Growth exponents with 3.99 walkers

M. B. Hastings*

CNLS, MS B258, Los Alamos National Laboratory, Los Alamos, New Mexico 87545

It is argued that the dielectric-breakdown model has an upper critical η_c equal to 4, for which the clusters become one dimensional. A renormalization group treatment of the model is presented near the critical η.

I. INTRODUCTION

The model of diffusion-limited aggregation (DLA) [1] has presented a great challenge to theorists. The model describes many phenomena, including viscous fingering [2], electrodeposition [3], and dendritic growth [4], but has also become important as a theoretical problem of its own. While the growth rules are simple, they are highly nonlocal and give rise to complex branching structures that cannot be described easily by any small perturbation of a smooth surface.

Despite much important recent theoretical work on the structure of DLA [5–7], these attempts have all involved approximations or phenomenological assumptions, without a fully controlled expansion. In analogy to critical phenomena, we would also like an ϵ expansion to provide a framework that can be systematically improved.

It is believed that DLA remains nontrivial in any finite dimension, so an expansion about an upper critical dimension is not possible [8]. We turn instead to another generalization of DLA, the dielectric-breakdown model (DBM) [9]. This model offers a continuously varying fractal dimension as a function of a parameter η, ranging from 2 at $\eta=0$ to approximately 1.7 at $\eta=1$ (DLA) to 1 at $\eta=\infty$. The model is equivalent to simultaneously releasing η random walkers and requiring that they all hit a given point for growth to occur. As the model remains nontrivial for $\eta \rightarrow 0^+$ [10], we seek instead an expansion about an upper critical η_c, for which the clusters become one dimensional. One attractive feature of this approach will be that near η_c the clusters are described in terms of one-dimensional branches, so that the branching structure of DLA is inherent.

Previous numerical studies have suggested $\eta_c=4$ [11], as well as providing some analytic explanation. A recent study of much larger clusters [12] also indicates a finite η_c between 4 and 5. This study found significant finite size corrections for clusters with $\eta \geq 4$, making it problematic to determine dimension with small clusters.

In this work we provide an analytic argument for $\eta_c=4$ based on branch competition, and present the lowest order in a $4-\eta$ expansion. The techniques are related to the branched growth model [6] and to singular Laplacian growth [13], while the way we evaluate growth processes in the long-time limit is close to the fixed-scale transformation [7].

We proceed as follows. First we argue the equivalence, at least near $\eta=4$, of the DBM to a reduced model based on one-dimensional branches with discrete tip-splitting events. Next, we analyze the competition of two branches and show that on large scales tip-splitting events proliferate for $\eta<4$, but are suppressed for $\eta>4$. Then we consider the competition of three branches (using numerical and analytical techniques) and show that these higher order effects suppress the tip splitting, leading to an attractive fixed point at a finite value of the tip-splitting rate, with no relevant perturbations of the fixed point. We then use this fixed point to determine fractal and multifractal dimensions and compare to numerics.

The renormalization group (RG) used involves expanding simultaneously in $4-\eta$ and the tip-splitting rate. A related tip-splitting expansion to systematically extend the branched growth model has been suggested previously [14]. We consider a system with a given ratio between microscopic and macroscopic cutoffs and evaluate the probability of various growth processes, to obtain corrections to the growth rate of the cluster and to the tip-splitting rate; we find that all such quantities can be written as a sum of logarithmic corrections to bare quantities. We then make an assumption that the logarithms may be resummed to produce power laws. This assumption relies on the renormalizability of the model; we have no proof of renormalizability, but in the last section we sketch how such a proof might proceed. Resummation of logarithms has been used for other nonequilibrium systems such as Barenblatt's equation [15]

II. REDUCED MODEL

Since we wish to have an RG in which power laws are obtained by resummation of logarithms, it is essential to remove all irrelevant variables from the problem. We construct such a model in two steps. First, we go from the conformal mapping model for DLA to a discrete version of the model. Next, we go to a reduced version of the model in which branches have vanishing aspect ratio and grow deterministically. The discrete model will be useful in providing a definition of tip-splitting events, which will provide the only source of randomness in the reduced model.

Recall the conformal mapping formulation [18] of DLA and the dielectric breakdown model: consider a function $F^{(n)}(z)$ that maps a straight line onto the boundary of the growing cluster after n growth steps. To obtain F^{n+1}, pick a point w with probability $|F^{(n)'}(z)|^{1-\eta}$. Define an elementary mapping $f^{(n+1)}(z)$ that produces a bump of linear size $\sqrt{\lambda}$ at w, where, to obtain the correct bump size in the physical plane,

$$\lambda = |F^{(n)'}(w)|^{-2}. \tag{1}$$

Then, define $F^{(n+1)}(z) = F^{(n)}(f^{(n+1)}(z))$.

Next, we consider a discrete version of the above model. Each elementary mapping f has square-root singularities located a distance of order $\sqrt{\lambda}$ from w. All points z between these singularities are mapped onto the surface of a given bump (although, after further growth steps, some of these points may be mapped onto bumps growing off the given bump). In the discrete model, we will first pick a point w as above; then, we find the nearest square-root singularities on each side of w, and grow a bump at a point equidistant between those singularities. This simple modification means that there is now a discrete set of growth sites (in any lattice formulation of the problem, one would also find a discrete set of growth sites).

Now, assume that the cluster has a roughly one-dimensional shape, with a tip near $z = z_i$ (we reserve the index i to label different such tips). If the branches were precisely one dimensional, near the tips the singular behavior of $F(z)$ would be given by

$$F(z) = F_i(z - z_i)^2, \tag{2}$$

with F_i some constant. Due to the finite size of particles in the model, $F(z)$ is given by a suitably regularized version of Eq. (2) near the tip. For $\eta > 2$, the integral of the measure $|F'(z)|^{1-\eta}$ diverges for small z, so that in the discrete model the probability measure will be concentrated on the one growth site at the tip, with rapidly decaying measure on the neighboring sites. The measure on neighboring sites will be nonuniversal and determined by the particular form of elementary mapping f we choose, which will define a particular regularization of the model.

