Diffusion limited aggregation as a Markovian process: site-sticking conditions

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Cylindrical lattice diffusion limited aggregation (DLA), with a narrow width $N$, is solved for site-sticking conditions using a Markovian matrix method (which was previously developed for the bond-sticking case). This matrix contains the probabilities that the front moves from one configuration to another at each growth step, calculated exactly by solving the Laplace equation and using the proper normalization. The method is applied for a series of approximations, which include only a finite number of rows near the front. The fractal dimensionality of the aggregate is extrapolated to a value near 1.68.

1. INTRODUCTION

Diffusion limited aggregation (DLA) [1] has been the subject of extensive study since it was first introduced. This model exhibits a growth process that produces highly ramified, self-similar patterns, which are believed to be fractals [2]. It seems that DLA captures the essential mechanism in many natural growth processes, such as viscous fingering [3], dielectric breakdown [4], etc. In spite of the apparent simplicity of the model, an analytic solution is still unavailable. Particularly, the exact value of the fractal dimension is not known. Some of the analytic approaches employed so far include the fixed scale transformation (FST) [5], real space renormalization group (RSRG) [6], conformal mapping [7], and conformal mapping [8].

In DLA there is a seed cluster of particles fixed somewhere. A particle is released at a distance from the cluster, and performs a random walk until it attempts to penetrate the fixed cluster, in which case it sticks. Then the next particle is released and so on. There are two common types of sticking conditions. The sticking condition described above is called “bond-DLA”, because it occurs when the random walker attempts to cross a perimeter bond between an unoccupied site and the aggregate. In an earlier paper [9], we solved the bond-DLA problem using a Markovian process. Here we apply similar methods to the “site-DLA” case, where sticking occurs as soon as the random walker arrives at a site that is a nearest neighbor to the aggregate. Since it is believed that the large scale structure of DLA is not sensitive to the type of sticking conditions used [10], one expects both problems to yield the same asymptotic fractal structures.

DLA can be grown in various geometries. In this paper we deal with the cylindrical geometry in two dimensions (2D), where the particles are emitted from a distant horizontal line at the top, while the seed cluster is a parallel line at the bottom, with periodic boundary conditions on the sides. We only consider relatively narrow cylinders, with widths ranging from $N = 2$ to $N = 10$. Even though the analysis in this paper is solely 2D, the same techniques can be applied in higher dimensions.

An exact solution of bond-DLA with $N = 2$ was published in 1998 [10]. A generalization of the same approach was used in order to solve slightly wider cases with $N$ between 3 and 7 [11]. The solution presented in the latter case is not exact, but still, it presents a well controlled series of approximations in the sense that any desired numerical accuracy could be obtained, provided that a sufficiently high-order of approximation is used. The difficulty with performing a high-order calculation is that its complexity grows exponentially.

The main idea in these references and in this paper is to follow the dynamics of the growing front. The shape of the interface determines the unique solution to the Laplace equation that determines the growth probabilities. The structure of the aggregate behind the interface is irrelevant and so is the history that led to the current interface. Each growth process changes the interface. We can therefore describe DLA as a Markovian flow in the space of interface configurations. The Markov states are the possible shapes of the interface, which are indexed by an integer, usually denoted by $i$ or $j$. $P_i(t) = P_i(t + 1)$, the probability that the interface is in state $i$ at time $t + 1$, depends only on the state of the interface at time $t$. The conditional transition probabilities from state $j$ to state $i$ make up the evolution matrix $E_{i,j}$, which is time independent. Thus, the dynamics of the Markov chain is described by the Master equations,

$$P_i(t+1) = \sum_j E_{i,j} P_j(t), \quad i = 1, 2, \ldots \quad (1.1)$$

Each matrix element $E_{i,j}$ corresponds to a particular growth process, and the sum of $j$ runs over all the interface configurations (whose number may be infinite).

In order to fully describe the dynamics, it is necessary to calculate the probabilities of all the possible growth processes, for each of the possible initial configurations of the interface. We calculate the growth probabilities.
by solving the discrete Laplace equation on a lattice for a function $\Phi$, which corresponds to the average density of random walkers,

$$\nabla^2 \Phi = 0.$$  \hfill (1.2)

In the dielectric breakdown model (DBM) $\Phi$ has an electrostatic meaning, so it is also commonly referred to as the “potential”.

Usually, the equation set $\{\text{1.2}\}$ is infinite because the number of possible shapes the interface may assume is unlimited. This may pose a problem for two reasons. For one, it is difficult to include all of the possibilities systematically. The case of bond-DLA with $N = 2$ is a counter-example, where the complete set of possible configurations can be easily characterized using a single parameter. This is because the interface has the shape of a step whose height $j$ can be any nonnegative integer $|j|$. For $N > 2$, however, it is very difficult to parametrise the shape of the interface, even with the use of more than one parameter, because complex overhangs may occur $|k|$. The second problem is that even if it was possible to account for a complete infinite set of configurations, it would still be awkward to analyze the Markov process, e.g., finding its fixed point. Instead of accounting for all the configurations, we make an approximation by employing some consistent truncation scheme on the list of configurations. In the $O$th-order approximation we include only the top $O$ rows of a configuration and truncate the rest; The list of configurations is sorted according to the maximal height difference, $\Delta m$, between the lowest and highest particles on the interface $|k|$. In the $O$th-order approximation, only a finite set of configurations with $\Delta m \leq O$ are taken into account. The configurations with $\Delta m > O$ are truncated so that only their top $O$ rows are taken into account (below the $O$th row all the sites are considered to be occupied). This truncation does not have a noticeable effect on the upward growth probability (the growth probability at the tip), because of the exponential decay of the potential inside deep fjords. Because of this exponential decay, the approximation converges very fast as a function of $O$. Unfortunately, the number of configurations diverges exponentially with $O$, so that the calculation can be carried out only for relatively low-order (depending on the width $N$ and on the strength of the computer).

