One is to take an ensemble of clusters with constant s and calculate their average k $s(l) \sim \langle l \rangle_s^{d_l}$. A second way to choose clusters of the same l and make the average over s: $\langle s \rangle_1 \sim l^{d_1}$. For percolation clusters at p_c , both averages give the same value for d_1 .¹²
However, for $p < p_c$ and large clusters, the two averages yield completely different results. For the constant s en-

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FIG. 1, Dependence on the cluster mass s of the mean-square radius of gyration $\langle R_g^2 \rangle$. Points represent averages over 1000 large branched polymers on square and simple cubic lattices. The slope of the double-logarithmic corresponds to $d_f=1.55\pm0.05$ [d=2] and $d_f = 2.0 \pm 0.05$ [d = 3]. Three different values of s₀ were used for $d = 2$ in order to test that the fractals were independent of s_0 , $s_0=15(\Delta)$, 20(0), and 30(\times).

semble one gets the lattice *animal* statistics with d_l varying semble one gets the lattice *animal* statistics with d_l varying from $d_l = 1.33$ for $d = 2$ to $d_l = 2$ for $d = 8^{13}$ However, for the constant-l ensemble, one obtains a new universality class: chemically one-dimensional branched polymer ensembles with $d_i = 1$ for all d. Numerical evidence will be given in the following as well as a theoretical interpretation. In Fig. 2 we plot the average mass s as a function of the chemical distance l for $d=2$ and $d=3$. The linearity of these plots suggests strongly that

$$
\langle s \rangle \sim l \tag{2}
$$

Before we proceed, we present exact results for the Cayley tree of coordination number $\sigma+1$, which describes¹ the critical exponents above $d_c = 8$. The distribution of $s(l)$ conditioned on the number of sites in shell l positive (so that the tree does not terminate at an earlier generation) is given for $p < p_c = 1/\sigma$ and $l >> 1$ by¹⁴

$$
Pr[s(l) - l(1-p)/(1 - \sigma p) \le v(Hl)^{1/2}]
$$

= $(2\pi)^{-1} \int_{-\infty}^{v} \exp(-u^{2}/2) du$, (3a)

where $H = (\sigma - 1)p(1 + p - 2\sigma p^2)/(1 - \sigma p)^3$. Hence, the conditional expectation value of $s(l)$ is, for $l >> 1$,

$$
\langle s(l)\rangle \sim (1-p)/(1-\sigma p)l \quad . \tag{3b}
$$

Thus the percolation clusters with $l \gg 1$ shells at $p < p_c$ are chemically one dimensional in contrast to the result $d_1 = 2$ for percolation clusters for $p = p_c$ on the same Cayley tree lattice and the same type of average.¹²

Fracta1 dimensions used thus far in statistical physics have been found to be nondecreasing functions of d ; indeed, it is

FIG. 2. Linear plot of the average of cluster mass $\langle s \rangle$ vs the chemical distance I. The fact that the data fall on straight lines suggests that $d_1=1$ for both $d=2$ and $d=3$.

hard to imagine how increasing d could serve to decrease a fractal dimension. Thus, from the results $d_l = 1$ for $d=1, 2, 3$ and for $d \ge 8$, we can argue that $d_1=1$ for all d and all p below p_c .

DISCUSSION

In order to understand the difference between the constant-l ensemble and the constant-s ensemble, we study the two different averages carefully. For the constant s ensemble, the average chemical distance is given by

$$
\langle l \rangle_s = \sum_{l,t} A_{st} l_{st} s p^s (1-p) / \sum_{l,t} A_{st} s p^s (1-p)^t , \qquad (4)
$$

where A_{st} and I_{st} are the number of configurations and the chemical distance of a cluster with s cluster sites and t perimeter sites. For $p \rightarrow 0$ Eq. (4) yields

$$
\langle I \rangle_{s} = \sum_{l,t} A_{st} I_{st} / \sum_{l,t} A_{st} \quad , \tag{5a}
$$

which represents the animal average.¹ For the constant- l ensemble, the average mass s is given by

$$
\langle s \rangle_{l} = \sum_{s,t} A_{st}^{l} s^{2} p^{s} (1-p)^{l} \sum_{s,t} A_{st}^{l} s p^{s} (1-p)^{t} . \tag{5b}
$$

In this case, for $p \rightarrow 0$ because of the factor p^s , the dominant configurations will be those with the minimum s. The minimum s for a given l is simply $s \sim l$, so we obtain $\langle s \rangle \sim l$ for all dimensions.

The result $d_1=1$ has implications for transport, for which topological concepts are physically relevant. We shall see that in the constant-l ensemble the fracton or spectral

FIG. 3. Results of exact enumeration of random walks on lattice animals using $s_0=20$; similar results were found for other values of s_0 . (a) Linear plot of P_0^{-2} vs t, where P_0 is the probability of returning to the origin at time t; (b) linear plot of $\langle I \rangle^2$ vs t, where $\langle I \rangle$ is the average chemical distance. The linearity supports the result of (6) that $d_s = 1$ and $d_w = 2$.

dimension $d_s = 2d_f/d_w = 1$ for all $d \ge 1$. We begin by noting that the chemical diffusion exponent d_w^l , defined through $t \sim l^{d_v}$, must satisfy the inequality $d_v \ge 2$, since $d_v' = 2$ for a Euclidean lattice. Thus, the number of distinct sites visited by the random walk $s(t)$ scales as $s(t) \sim t^{1/d_w t}$. But $s(t)$ by the random walk $s(t)$ scales as $s(t) \sim t^{1/4}$. But $s(t)$
 $\sim t^{4s/2}$, and $d_s \ge 1$ for any connected fractal. Hence the only way that we can simultaneously satisfy $d_w^l \geq 2$ and $d_s \geq 1$ is to have

$$
d_w^l = 2 \t{6a}
$$

and

$$
d_s = 2d_f/d_w = 1 \quad . \tag{6b}
$$

To test (6) by direct simulation, we have used the method of exact enumeration of random walks on fractal structures.¹⁵ In this fashion we have obtained the exact statistics for 1000 different clusters each containing at least $l = 150$ shells.¹⁶ Results for the probability of a random walk being at the origin at time t are shown in Fig. $3(a)$, and results for the average chemical distance $\langle l \rangle$ are shown in Fig. 3(b). For the high degree of linearity of both plots we conclude that the corresponding values of d_s and d_w^l agree with the predictions of Eqs. (6b) and (6a). We also calcu-

lated the mean-square displacement $\langle R^2 \rangle$ for $d=2, 3$ and the corresponding values of d_w agree with the prediction of (6b) that $d_w = 2d_f$. For an arbitrary fractal, the conductivity exponent $\tilde{\mu}$ can be related to d_f and d_w by¹ $\tilde{\mu} = (d_w - d_f) + (d - 2)$. From Eq. (6b) follows a direct relation between the conductivity and the fractal dimensionality for these topologically one-dimensional clusters, $\tilde{\mu} = d_f + (d - 2).$

In summary, we have developed a new Monte Carlo method for generating large percolation clusters below p_c . The method produces clusters in the universality class of lattice animals for the constant-s ensemble. For the constant-I ensemble, we find clusters that are topologically linear. We argue that the fracton dimension $d_s = 1$ for these topologically one-dimensional cluster and confirm this result numerically.

ACKNOWLEDGMENTS

We wish to thank S. Alexander, D. Ben-Avraham, D. C. Hong, D. Movshovitz, R. Nossal, D. Stauffer, and especially I. Majid for helpful discussions, and National Science Foundation, Office of Naval Research, and Army Research Office for financial support.

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