Consider a branch that grows without splitting. While the length of the branch increases constantly in time, the width remains of the order of the microscopic scale. Thus, at large scales such a branch looks like a singular configuration with vanishing aspect ratio. At the upper critical η, the assumption of growth without splitting will be valid at large scales, while below the upper critical η the clusters are approximately described by a collection of one-dimensional branches, implying that the aspect ratio is an irrelevant variable near the upper critical η. So, in constructing the reduced model, we will take all branches with vanishing aspect ratio.

As the aspect ratio vanishes, all of the growth measure becomes concentrated near the growth tip, on a scale much less than the length of the branch. However, even though the aspect ratio vanishes, due to the discretization there is some growth measure on sites neighboring the growth tip, and growth may arise on any of these sites, with some nonuniversal probability. This is a tip splitting event. Below, we will assign a tip-splitting rate, and consider how this rate renormalizes. As we expand to higher orders in tip splitting, we include more growth configurations, so that to sufficiently high order we restore the full set of clusters found in the original model.

We now determine the growth measure for a branch, based on the proper regularization of Eq. (2). The correct

microscopic regularization of the model is at fixed length in the physical plane, leading to a cutoff at length of order $1/\sqrt{|F'|}$ in the z plane. Thus, the correctly regularized value of F' at the growth tip is

$$\sqrt{F_i}. \tag{3}$$

Numerically, one may implement this by evaluating F' a short distance from z. We note that the difference in F' depending on regularization means that different short-distance regularizations may imply completely different physical models; this may be behind some of the differences found between diffusion-limited aggregation and Laplacian growth [19].

Equation (3) is different from that taken in the idea of singular Laplacian growth [13], and reflects the correct regularization of the problem in the physical plane. Similarly, the correctly regularized growth measure at the tip, which in the discrete model is an *integral* of $|F'|^{1-\eta}dz$ over the region between singularities, is

$$v_i = \frac{\sqrt{F_i}^{-\eta}}{\sum_i \sqrt{F_i}^{-\eta}}. \tag{4}$$

Further, we assume in constructing the reduced model that, if there is a collection of growth sites, at large scales it is valid to grow each site deterministically at a velocity proportional to Eq. (4), ignoring the shot noise inherent in the discrete formulation of the model. As the branches become long compared to the walker scale, this assumption is valid. All the randomness in the reduced model will arise via tip splitting.

In what direction does a tip grow? In our model, each microscopic growth step is produced by a mapping f, growing the surface in the z plane normal to itself at $z = z_i$. For a nonsingular configuration, this grows the surface in the physical plane normal to itself; however, the tip of a one-dimensional configuration has no normal direction, and we are forced to rely on the conformal mapping definition of growth. In the conformal mapping model, growth at z_i for time dt with velocity v_i can be obtained by composing F with a function $f = z + v_i dt[\lambda/(z_i - z)]$. As growth progresses, the singularities z_j move, as the point that is mapped to a singularity j of F is $f^{-1}(z_j) = z_j - v_i dt[\lambda/(z_i - z_j)]$. This leads to

$$\partial_t z_i = \sum_{j \neq i} \frac{1}{z_i - z_j} F_j^{-1} v_j. \tag{5}$$

Our model of growth causes a tip z_i to grow in the direction F_i in the complex plane, but as F_i may change in time the tips may curve. This differs from the model of singular Laplacian growth in which branches always grow in a straight line, and in which there are additional terms in the motion of each tip due to growth at that tip. However, with correct regularization in which the map function f is chosen to produce a bump of small but finite size, one may show that z_i does not move due to growth at the tip i itself.

If the branches are straight, then $F(z)$ has a finite number of singularities at branch points and growth tips. Any singularity z of F that is not a growth tip obeys an equation of motion

$$\partial_t z = \sum_i \frac{1}{z - z_i} F_i^{-1} v_i. \tag{6}$$

If the branches curve, additional singularities are continuously produced.

Thus we present the reduced model: Let the cluster be described by a mapping $F(z)$ that produces a cluster made of one-dimensional branches, with growth tips labeled by i. Grow each tip at a velocity given by the growth measure of Eq. (4) multiplied by a growth velocity v.

In addition, tips split. Assign a rate g, which is an appropriately defined rate at which each tip has a tip-splitting event; the definition of g is to a certain extent arbitrary and will be discussed more below. This rate is measured with respect to the time integral of the growth probability measure on the given tip, so that tips with greater growth probability measure split more readily. The initial conditions for the two daughter branches are randomly chosen, as one or another daughter may have the majority of the growth probability. A regularization is necessary; as we show below, if the two daughter tips are created an infinitesimal distance apart with a finite asymmetry in the initial conditions, one tip will immediately dominate the growth over the other. Thus, we will need to assign a short-distance cutoff, so that the two tips survive for some minimum time, or to some minimum finite separation. In the RG we will use a particular cutoff; however, the precise form of the cutoff will not be important.

III. GEOMETRY

Throughout, we will work in cylindrical geometry in the long-time regime. The size of the individual particles in the original model defines a microscopic cutoff length l, which will provide the minimum distance at which branch pairs are created. The horizontal width of the cylinder in which the cluster grows defines a macroscopic length scale L. These cutoffs in length are related to cutoffs in time for branches, such that the minimum time a branch exists is of order l/v. In cylindrical geometry, the ratio between these cutoffs is fixed and the front grows upward at constant velocity. Below we will expand in the number of tip-splitting events, assuming that the cluster is evolved for a finite time T, so that the average number of tip splittings gT serves as an expansion parameter; T must be taken infinite at the end to obtain the long-time regime.