In the case of site-DLA, the situation is a bit simpler than in bond-DLA, because it is generally harder for the random walker to penetrate deep into a fjord. A particle will only be able to enter fjords that are three sites wide or more, unlike the case of bond-DLA, where a particle can go into a single column fjord. This makes the solution of site-DLA with $N = 2$ and $N = 3$ much simpler, because they both have only a finite number of interface configurations. The narrowest cylinder that can have an arbitrarily deep fjord (a configuration with an arbitrarily large $\Delta m$) arises for $N = 4$, and thus there is an infinite number of configurations. However, there can be no fluctuations in the width of the fjord, so in this sense this case resembles the $N = 2$ case in bond-DLA. For $N > 4$ the approximation method must be used, but generally, for the same $N$ and $O$ the number of configurations in site-DLA is much smaller than in bond-DLA, so it is possible to perform higher-order calculations for wider cylinders.

Once an order of approximation $O$ is chosen, there is only a finite number of configurations, $N_c(N,O)$, which depends both on $N$ and on $O$. The Markov process is then closed and irreducible. Closed means that $\sum_{i=1}^{N_c} E_{i,j} = 1$ for $j = 1, \ldots, N_c$, and irreducible means that there is a finite probability to go from any initial state $j$ to any final state $i$ during a finite number of time steps. A basic theorem in Markov theory states that a closed and irreducible process necessarily has a single fixed point $|L|$. This fixed point represents the steady-state probabilities for the various interface configurations in the asymptotic time limit. The theorem is also true for an infinite number of states, so one can conclude that the unapproximated process also converges to a steady state. As mentioned, this steady state is characterized for example by a time independent average density $\rho$.

The fixed point equations are,

$$P_i^* = \sum_j E_{i,j} P_j^*, \quad i = 1, 2, \ldots$$  \hfill (1.3)

This means that $\mathbf{P}^*$ is the normalized eigenvector of the evolution matrix $\mathbf{E}$ with an eigenvalue of 1. Once the steady state $\mathbf{P}^*$ is calculated, it is possible to evaluate the steady-state average upward growth probability,

$$\langle p_{\text{up}} \rangle^* = \sum_{j=1}^{N_c} P_j^* p_{\text{up}}(j),$$  \hfill (1.4)

where $p_{\text{up}}(j)$ is the total upward growth probability for configuration $j$. The average steady-state density of the aggregate is then given by

$$\rho(N) = \frac{1}{N \langle p_{\text{up}} \rangle^*}.$$  \hfill (1.5)

Here, the density is written explicitly as a function of $N$. By $\rho(N)$ we denote the true value of the density, in the limit $O \rightarrow \infty$. We denote the result of the $O$th-order approximation by $\rho_o(N,O)$.

As mentioned, the number of configurations grows exponentially with $O$ and $N$, so it becomes infeasible to make the calculation for high values of $O$ and $N$. We perform calculations for $N \leq 10$. The calculated densities and the number of configurations are presented in Sec. $4$. We find that in order to obtain a relative accuracy of about $10^{-4}$, it is necessary to go up to $O = N - 2$, or $O = N - 1$. This is achieved for $N \leq 8$, but for $N = 9, 10$ it is too heavy a task for our computer resources. In spite of this, we are able to successfully extrapolate $O$ to infinity for $N = 9$ and $N = 10$. The calculated densities are compared to direct measurements from cylindrical site-DLA simulations, and are found to be the same up to
the accuracy of the simulation, which is about 0.01% or better.

The fractal dimension $D$ is extracted from the assumption that $\rho(N) \propto N^{-(d-D)}$, where $d = 2$ is the Euclidean dimension. In general one should also expect some corrections to scaling, especially for low $N$'s, i.e.,

$$
\rho(N) = AN^{-(d-D)}(1 + B/N^\theta + \ldots),
$$

where $A$ and $B$ are some constants, $\theta$ represents the leading correction exponent, and the dots stand for a series of higher powers of $1/N$. This scaling hypothesis is validated by both the analytic enumeration computation and by the simulations, which were conducted up to $N = 128$. The best fit of such a model to the enumeration data results in an estimate of the fractal dimension $D \approx 1.671 \pm 0.001$. The same fit is also performed with the simulation data, yielding $D \approx 1.66$ often found in the literature.