In radial geometry, the ratio between cutoffs is constantly changing, leading to discrepancies between different measures of the dimension [16]. An interesting future problem will be to understand radial geometry in our framework, or to deal with the affine regime in cylindrical geometry [17].

In cylindrical geometry, the intersection of the cluster with a line at constant height is a fractal with dimension D between 0 and 1. The cluster grows upward with velocity v_{ren}. As the area of the cluster increases at a constant rate in
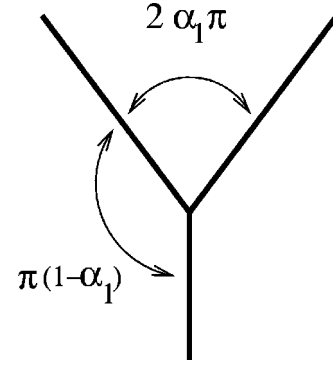

FIG. 1. Competition of two branches. Opening angles are indicated in terms of α_1.

time, v_{ren} is related to the ratio of scales and the microscopic velocity v by

$$v_{\mathrm{ren}} \propto v(l/L)^D. \tag{7}$$

Later, we will compare the analytic results to numerics on the DBM in radial geometry, so we must assume that any difference due to geometry is small. This difference is small for DLA, roughly the difference between 1.66 and 1.71, and we assume that we may add 1 to the dimension given by Eq. (7) to obtain the dimension in radial geometry.

IV. COMPETITION OF TWO BRANCHES

Consider two competing branches, the first order in g in the reduced model. We linearize near a symmetric configuration of the two branches. The branch shape depends on the initial conditions. However, in the long-time limit, two symmetrically competing branches will grow straight. Physically, the angle between the two branches cannot be too small due to the mutual screening effects; neither can it be too large or the branches would end up growing back toward their parent. We will compute this angle below. If initially the branches are not at the given angle, they will curve and approach this angle; we have observed this curving in numerical simulations of the reduced model.

If the branches are straight in the physical plane, F is a degenerate Schwarz-Christoffel map. We define $F(z)$ by its derivative:

$$F'(z) = (z-y)^{-\alpha_1}(z+y)^{-\alpha_1} z^{-\alpha_2}(z-x)(z+x), \tag{8}$$

describing growth tips at $z = \pm x$. We have $2\alpha_1 + \alpha_2 = 1$. In Fig. 1 we show the resulting configuration and relate the angles to α_1 and α_2.

We will use a trick to describe the dynamics of this system. The reduced model above has a specified dynamics for the motion of the growth tip singularities x. The model of singular Laplacian growth, a different model, which admits solutions with straight branches of *arbitrary* opening angle, has a different set of solutions for the motion of x. The equations of motion of the two models match only when

$$\partial_z \left(\frac{F'(z)}{z \pm x} \right) = 0, \tag{9}$$

for $z = \mp x$. This use of singular Laplacian growth is simply a trick to derive the constraint (9) that a Schwarz-Christoffel map must obey to grow straight under the reduced model dynamics.

If the map remains Schwarz-Christoffel, we use Eq. (5) to find the motion of x, as well as Eq. (6) to describe the motion of y. We find

$$\partial_t x = \frac{1}{2} \frac{1}{2x}, \tag{10}$$

$$\partial_t y = \frac{1}{2} \left(\frac{1}{y-x} + \frac{1}{y+x} \right), \tag{11}$$

where we normalize $F_i = 1$ for the two different tips $i = 1,2$. We note that for this configuration F_i is constant in time.

Requiring that $\partial_t y / \partial_t x = y/x$, we find that

$$y = \sqrt{5} x. \tag{12}$$

Requiring Eq. (9), to obtain straight growth, we find

$$\alpha_1 = 1/5, \quad \alpha_2 = 3/5, \tag{13}$$

which implies that the competing branches have a 72° degree opening angle. In numerical simulations with η near 4 [12], this characteristic opening angle can be clearly seen.

Having found F when the two branches are symmetric, we now consider, to linear order, to competition of two asymmetric branches. Let the branches have growth measures v_1 and v_2. Define $\delta = \ln F_1/F_2$. We will find that the dynamics is unstable, and one of the two branches will win; as that branch wins, it will curve, until it becomes parallel to its parent. However, to linear order, we may ignore the curvature, and assume that the map retains the Schwarz-Christoffel form. Above, we noted that the branches grow in the direction F_i; while the competition moves the singularities z_i, leading to changes in F_i and curvature of the branches, Eq. (9) implies that to *linear* order the motion of singularities does not change the angle at which the branches grow.

Equation (8) generalizes to

$$F'(z) = (z - y + \delta_1)^{-\alpha_1} (z + y + \delta_2)^{-\alpha_1} (z + \delta_3)^{-\alpha_2} (z - x + \delta_4)(z + x + \delta_5). \tag{14}$$

Assume the various δ are all small. Assuming that the map retains this form, one can use the equations of motion for all five singularities to determine the dynamics of the map. Regardless of whether v_i is chosen from Eq. (4) or chosen arbitrarily, Eqs. (5) and (6) lead to constraints on the possible resulting δ which reflect constraints following from the assumption that the Schwarz-Christoffel map is degenerate. As a result, the competition of two branches starting from an almost symmetric configuration occurs in a two-dimensional parameter space, specified by δ and by the overall length scale of the branches.

After some algebra, one finds $\partial_t \delta = (v_1 - v_2)/t - (\delta/t)$, or

$$\partial_t \delta = \left(\frac{\eta}{2} - 1 \right) \frac{\delta}{t}. \tag{15}$$

The factor of $1/t$ arises from Eq. (10), giving $x = \sqrt{t/2}$. This factor implies

$$\delta \propto t^{\eta/2 - 1}. \tag{16}$$

The factor $t^{\eta/2}$ in the above equation reflects the branch competition. The factor t^{-1}, present even at $\eta = 0$, reflects the fact that if both branches grow at constant velocity the difference in the lengths of the two branches remains constant, while the total length of each branch and the separation between branches increase linearly in t, so that the difference in length scaled by total length behaves as t^{-1}.

For $\eta = 4$, δ grows linearly in time. For large enough δ, nonlinear effects take over and one branch dies. Thus, assuming the branches are created after a tip-splitting event with a probability that is not singular at $\delta = 0$, the probability of both branches surviving for time t is proportional to $1/t$ at $\eta = 4$. On the other hand, the number of possible tip-splitting events in time t is proportional to t. Thus, the probability of creating a branch in time t that survives for time t is independent of t. This will become more clear in the next sections when we consider interaction of three branches. For $\eta > 4$, this probability decays for large t; on the other hand, for $\eta < 4$, this probability increases, and tip-splitting events proliferate. Defining $\epsilon = 4 - \eta$, the lowest order β function is

$$\beta(g) = \frac{\epsilon}{2} g. \tag{17}$$

V. RENORMALIZATION GROUP

The renormalization group is based on simultaneously expanding in g and $4 - \eta$. In this section we outline how the RG works; in the next section we will discuss the implementation of the RG.

We define survival of two subbranches by requiring that neither of the two subbranches has more than some given percentage of the total growth probability. Then we define g as the probability in time t that two branches are produced which survive for time t, which relates the arbitrariness in survival to an arbitrariness in the renormalization scheme. Alternatively, define g as the probability in time $\tilde{T}$ that two branches are produced which survive up to a separation $\tilde{L} \propto v\tilde{T}$; this second definition will be more convenient and will be used in the numerical work below. The scale $\tilde{L}$ is intermediate between the scales l and L.

We will compute two RG functions, the renormalization of the growth velocity and the renormalization of the tip-splitting rate g. Consider the renormalization of growth velocity to first order in g at $\eta = 4$. If there is only one branch

in the system, this branch grows upward with velocity v. If the branch splits into two subbranches, the growth velocity is reduced until eventually one of the two subbranches wins and the original growth velocity is restored at long times, where no further tip-splitting events intervene so long as we work to first order in g. The probability that the subbranches survive to distance $\tilde{L}$ scales as $1/\tilde{L}$.

The probability that both branches survive exactly time t and distance vt scales as $1/t^2$. If the two branches survive for time t, the height of the cluster at long times is reduced by an amount of order vt compared to the height of the cluster without tip splitting. More precisely, evolve the cluster for total time T, so that the probability of a single such tip splitting event is gT/t^2, and compute the average height h of the cluster after time T, to find

$$h = vT - gTc \int \frac{dt}{t}, \qquad (18)$$

where c is some constant. This yields the renormalized velocity

$$v_{\text{ren}} = v \left(1 - \frac{gc}{v} \ln \tilde{L}/l \right). \qquad (19)$$

Interpreting Eq. (19) as the first term in the expansion of a power law given by Eq. (7), we find that the dimension of the cluster is given by

$$D = gc/v. \qquad (20)$$

For $\eta < 4$, the number of tip-splitting events proliferates. The average number of branches in a system at macroscopic scale $\tilde{L}$ scales as

$$\tilde{L}^{(4-\eta)/2}, \qquad (21)$$

as seen by the lowest term in the β function above. Go to second order in g^2 to compute the next term in the β function. If two tip splittings occur, there are now three competing branches, and the enhanced competition reduces the chance that any two of them will survive till long times. There is a simple physical reason for the enhanced competition. Equation (16) may seem surprising, as it implies that for $\eta < 2$ the branches do not compete, while it is known that for any $\eta > 0$ a smooth surface is unstable. However, the factor t^{-1} in Eq. (16) is due to the increasing separation of the growth tips over time. Starting with perturbations on a smooth surface, there is no such mechanism causing the perturbations to spread in space. Similarly, if there is a large number of competing branches, they are forced closer to each other and are unable to spread apart from each other as rapidly, enhancing the competition. In Fig. 2, we show various possibilities. In (a), the small branch in the middle is actually reducing the competition of the two outer branches, while in (b) and (c) the competition of the two larger branches is enhanced. To determine which of these effects is stronger requires a calculation.
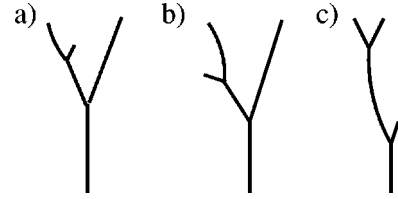

FIG. 2. Competition of three branches. Various possibilities.

Let the second splitting occur at time t after the first splitting. If one of the two branches resulting from the second splitting dies after a time much less than t, the second splitting has no affect. Thus, the probability that the second splitting will affect the evolution of the first pair of branches is proportional to $\int dt/t$, again yielding a logarithm as desired.

Precisely, consider the number of surviving pair of branches at scale $\tilde{L}$ that are produced in time T. If there are no tip-splitting events, this probability is zero; if there is one it is given by the calculation above. If there are two, the branches compete and one must integrate over the initial time at which the two branches are created as well as over the initial conditions after each tip-splitting event. It is convenient to define $\tilde{g}$ to be the *rate* at which *any* tip-splitting event occurs. Only some fraction of these events lead to a pair of branches surviving for sufficient time, so that $g < \tilde{g}\tilde{T}$. The number of surviving pairs, to order $\tilde{g}^2$, is

$$P_1 \tilde{g} T e^{-\tilde{g}T} + \int dt P_2(t) \frac{\tilde{g}^2}{2} T e^{-\tilde{g}T} + \cdots = P_1 \tilde{g} T - P_1 \tilde{g}^2 T^2$$

$$+ \int dt\, P_2(t) \frac{\tilde{g}^2}{2} T + \cdots \qquad (22)$$

where P_1 is the probability that one tip-splitting event gives rise to a surviving pair of branches, while $P_2(t)$ is the probability that two such events produce a surviving pair, with t the time difference between events. Note that $P_1 \propto l/\tilde{L}$.