The differences between bond-DLA and site-DLA are manifested in the boundary conditions for the Laplace equation, and in the way the growth probabilities are extracted from the potential $\Phi$. The boundary conditions at the top are,

$$
\lim_{m \to \infty} \frac{\partial \Phi(m,n)}{\partial n} = 1, \quad n = 0, \ldots, N - 1,
$$

where $\hat{\mathbf{n}}$ is the vertical direction (the growth direction), and $\hat{\mathbf{m}}$ denotes the periodic lateral direction. This describes a uniform flux of incoming particles. In the original DBM papers \cite{14,16} a uniform potential is used instead of a uniform gradient, but if the distant boundary is very far, then the differences between the solutions for the two cases is exponentially small \cite{16}. The determination of the boundary conditions on the aggregate should be done with care. In the case of bond-DLA the potential is set to 0 on the aggregate itself, while in site-DLA the potential should be set to 0 on nearest neighbors sites, i.e., on sites where growth might occur. Also, the derivation of the growth probabilities from the potential in site-DLA is done a bit differently than in bond-DLA, as explained in the next section.

The Laplace equation with these boundary conditions can be solved exactly \cite{14,16}. The idea is to divide the plane (or space in higher dimensions) into two parts: the upper part is an empty semi-infinite rectangle that begins at the row of the highest site on the lower boundary and continues upward ad infinitum. The lower boundary is the set of sites on which the potential $\Phi$ is set to 0, and it depends on the type of sticking-conditions used: In the case of bond-sticking conditions the boundary is the aggregate itself, whereas in the case of site-sticking conditions it is the set of sites that are nearest neighbors to the aggregate. The lower part contains the aggregate and extends from the highest row downwards. The row that contains the highest particle in the aggregate is usually set as a reference row with $m = 0$. Thus, in bond-DLA, the upper part has $m \geq 0$, and the lower part has $m \leq 0$, and in site-DLA, the upper part has $m \geq 1$, and the lower part has $m \leq 1$, as explained in more detail in Sec. \cite{14}. Note that in either case the dividing row is considered to belong to both parts. In the upper part, it is possible to express the potentials in row $m + 1$ as a linear combination of those in row $m$,

$$
\Phi(m + 1, n) = 1 + \sum_{n'=0}^{N-1} \Phi(m, n') g_N(n - n').
$$

This is especially useful for the bottom row of the upper part, $m = 0$ or $m = 1$ (depending on the type of sticking conditions). The boundary Green’s function $g_N(n)$, appearing in Eq. \cite{14,16}, is given by

$$
g_N(n) = \frac{1}{N} \sum_{l=0}^{N-1} e^{-\kappa_l \cos(k_l n)}. \quad (1.9)
$$

The finite set of allowed wave-vectors $k_l = \frac{2\pi}{N}l$ for $l = 0, \ldots, N - 1$, is imposed by the horizontal periodicity. The factor $\kappa_l$ is related to $k_l$ through the dispersion relation

$$
sinh(\kappa/2) = \pm \sin (k/2), \quad (1.10)
$$
or more explicitly,

$$
e^{-\kappa(k)} = 2 - \cos(k) - \sqrt{(2 - \cos(k))^2 - 1}. \quad (1.11)
$$

An interesting property of the Green’s function is that

$$
\sum_{n=0}^{N-1} g_N(n) = 1. \quad (1.12)
$$

This property was proved algebraically in Ref. \cite{16} and was used in Refs. \cite{16,14} to check the computations of the Green’s function. It is also used in the sample calculation of Sec. \cite{11,13} in the current paper for the same purpose.

Usually, there is no general derivation for the solution in the lower part. In spite of that, the number of sites in the lower part is finite and not too large, so it is possible to simply write the equations for each of the potentials. The solution of the resulting finite and linear set of equations is then straightforward.

The paper is organized as follows: In Sec. \cite{11} we present in detail the differences in the computation of the growth probabilities between bond and site sticking conditions. This presentation also explains the connection with the Laplace equation more rigorously. After that, we perform a few sample calculations, for $N = 2$ and $N = 3$, in order to demonstrate the method presented in the introduction. We then report the results of the computations for $N$ between 4 and 10 for various orders of approximations $O$. We point out that the results collapse onto a universal function that enables the extrapolation $O \to \infty$. 
for \( N = 8, 9 \) and 10. This extrapolation reduces the error appreciably. In Sec. II we present the simulation we made in order to verify our theoretical predictions. This presentation also explains how the boundary Green’s function \( g_N(n) \) is used in some way as a probability function, in order to make the simulation more efficient. We summarize in Sec. IV.

II. ENUMERATION

Our computation method is referred to as enumeration, because it involves a systematic processing of some complete lists of configurations.