If $t \gg \tilde{T}$, then the branch creation events are independent, and we find that $P_2 = 2P_1$, as either of the two creation events may give rise to a branch pair at scale $\tilde{L}$, so that terms of order T^2 cancel in the above equation. Otherwise, $2P_1 - P_2$ is of order $1/t$; assume

$$P_2 = 2P_1 - c_2/|t|, \qquad (23)$$

for some constant c_2. Then, the bare constant g is determined by

$$g = P_1 \tilde{g} \tilde{T}, \qquad (24)$$

and the probability of producing a surviving branch pair at scale $\tilde{L}$ in time $\tilde{T}$ is given by

$$\tilde{T} \left(P_1 \tilde{g} - \frac{c_2}{2} \tilde{g}^2 \int \frac{dt}{t} \right) = g - c_2 \frac{g^2}{\tilde{T} P_1^2} \ln \tilde{L}/l. \qquad (25)$$

This yields the β function, taking into account velocity renormalization,

$$\beta(g) = \frac{\epsilon}{2}g - c_2 \frac{g^2}{\widetilde{T}P_1^2} + c\frac{g^2}{v}. \qquad (26)$$

To evaluate c_2, as well as c in Eq. (20), we must turn to a numerical renormalization group as discussed in the next section, summing over different possible branch creation events. We will numerically evaluate $P_2(t)$ for a fixed $t \gg l/v$, and then use the scaling arguments given here to obtain $P_2(t)$ for any t and get the lowest order β function. Similarly, c can be obtained by considering only one set of initial conditions after the tip-splitting event and using scaling arguments. The RG requires numerical work, but remains essentially an analytical treatment, in the same sense that we may refer to an RG in field theory as analytical despite possible use of a computer to perform loop integrals.

There is an interesting question related to the correct form of the β function for various definitions of g, whether g is the rate at which branch pairs are produced that survive to scale $\widetilde{L}$ or until time $\widetilde{L}/v$. The second definition is what is needed to determine the number of branch pairs in the system. At time t after the first tip-splitting event, let there be a second tip-splitting event, so that one of the second pair of branches survives only for a time t' much less than t. Then, when the two remaining branches reach separation $\widetilde{L}$, a time $\widetilde{L}/v + t'$ has elapsed, rather than a time $\widetilde{L}/v$. We will find that, depending on which definition of g is used, $P_2(t)$ will differ by an amount of order $t'/\widetilde{L}$. Note that this is independent of t, differing from the form we have assumed in Eq. (23). This yields a change in $\int dt P_2(t)$ independent of L, and of order t'; integrating over initial conditions for the second branching event will yield a logarithmic correction to $\int dt P_2(t)$. However, since the velocity is renormalized, there is an additional term in the β function for the first definition, equal to g^2c/v, which gives the same correction to $P_2(t)$. However, we will not need to consider this complication, because for fixed t' and large $\widetilde{L}$, the change in $P_2(t)$ is negligible and this is the regime in which we perform the numerical calculations.

Similarly, there may also be slight differences in the definition of g between requiring that the branch pair grow until *height* $\widetilde{L}$ or until *separation* $\widetilde{L}$. Although at long times the surviving branch pair grows with the characteristic 72° angle, and the height and separation are related, there can again be deviations in the separation by an amount of order $1/\widetilde{L}$. If the present work, concerned with the stationary regime in the cylindrical geometry, is extended to the affine regime, perhaps these deviations in separation will be found to be connected with different scaling in the horizontal and vertical directions.

VI. NUMERICAL RENORMALIZATION GROUP

The reduced model was implemented numerically in a discrete version, such that the program alternates between growth tips on different time steps, advancing each growth tip by an amount proportional to the growth probability measure. To solve Laplace's equation quickly, the method of

iterated conformal maps [18,12] is used, using "strike mappings" [18] to obtain branches of vanishing aspect ratio, and computing the Jacobian at the tips by appropriate regularization.

To obtain dynamics in the scaling regime well below the macroscopic cutoff, we simply take this cutoff to infinity, which poses no difficulty in a conformal mapping implementation of the reduced model: the surface that is mapped onto the growing cluster is the real line, while the map $z \rightarrow z^2$ is used to produce a single growing tip as an initial condition. To evaluate the β function, we run the simulations until the two most active branches become more than a large, but finite, distance $\widetilde{L}$ apart. Of course, if it were not necessary to perform the calculations numerically, this distance would be taken to be infinite. To produce tip splittings, we use a function whose derivative is given by Eq. (8) to produce a pair of growth tips, choosing the initial separation between tips to be small. Interestingly, this function can be obtained in closed form as (for $x=1$)

$$F(z) = z^{2/5}(z^2 - 5)^{4/5}. \qquad (27)$$

The strike mappings take a particularly simple form in this geometry. We have $f(z) = \sqrt{z^2 - \lambda}$. Using the shape of the map $F(z) \propto F_i(z - z_i)^2$ near the tip, this increases the length of the branch by $F_i\lambda$. The regularized value of $F'(z)$ near the tip is $\sqrt{F_i}$, but λ is taken proportional to $|F'|^{-2}$, so that we produce strikes of constant length in the physical plane.

With this geometry, the program runs significantly faster than such a program in radial geometry, due to the simple form of the map functions. It may be worth investigating this as a means of speeding up simulations using the conformal mapping model.

The errors due to discretization can be surprisingly large, so that even after thousands of time steps there are noticeable, though small, deviations from the linearized branch competition dynamics discussed above. We have verified that these errors are reduced as the discretization is reduced, but we have had to make some compromises to obtain a sufficiently fast program.

To obtain a range of different initial conditions for branches after splitting, we use the discretized version of the reduced model, but we introduce a factor f that multiplies the growth velocity of one of the daughter branches on the *first* step after splitting. When this factor is close to 0, that daughter tends to lose; when it is close to 1, that daughter tends to win; a balance arose when f is near $f_0 \approx 0.278$. We are able to start the branches sufficiently close that they compete roughly equally for tens of thousands of growth steps.

As discussed above, we fix the time t of the second splitting (chosen to be 500 steps for each of the two branches), pick one of the two branches to split at random with relative probability equal to the relative growth measure on the tips, and then evolve the three branches. Typically, for the two most active branches to obtain the chosen separation requires of order another 3000 growth steps per branch.

We wish the initial conditions for the second tip-splitting event to have the same microscopic cutoff as for the first tip-splitting event. In order to do this, the same mapping of

Eq. (27) is used for both tip-splitting events, with an appropriately scaled value of x, and the overall velocity scale after the second tip-splitting event is chosen such that those two daughters initially have the same step size in the *physical plane* as the two daughters after the first tip-splitting event.

We tried two methods of handling the integration over initial conditions. First, a Monte Carlo technique: initial conditions are chosen randomly and we count the fraction of initial conditions that give rise to a surviving branch pair. To speed the Monte Carlo calculation, we sampled only a subset of initial conditions, chosen to include all conditions that could give rise to a surviving pair. By having the program randomly choose which of the two branches after the second branching event would get the first growth step, we ensured that the distribution of initial conditions for this event was symmetric between the branch growing inward and the branch growing outward. The Monte Carlo technique suffered from the problem that, to obtain a sufficient number of surviving branch pairs in the available computer time, we had to adopt a fairly broad definition of ''surviving'' and keep $\tilde{L}$ finite. The correct limit for the renormalization group is to take $\tilde{L} \gg l$. In this limit, it does not matter how the survival of a branch pair is defined, but for finite $\tilde{L}$ we more closely approximate the desired results if we take the definition of survival to be very narrow, so that the two branches must be almost identical in growth measure. This was accomplished by manually searching for initial conditions that gave rise to a surviving branch pair (with an extremely narrow definition of survival so that δ for the two surviving branches was almost exactly zero) and numerically computing the derivative of δ with respect to the initial conditions to obtain P_1 and P_2.

If we fix the initial conditions of one of the tip-splitting events to produce a very asymmetric pair of daughters so that after a brief time only one daughter survives, and choose the initial conditions of the other tip-splitting event randomly, the probability that a branch pair survives to scale $\tilde{L}$ must approach P_1. Due to the discretization errors in our program, this probability is within a few percent of P_1, but not exactly equal to P_1; we have verified that this difference also disappears as the discretization is reduced. The numerical evaluation of $P_2 - 2P_1$ suffers from the problem that the large contributions resulting from the very narrow region where all three branches compete may be swamped by small errors over the large region of all other initial conditions. Thus, we have had to adapt some criterion for determining what range of initial conditions to integrate over. This necessarily introduces some error and makes our results for the β function somewhat subjective. It is hoped that improved numerical techniques will at some point improve this situation. One reason for the difficulty is that the processes in Fig. 2 contribute to the β function with different signs. Another reason for these small errors is discussed at the end of the last section in terms of corrections of order $1/\tilde{L}$ which are logarithmically divergent when integrated over initial conditions for the second surviving branch pair; perhaps using a different definition of g will improve the situation.

The constant c in Eq. (20) is obtained by evaluating a process with a single tip splitting. We consider the change in height of the dominant branch of the pair as compared with the height of a branch without splitting. The simulation of the branch pair was run for approximately $50\,000$ steps per branch. The change in height fits very well the form $c - c_1/\sqrt{t}$, with c_1 some other constant; using this form we were able to obtain the asymptotic change in height by extrapolation. This quantity c can be obtained much more accurately than c_2.

Using Eq. (20) evaluated at the fixed point of Eq. (26), I have obtained that

$$D \approx 0.46\epsilon. \tag{28}$$

Using different estimates for the range of initial conditions over which to integrate, I have obtained a lower estimate of $D \approx 0.40\epsilon$ and an upper estimate of $D \approx 0.51\epsilon$. I then compared these results to the dimensions obtained numerically [12]. The RG result seems high, for at $\eta = 3$ we have $D \approx 0.26$ and at $\eta = 3.5$ we have $D \approx 0.16$, where these results are obtained by subtracting unity from the dimensions in radial geometry. However, fitting the dimensions obtained numerically for $\eta = 0,1,2,3$ to a polynomial in ϵ, I found that the lowest order result is

$$D \approx 0.45\epsilon, \tag{29}$$

in good agreement with the RG result. I did not include $\eta = 3.5$ in the polynomial fit as this dimension is known less accurately than the others and has an inordinate effect on the lowest order term in ϵ; taking $D = 0.17$ at $\eta = 3.5$ leads to $D \approx 0.48\epsilon$, while taking $D = 0.16$ leads to $D \approx 0.41\epsilon$.

Let us now consider the multifractal spectrum [20,21]. Let x be a point in the physical plane, with $z = F^{-1}(x)$. The harmonic measure is $|F'(z)|^{-1} dx = dz$. Define $p(x)$ to be the *normalized* harmonic measure

$$p(x)dx = \frac{|F'(z)|^{-1} dx}{\int (dx'/l) F'(z')^{-1}}, \tag{30}$$

and the exponents $\tau(q)$ by

$$\left\langle \int \frac{dx}{l} p^q(x) \right\rangle = \left(\frac{l}{L} \right)^{\tau(q)}, \tag{31}$$

where the angular brackets denote averaging over realizations of the cluster. For an isolated branch in cylindrical geometry, if we pick a parametrization such that $F(z) \propto z^2$ near the tip, then the denominator of Eq. (30) is of order $\sqrt{L}/l$. For $q > 2$ the integral of Eq. (31) is divergent near the tip and is cut off at length scale l. For $0 < q < 2$ this integral is divergent away from the tip, and is cut off at a physical length scale L, when the power law behavior of the electric field crosses over to an exponential decay. For $q \leq 0$, these exponents are ill defined in this geometry. For an isolated branch, we have $\tau(q) = q/2$ for $q > 2$ and $\tau(q) = q - 1$ for $q < 2$.