A. The differences between site and bond sticking conditions

Before proceeding with the actual calculations, we point out the differences in the computation of the growth probabilities between bond and site sticking conditions, because these differences are the essence of this paper. In order to point out the differences, we first review the method for computing the growth probabilities with bond-sticking conditions. The first step is to solve the Laplace equation (1.2) on a lattice, where the boundary conditions are \( \Phi = 0 \) on the aggregate, and \( \partial \Phi / \partial m = 1 \) on the distant boundary. In the case of cylindrical geometry there are periodic boundary conditions on the sides, see Fig. 1. The sticking probability per bond is then given by

\[
p_b = \frac{\Phi_b}{\sum_{b'} \Phi_{b'}}. \tag{2.1}
\]

where the subscript \( b \) refers to a perimeter bond and \( \Phi_b \) refers to the potential difference across such a bond. Because the potential is null on the aggregate, this difference is equal to the value of the potential in a nearest neighbor site. Finally, the growth probability per site is computed by multiplying the sticking probability per bond by the number of bonds associated with the site, \( N_b \), see Fig. 2.

Why does this procedure give the exact growth probabilities? In order to answer this question we must return to the original definition of DLA, that involves a single random walker. The random walker is injected into a random site near the remote boundary and it diffuses until it attempts to penetrate the aggregate, in which case it gets stuck. By “penetrate” we mean that it is not sufficient for the random walker to be in a nearest neighbor site to the aggregate, but that it has to attempt to cross a perimeter bond in order for it to stick. A possible way of measuring the growth probabilities for a particular interface configuration is to send many random walkers, one after the other, and remove them after they stick. One has to keep track of how many particles get stuck in each site. Eventually, the growth probabilities per site are estimated by the fraction of particles that got stuck in each site. Instead of releasing the random walkers one at a time, it is more efficient to release many of them simultaneously, and let them perform a random walk without interacting with each other. Moreover, instead of releasing a large amount of particles in a single batch and waiting until all of them stick, it is also possible to inject them at a constant rate near the boundary, i.e., in each time step inject a new particle into each site near the boundary with a uniform probability \( r \). The advantage in this way of performing the measurement is that after an initial equilibration time the system arrives at a steady state, which is characterized by a time-independent average number of random walkers in all of the sites, including sites that are not near any of the boundaries. In the steady state the average number of random walkers entering into the system in each time step at the upper boundary is equal to the average number of random walkers vanishing out of the lower boundary.

Denote the average number of random walkers in each site in the steady-state by \( \Phi(m,n) \). The crucial point is that \( \Phi \) is time independent. In order to calculate \( \Phi \) we note that it satisfies the discrete Laplace equation

\[
0 = \nabla^2 \Phi(m,n) \equiv -4 \Phi(m,n) + \Phi(m+1,n) + \Phi(m-1,n) + \Phi(m,n+1) + \Phi(m,n-1), \tag{2.2}
\]

because every random walker is equally probable to go to any one of its nearest neighbor sites. Thus, on a general lattice (or graph) the Laplace equation states that the value of \( \Phi \) at each site is equal to the mean value of \( \Phi \) on its nearest neighbor sites. Special care should be give to sites near the boundaries. Near the upper boundary each site has only three nearest neighbors, and particles are added at a constant rate \( r \), therefore,

\[
\Phi(m,n) = \frac{1}{4} \left[ \Phi(m,n-1) + \Phi(m,n+1) + \Phi(m-1,n) + \Phi(m,n+1) + \Phi(m+1,n) + \Phi(m,n-1) + r \right]. \tag{2.3}
\]

Note that the last term on the left before \( r \) is \( \Phi(m,n) \), instead of \( \Phi(m+1,n) \), because the particles that randomly choose to go up are unable to do so because of the boundary, and therefore they remain in the same place. Now, let us define \( \Phi(m+1,n) \equiv \Phi(m,n) + 4r \) as a fictitious density above the boundary. Then we see that Eq. (2.3) turns into the standard Laplace equation. This shows that instead of using the injection rate parameter \( r \), it is possible to use the regular Laplace equation with the Neumann type boundary conditions that require the specification of the electric field, which corresponds to the difference in the potential across the upper boundary. Since the value of \( r \) does not change the growth probabilities, we are free to choose any value for it. If, for example, we choose \( r = 1/4 \) then the boundary conditions at the top are

\[
\frac{\partial \Phi}{\partial m} \equiv \Phi(m+1,n) - \Phi(m,n) = 1, \tag{2.4}
\]
for \( n = 0, 1, \ldots, N - 1 \). We choose the upper boundary to be very far away from the lower one, because this simplifies the analytic expressions involved in the solution of the Laplace equation, while leaving the sticking probabilities practically unchanged.

Near the bottom boundary the situation is a bit different. Each random walker that attempts to go into the aggregate is taken out of the system. The steady state equation for these sites is therefore

\[
\Phi(m, n) = \frac{1}{4} \sum_{\text{nn}} \Phi(m', n'),
\]

(2.5)

where the sum is taken over all the sites \((m', n')\) that are nearest neighbors (nn) to \((m, n)\). At the lower boundary the situation is similar, because once again, we obtain the regular Laplace equation, if we choose the boundary conditions \(\Phi = 0\) on the aggregate itself.