It is also possible to compute corrections to the multifractal spectrum in the RG. Various multifractal exponents may be defined, including quenched and annealed exponents [22]. It has been argued [23] that asymptotically all these exponents are identical for DLA, but that for finite size systems the apparent exponents may be quite different. The different exponents all involve different ways of choosing how to weight different realizations of the cluster when performing the average in Eq. (31). Within the RG framework, we need to have a multiplicatively renormalizable operator in order to obtain power laws from the lowest order computation. This requires choosing the correct set of exponents and the correct average, as will be discussed below.

Let us first consider corrections to $\tau(q)$ for $q > 2$. The integral of Eq. (31) must be summed over all configurations of the cluster. The configuration with only one branch gives the zeroth order result. Let $\int p^q$ for the configuration with a single branch be equal to $P_0(q)$. At first order in g one must sum over configurations with two branches also. One must integrate $\int p^q - P_0$ over the full trajectory of the two branches, starting with the two branches almost equal and continuing until one branch has completely won out. This trajectory can be obtained numerically. Note that the integral of $p^q(z)$ will be dominated by the field near the tips, and so it suffices to know F_i at each tip:

$$\int \frac{dx}{l} p^q(x) \propto \left(\frac{l}{L}\right)^{q/2} \sum_i F_i^{-q/2}. \qquad (32)$$

Suppose the integral over the branch trajectory of $\int p^q - P_0(q)$ is equal to $-txP_0$, where t is the time the two branches exist. Integrating over initial conditions of the two branches, we have that the left-hand side of Eq. (31) is equal to

$$\left(\frac{l}{L}\right)^{q/2} (P_0 - xgP_0 \ln L/l + \cdots) \qquad (33)$$

giving $\tau_\eta(q) = q/2 + xg$.

How should we perform the integral over the branch trajectory? Each configuration along the trajectory corresponds to a different realization of the cluster, and, depending on how we choose to weight different realizations, we must weight the integral over the trajectory differently. We choose to weight the integral by

$$\left(\sum_i \sqrt{F_i}^{-\eta}\right)^{-1} dt, \qquad (34)$$

which corresponds to changing the time scale such that each branch grows at a rate proportional to $\sqrt{F_i}^{-\eta}$, rather than that given by Eq. (4). However, this is exactly what happens with a large number of branches if one of the branches splits: in this case, the denominator of Eq. (4) involves contributions from all branches and is insensitive to the splitting on the single branch, so that we expect that this choice of weighting function will define $\langle \int p^q \rangle$ in a manner that is multiplicatively renormalizable.

Further, with this choice, the dimensions will automatically obey the electrostatic scaling law [24] order by order. This scaling law adapted to cylindrical geometry is

$$1 + D = \tau(2 + \eta) - \tau(\eta). \qquad (35)$$

The electrostatic law is obtained, in this geometry, by noting that the growth velocity is proportional to the average, using the growth probability measure, of λ over tips: this average scales as $\tau(2 + \eta) - \tau(\eta)$. Since this relation between the growth velocity and the average of λ holds for each branch configuration separately, it holds for the exponents as we have defined the average above.

We have obtained the lowest order results that

$$\tau(6) = 3 + 1.77D, \quad \tau(5) = 2.5 + 1.35D,$$

$$\tau(4) = 2 + 0.77D, \quad \tau(3) = 1.5 - 0.23D. \qquad (36)$$

We report these results in terms of D by using Eqs. (20) and (33) as these calculations are more accurate than that for Eq. (26). Note that even at lowest order in ϵ the $\tau(q)$ spectrum does not have any simple form such as a log-normal distribution or gap scaling. By looking at larger q, we find that the Turkevich-Scher [25] scaling law does not hold as an equality in this expansion. It holds only as an inequality.

For $0 < q < 2$, a similar calculation can be performed, although it will be slightly more complicated as the integral of $p^q(z)$ is no longer dominated by the tip and must be considered over the full branch. Further, the cutoff L of cylindrical geometry must be kept finite, rather than being taken infinite as we have done in the calculations above, to keep the integral of p^q finite.

One further complication is that $\tau(q)$ is not an analytic function of $4 - \eta$ near $q = 2$. The $\tau(q)$ above correspond to an $f(\alpha)$ spectrum with two points: $f = 0.5, \alpha = 0$, the zero-dimensional set of singularities near the tips, and $f = 1, \alpha = 1$, the rest of the branch forming a one-dimensional set. As η decreases, the singularities near the tips soften while the dimension of the set of tips increases, and the function $f(\alpha)$ becomes a curve rather than a set of discrete points. The function $\tau(q)$ above is not analytic in q as for $q > 2$ the integral of p^q is dominated by $\alpha = 0$, while for $q < 2$ it is dominated by $\alpha = 1$. Similarly, for fixed q near 2, as η is decreased the value of α, which controls $\tau(q)$, may jump discontinuously from near 0 to near 1, or vice versa. It may be possible to surmount this problem by expanding the left-hand side of Eq. (31) in $q - 2$ and trying to resolve the logarithms that result as a sum of different power laws.

VII. RENORMALIZABILITY

Clearly, it will be very difficult to prove renormalizability, since we find it difficult to evaluate even lowest order processes, but renormalizability is essential for the RG we employ. Further, if we prove multiplicative renormalizability for the theory with two parameters v, g, then the fractal nature of the DBM cluster will follow without any detailed calculation of β functions: it is clear that v has no effect on the RG flow of g, and if g has an attractive fixed point then

without fine-tuning the theory must arrive at a critical point with nontrivial exponents. If instead g had a repulsive fixed point, we would observe very different critical behavior: for $\eta > 4$, there would be a phase transition in the behavior of the system as a function of the bare coupling constant from one dimensional to fractal; the bare coupling constant could perhaps be adjusted using a noise reduced version of the model. Also, for fixed bare g, there would be a discontinuous change in the dimension of the cluster as a function of η from $D > 0$ to $D = 0$. So let us sketch how such a proof might proceed.

Consider a collection of competing branches with separation distances of order L_1. Let one branch have a single tip-splitting event such that after a time T_2 only one of the two subbranches survives, with $vT_2 \ll L_1$. While both subbranches survive the total growth measure on the pair is reduced compared to that on the subbranch, but at times much greater than T_2 the growth measure of the surviving subbranch asymptotically approaches that of the parent, and at scale L_1 it seems simply as if the branch with the tip-splitting event had grown with a renormalized velocity for a brief time. After integrating over T_2, the renormalization of the velocity is of order $\ln L_1/l$.

It would be disastrous if instead there were a logarithmic divergence that depended on L_1, such as $L_1 \ln L_1/l$, as this would change the growth rules of the theory and the manner in which branches compete. However, since we are interested in the divergence as $T_2 \to 0$, we can restrict ourselves to $vT_2 < L_1$ and formally expand the growth velocity in a power series of vT_2/L_1 (this is possible since, for T_2 small, the influence of the branch pair on the other branches is small), so that the growth velocity is

$$\sum_k \int \frac{dT_2}{T_2} a_k (vT_2/L_1)^k. \tag{37}$$

The zeroth-order term in this series yields a logarithmic divergence of desired form, while the higher terms are not divergent.

It would equally be disastrous if the growth measure of the surviving subbranch were not to asymptotically approach that of the parent. However, this follows from properties of Laplace's equation: at long times the surviving tip is at a height much greater than the dead subbranch, and the dead subbranch has only a small effect on the growth probabilities near the surviving tip.

This show that processes with a single branching just renormalize v. Consider several branchings. Each set of branchings is defined by a tree diagram indicating the topology of the branchings, and a set of times t indicating the times at which branching take place as well as a set of initial conditions for each branch pair. To the initial conditions corresponds another set of times, the times that the two branches survive. For fixed topology, one must integrate over these times and evaluate the average rate at which the cluster grows or produces branches. Let us order the times from smallest to largest, and send groups of these times to zero. If a set of times t_i are sent to zero together, with some other times t_a being held fixed, one finds, as above, logarithmically

divergent renormalizations of v and g. However, by expanding in t_i/t_a as above, we again obtain the desired result that the logarithmically divergent terms depend only on the logarithm of the ratio of t_a/t_i.

These arguments sketch the renormalizability of the theory. One must also show, for example, that there are no divergent contributions to the rate at which one branch splits into three.

Also, in defining the reduced model, we ignored shot noise in the velocity of a given branch; however, the process of tip splitting, which renormalizes the average velocity, will reintroduce some noise in the velocity. The noise in the velocity of a branch is irrelevant at long time; fortunately, then, while the renormalization of velocity is logarithmically divergent, the rms fluctuations in the velocity are convergent at short times, behaving as (taking the branch pair to survive for time t) $\int (dt/t^2)t^2$.

In the continuous model, δ increases in time, and the probability of having $\delta = 0$ decreases in time, such that this probability, multiplied by the branch length, remains constant. Consider now the case of a discrete formulation of the model, to see the effects of shot noise or other fluctuations in the velocity. Suppose two competing branches have lengths $1 + \delta, 1 - \delta$. Take a discrete growth step, adding length 2δ to one of the branches, with probabilities $1/2 \pm \delta$. The probability of having the two branches symmetrically distributed after the discrete growth step is $1/2 - \delta$. If the initial configuration of δ is chosen uniformly near $\delta = 0$, we find that the probability of having $\delta = 0$ is again decreased with this probability, multiplied by the branch length, again remaining constant to linear order in δ. To second order in δ we will find differences between the continuous and discrete models.

One can do a similar calculation for the case in which the growth of a branch stagnates due to a tip-splitting event. The probability of a given branch having a tip-splitting event is $1/2 \pm \delta$, while the tip-splitting event will slow that branch for a time $1/2 \mp \delta$ during which the other branch grows at a velocity $1/2 \mp \delta$. Again one can show that the probability of having $\delta = 0$, multiplied by branch length, remains constant, to linear order in the time of the tip-splitting event.

This comparison between continuous and discrete models is why we emphasize that the rms fluctuations induced by tip splitting are convergent. Suppose instead that the rms fluctuations were not convergent. Then, one would find in Figs. 2(a) and 2(b) that c_2 was divergent when integrating over initial conditions for the second branching event, which would lead to divergences of the form $(\ln L/l)^2$, destroying renormalizability.

VIII. CONCLUSION

We have presented the lowest order in an $\epsilon = 4 - \eta$ expansion, obtaining good agreement with numerical results. For more accurate comparison with DLA, for which $\epsilon = 3$, extension to higher order with further branching processes is necessary. Due to the need for numerical techniques to evaluate even lowest order processes, it is unclear if higher order terms can be computed accurately.

It is also necessary to improve the numerical evaluation of

lowest order processes. To numerically simulate the reduced model, some discretization and cutoff is necessary. We have used a particular cutoff, but perhaps other cutoffs are preferable. Indeed, the discrete random walker formulation of the DBM provides another cutoff that may lead to more accurate results; one can simulate the DBM with growth confined to occur on only two or three different tips to generate a system with a fixed number of branches.

It is also interesting to consider the extension to higher dimensions. While conformal mapping techniques were very useful in all the calculations above, the basic idea, determining the relevance of tip splitting based on the competition of two branches, should be applicable in any dimension. While there is a lower bound on the dimension of DLA in higher dimensions [26], there does not seem to be any such bound for the DBM, which would prevent the existence of an upper critical η.

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