The growth probability in each site is evaluated as the average number of random walkers that stick in that site per unit time, normalized by the total number of particles sticking in a time step across the total length of the lower boundary. An average of 1/4 of the particles in a site choose to go in each direction. Particularly, a fraction of 1/4 of the particles vanish after choosing to go via bonds that connect to the aggregate. The average total number of particles sticking in a site would be a sum over all of its interface bonds, \(\sum_{\text{p}} \Phi/4 = N_{\text{p}} \Phi/4\). In the steady-state, the average total number of sticking random walkers is equal to the average total number of random walkers injected into the system. Near the upper boundary, a random walker sticks after it moves into it. This differentiates between the boundary of the aggregate with a layer of circled sites, as shown in the figure. Therefore the normalization factor is \(N/4\) and the growth probability in each site is \(N_{\text{p}} \Phi/N\). In Ref. [14] we arrive at the same result using the discrete Gauss theorem.

The situation in site-DLA is different in the boundary conditions used near the aggregate, and in the expression for the growth probabilities. Now, random walkers never arrive at sites that are nearest neighbors to the aggregate, because as soon as they do they get stuck and are immediately removed from the system. We therefore impose \(\Phi = 0\) not on the aggregate itself, but rather on its nearest neighbor sites, see Fig. 3. In general, the boundary for the Laplace equation is obtained by coating the aggregate with a layer of circled sites, as shown in the figure. This differentiates between the boundary of the aggregate itself and the boundary for the Laplace equation, in the sense that it is possible that two different aggregates would have the same boundary for the Laplace equation, see Fig. 4. One can think that a random walker does not interact directly with the boundary of the aggregate, but rather, it interacts with the circled sites that make the boundary for the Laplace equation. This means that a random walker that obeys site-sticking conditions cannot be used as a probe in any way to determine which of the two aggregates in the figure are present. Consequently, any two different aggregates that have the same boundary for the Laplace equation must have the exact same set of growth probabilities and can be therefore considered as equivalent. Thus, from now on when we refer to an interface configuration, we relate to the shape of the boundary for the Laplace equation. The probability to be in such a configuration is a sum over all the underlying aggregate configurations. Another effect of the transition to the Laplace boundary is the narrowing of fjords. The padding of the aggregate by circled sites causes all the fjords to be narrower by two sites. Thus, a random walker can only penetrate into aggregates that have branches that are at least three sites apart.

As in the case of bond-DLA, the sticking probabilities are evaluated as fractions of the average number of random walkers that stick per unit time. Only now, we must sum over bonds that lead into the site, rather than out of it, as is the case in bond-DLA. The growth probability per site is therefore,

\[
p_{\text{site}}(m, n) = \frac{1}{N} \sum_{\text{nn}} \Phi(m', n'),
\]

(2.6)

where \(p_{\text{site}}(m, n)\) is the total sticking probability at the perimeter site \((m, n)\), see Fig. 5. Unlike the case of bond-sticking conditions, where a single potential determines the sticking probability in a particular site, now the potentials in several different sites contribute. This is because in bond-DLA the random walker sticks before it moves out of the site, whereas in site-DLA the random walker sticks after it moves into it. This difference gives the upper most tip of the aggregate even a greater advantage relative to bond-DLA, because a single particle tip gathers contributions from three sides in site-DLA, whereas in bond-DLA the only contribution is from above. This comes in addition to the screening property of the Laplace equation (common to both types of sticking conditions), which causes the sticking probabilities to be very far away from the lower one, because this simplifies the analytic expressions involved in the solution of the Laplace equation, while leaving the sticking probabilities practically unchanged.

**B. Exact solutions for \(N = 2, 3\)**

The best way of explaining the enumeration method is by showing some sample calculations in detail. We present here the two simplest cases, namely, \(N = 2\) and \(N = 3\). In these relatively simple cases there is only a finite number of configurations, so it is possible to get an exact solution with no need for approximations.

For \(N = 2\), the interface of the aggregate itself has an infinite number of possible configurations, because it has the shape of a step whose height \(j\) can be any nonnegative integer \(\geq 1\). However, in site-DLA there are only two distinct states: \(j = 0\) and \(j > 0\). The case \(j = 0\) refers to a flat interface, i.e., the two columns have the same height, and a growth process will create a step with \(j = 1\), with probability 1. For any step size \(j > 0\) there are only two sites where a random walker may stick: above the
highest particle in the aggregate, or on its side, see Fig. 4. There is no possibility for the random walker to penetrate into a fjord in $N = 2$, because it is too narrow, and the particle would stick at its entrance. The two configurations are indexed by $i = 1$ and $i = 2$ respectively and are shown in Fig. 3.

We now begin building the evolution matrix $E$, by finding the growth probabilities for each of the two configurations. As mentioned, configuration $i = 1$ turns into $i = 2$ with probability 1, hence $E_{1,1} = 0$ and $E_{2,1} = 1$. It is important to keep track of the total upward growth probability for each configuration, $p_{\text{up}}(i)$, that corresponds to events in which a newly stuck particle is higher than all of the particles in the aggregate. In this case $p_{\text{up}}(1) = 1$. In order to solve for $i = 2$, we first have to compute the Green’s function according to Eq. (1.9), which gives
\[
g_{2}(0) = 2 - \sqrt{2} = 0.5858, \\
g_{2}(1) = \sqrt{2} - 1 = 0.4142. \\
\] (2.7)

We check our calculations by verifying that $g_{2}(0) + g_{2}(1) = 1$, as expected from Eq. (1.12). The potential $\Phi$ near the growth sites can be expressed in terms of the variable $x \equiv \Phi(1,0)$ according to Eq. (1.8), as shown in Fig. 3. We usually set the row containing the highest particle in the aggregate as the reference row, with $m = 0$. Thus, the row $m = 1$ always contains the highest circled site that belongs to the Laplace boundary. Each of the sites in row $m = 1$ contributes to the potentials in the sites in row $m = 2$. The weight of the contribution is equal to the value of the Green’s function $g_{N}(n)$, where $n$ is the horizontal distance between the contributing site in row $m = 1$ and the evaluated site in row $m = 2$. In this simple case there is only one site with a nonzero potential, namely, $\Phi(1,0)$, which is yet unknown, and which we denote by $x$. The site $(1,1)$ on its side is nearest neighbor to the aggregate and therefore we set $\Phi(1,1) = 0$. Thus, the potential of the sites in row $m = 2$ have only a contribution from $x$. More specifically, $\Phi(2,0) = 1 + g_{2}(0)x$ because it is right above $x$, and $\Phi(2,1) = 1 + g_{2}(1)x$ because it is removed by one site. The potential $\Phi(2,0)$ does not contribute to any growth process, but is important for solving for $x$. The variable $x$ is found using its Laplace equation,
\[
4x = 1 + g_{2}(0)x, \\
\Rightarrow x = \frac{2 - \sqrt{2}}{2} = 0.2929. \\
\] (2.8)

Growth in site $(0,0)$ results in the flat configuration $i = 1$. It can only occur via one bond from site $(1,0)$, denoted by a bold double arrow (4) in Fig. 4. Hence,
\[
E_{1,2} = \frac{x}{2} = \frac{2 - \sqrt{2}}{4} = 0.1464, \\
\] (2.9)

where the denominator comes from the normalization factor $N = 2$. Growth can also occur in site $(1,1)$. This time there are three different bonds coming from two sites: there are two bonds coming from $(1,0)$ and an additional one coming from $(2,1)$. This upward growth results in the same configuration, so
\[
E_{2,2} = p_{\text{up}}(2) = \frac{1}{2} \left[ 2x + 1 + g_{2}(1)x \right] = \frac{2 + \sqrt{2}}{4} = 0.8536. \\
\] (2.10)

This concludes the calculation of all of the growth processes. The resulting evolution matrix is
\[
E = \begin{bmatrix} 0 & 0.1464 \\ 1 & 0.8536 \end{bmatrix}. \\
\] (2.11)

We verify that the matrix is properly normalized by noting that the sum of the terms in each of its columns is equal to 1, i.e.,
\[
\sum_{i=1}^{2} E_{i,j} = 1, \ j = 1, 2. \\
\] (2.12)

The general theorem mentioned in the introduction ensures the existence of a single eigenvector with an eigenvalue of 1, or in other words, a fixed point vector $P^{*}$ that satisfies,
\[
P^{*} = EP^{*}. \\
\] (2.13)

The fact that the process is closed is manifested in Eq. (2.12). The process is also irreducible because there is a finite probability to go from any initial state to any final state during a finite number of time steps. The fact that there is a single fixed point implies that starting from any initial state, the system will converge to the fixed point. This fixed point represents the asymptotic time probabilities for seeing either one of the two possible configurations.

The eigenvalues are the roots of the characteristic polynomial,
\[
\lambda_{0} = 1, \\
\lambda_{1} = -\frac{2 - \sqrt{2}}{4} = -0.1464, \\
\] (2.14)

and the normalized fixed-point vector $P^{*}$ is given by
\[
P_{1}^{*} = \frac{5 + \sqrt{2}}{17} = 0.1277, \\
P_{2}^{*} = \frac{12 + \sqrt{8}}{17} = 0.8723. \\
\] (2.15)

The steady-state weights enable us to calculate the average upward growth probability,
\[
\langle p_{\text{up}} \rangle^{*} = \sum_{i=1}^{2} P_{i}^{*} p_{\text{up}}(i) = \frac{12 + \sqrt{8}}{17} = 0.8723, \\
\] (2.16)

which is connected to the mean density,
\[ \rho(2) = \frac{1}{2} \left( \frac{p_{\text{up}}}{p_{\text{down}}} \right)^2 = \frac{6 - \sqrt{2}}{8} = 0.5732. \]  

(2.17)

It is also possible to calculate the rate of convergence to the steady state. In general, the rate of convergence is determined by the largest eigenvalue of \( \mathbf{E} \), other than 1. Suppose that at time \( t = 0 \) the state of the system differs from the steady state \( \mathbf{P}(0) \neq \mathbf{P}^* \). The difference vector

\[ \mathbf{v}(0) \equiv \mathbf{P}(0) - \mathbf{P}^*, \]

(2.18)

belongs to the linear subspace of vectors \( \mathbf{V} = \{ \mathbf{v} | \sum v_i = 0 \} \), because both \( \mathbf{P}(0) \) and \( \mathbf{P}^* \) are normalized probability vectors and thus the sum of their components is equal to 1. Now, Eq. (2.12) ensures that \( \mathbf{V} \) is an eigen-subspace of \( \mathbf{E} \), and as such it must contain at least one eigenvector. Since in this simple case the space of configurations is only two-dimensional, then \( \mathbf{V} \) is one-dimensional, and \( \mathbf{v}(0) \) is necessarily an eigenvector with the eigenvalue \( \lambda_1 = -0.1464 \). After \( t \) time steps the state of the system is

\[ \mathbf{P}(t) = \mathbf{E}^t \mathbf{P}(0) = \mathbf{P}^* + \lambda_1^t \mathbf{v}(0). \]

(2.19)

Therefore, the deviation from the steady state decays exponentially,

\[ \mathbf{P}(t) - \mathbf{P}^* = \lambda_1^t \mathbf{v}(0) = (-1)^t e^{-\tau} \mathbf{v}(0), \]

(2.20)

where

\[ \tau = -\frac{1}{\log |\lambda_1|} = 0.5584. \]

(2.21)

This means that a single time step is practically sufficient to arrive at the steady state. All of these theoretical predictions agree with results obtained from numeric simulations, up to the accuracy of the simulation, which is better than \( 10^{-5} \). This dynamics is actually exactly the same as the first-order approximation of the frustrated climber model in Ref. [14], except that the analysis of the temporal convergence is a little bit more refined there.

The solution of the case \( N = 3 \) is also relatively simple, because again there is only a finite number of growth configurations. This is because the width of the widest possible fjord is two sites, which is still insufficient for a random walker to penetrate, i.e., a random walker sticks as soon as it enters into a fjord. The three possible configurations are indexed in Fig. 8. These are the same as the three configurations of the first-order approximation for bond-DLA with \( N = 3 \) [14]. As in the example of \( N = 2 \), we proceed to calculate the probabilities for every growth process in each of the configurations. Once again, we first calculate the Green’s function,

\[ g_3(0) = \frac{6 - \sqrt{2}}{3} = 0.4725, \quad g_3(1) = g_3(2) = \frac{1 - g_3(0)}{2} = \frac{\sqrt{3} - 3}{6} = 0.2638. \]

(2.22)

The first configuration, \( i = 1 \), grows with probability 1 into configuration \( i = 2 \). Thus, \( E_{1,1} = 1 \) and \( E_{1,3} = E_{3,1} = 0 \), and also \( p_{\text{up}}(1) = 1 \). The potential diagram for \( i = 2 \) is shown in Fig. 8. Because of symmetry it is possible to conclude that \( \Phi(1,0) = \Phi(1,2) = x \).

The Laplace equation for \( x \) is

\[ 4x = x + 1 + [g_3(0) + g_3(1)] x, \]

\[ \Rightarrow x = \frac{9 - \sqrt{2T}}{10} = 0.4417. \]

(2.23)

The sticking probability at \( (0,0) \) is \( x/3 \), because there is a single connecting bond, and because the normalization factor is \( 1/3 \) for this case. The resulting configuration is \( i = 3 \), however, a sticking event at \( (0,2) \) also leads to \( i = 3 \), so that \( E_{3,2} = \frac{2}{3} x = \frac{9 - \sqrt{2T}}{15} = 0.2945 \). The other possibility is an upward growth at (2,1), that results in the initial configuration \( i = 2 \). Thus, \( E_{2,2} = p_{\text{up}}(2) = 1 - E_{3,2} = \frac{6 + \sqrt{2T}}{15} = 0.7055 \), and \( E_{1,2} = 0 \).

The potential diagram for \( i = 3 \) is shown in Fig. 9. The Laplace equation is

\[ 4x = 1 + g_3(0)x, \]

\[ \Rightarrow x = \frac{6 - \sqrt{2T}}{5} = 0.2835. \]

(2.24)

A sticking event in \( (0,1) \) leads to \( i = 1 \), therefore \( E_{1,3} = x/3 \). The other possible sticking events at \( (1,0) \) or \( (1,2) \) involve upward growths, that result in \( i = 2 \). Thus, \( E_{2,3} = p_{\text{up}}(3) = 1 - x/3 = \frac{9 + \sqrt{2T}}{15} = 0.9055 \). This completes the calculation of all of the element of the evolution matrix:

\[ \mathbf{E} = \begin{bmatrix} 0 & 0 & 0.0945 \\ 1 & 0.7055 & 0.9055 \\ 0 & 0.2945 & 0 \end{bmatrix}. \]

(2.25)

The normalized fixed point of the matrix is

\[ \mathbf{P}^* = \begin{bmatrix} 0.0210 & 0.7562 & 0.2227 \end{bmatrix}. \]

(2.26)

This enables the computation of the average upward growth probability, and of the average density:

\[ \langle p_{\text{up}} \rangle^* = \sum_{j=1}^{3} P_j^* p_{\text{up}}(j) = 0.756245, \]

\[ \rho = \frac{1}{3 \langle p_{\text{up}} \rangle^*} = 0.440774. \]

(2.27)

The second largest eigenvalue determines the characteristic time constant of the exponential convergence to the steady state,

\[ \tau = -\frac{1}{\log |\lambda_1|} = 0.56. \]

(2.28)
C. Approximations for \( N > 3 \)

The two examples of the previous sections, for \( N = 2 \) and \( N = 3 \), are special because there is only a finite number of possible configurations; a random walker cannot enter a fjord whose width is less than three sites when using site sticking conditions. The case \( N = 4 \) is the narrowest cylinder that can have a fjord that is three sites wide. Since this fjord can be arbitrarily deep, there is an infinite number of configurations. In spite of that, every configuration that has a fjord, which is more than one site deep, is uniquely determined by its depth, i.e., there is only one configuration with \( \Delta m = 2 \), a single configuration with \( \Delta m = 3 \), and in general: a single configuration with a specific \( \Delta m \), if \( \Delta m \geq 2 \). The unique configuration with \( \Delta m = 2 \) is shown in Fig. 10, along with the single configuration with a specific \( \Delta m \) that is larger than two. Other than that, there are four possible configurations with \( \Delta m = 1 \), which are shown in Fig. 11, and finally, the trivial flat configuration, with \( \Delta m = 0 \).

This case resembles bond-DLA with \( N = 2 \) [13], in the sense that in both cases there is an infinite number of configurations, but this infinity can be represented using a single parameter. In Ref. 13 this parameter is called “the step size” and is denoted by \( j \), but actually it is the same as \( \Delta m \). The case of site-DLA with \( N = 4 \) is a bit different, because there are four configurations with \( \Delta m = 1 \) instead of one. There is also a resemblance between the solution of the Laplace equation for the two cases, because in both cases the Laplace equation is solved on a single column with zero boundary conditions on the sides. Thus, in both cases there is an exponential decay of the potential inside the fjord, which is governed by the multiplicative factor \( e^{-\kappa j} = 2 - \sqrt{3} \). This enables us to treat the current case in an analogous way to the previous one. This could have given us analytic expressions for the Markovian matrix \( E_{i,j} \), \( i,j = 1, 2, \ldots, \infty \), for the steady-state vector \( P^s \), \( i = 1, 2, \ldots, \infty \), and for the distribution of gaps inside the aggregate. However, we omit the presentation of this calculation because it is not of main interest of this work, and so we treat the case of \( N = 4 \) in the same way as \( N > 4 \).

For \( N > 4 \) the boundary may be complex, and it cannot be easily characterized because the width of a fjord can fluctuate and overhangs may appear. We therefore use the approximation scheme described in the introduction, which was also used for bond-DLA [14]. The calculation procedure involves going over all the possible configurations to some order, and calculating their set of growth probabilities. It is feasible to perform this task manually when the number of configurations is relatively small, but as \( N \) and \( O \) increase, the number of configurations grows exponentially and it becomes impractical to do so. We use the same computer program that was used for bond-sticking conditions, after making the necessary adjustments due to the site-sticking conditions. Manual calculations may still be important as test cases to check the operation of the program.

The program goes over all of the possible configurations systematically. It starts with the trivial flat configuration (\( \Delta m = 0 \)), which is indexed by \( j = 1 \). This configuration has only one possible growth process, which occurs with probability 1, that turns the interface into configuration \( j = 2 \), which has a single bump. The program then continues to \( j = 2 \) and analyzes its growth probabilities. Every growth process changes the shape of the boundary. Each time a particle sticks in a certain site, the program has to identify the newly formed configuration. In order to do so, it marks all of the nearest neighbors of the newly attached particle, because new particles may stick there. The new configuration is searched for in the existing list of configurations, which were already analyzed by the program. If it does not exist then it is added at the end of the list. In either case the program identifies the index of the resultant configuration \( i \). Now, if the index of the original configuration is \( j \), then the growth probability is stored in the matrix element \( E_{i,j} \).

A configuration is characterized using the set of sites that are connected to infinity because these are the sites that are accessible to the random walker. Of course, any site that is higher than the highest site on a certain boundary is connected to infinity. Hence, it is sufficient to specify only the set of sites that are not higher than the highest site (the region \( m \leq 1 \)). A single growth process may cause a whole region of sites to disconnect from infinity, for instance by sealing off an entrance to a fjord. This means that it is not sufficient to mark the nearest neighbors of a newly attached particle, but that it is necessary to recheck the complete set of sites that are connected to infinity. We perform this by an algorithm that marks this set recursively.

Special care has to be taken for upward growth processes, because they may cause \( \Delta m \) to exceed \( O \). In case this happens, the bottom row of the configuration is truncated. Finally, symmetry has to be taken into account. Rotations around the axis of the cylinder and reflections about any vertical axis do not change the growth probabilities or the steady-state weights, so the set of all of the symmetric configuration are represented by a single canonical choice. More specifically, a configuration is represented by a binary word that consists of \( N \times O \) digits that correspond to the sites: The empty sites that are on the exterior are given a value of 1, and the rest of the sites are assigned with zeros. We choose the canonical form as the word that has the maximal numerical value.

After the complete list of configurations is processed, the calculation of the evolution matrix is completed, and it is closed, i.e., \( \sum_j E_{i,j} = 1 \) for every \( j \). Then the steady-state vector \( P^s \) is calculated iteratively by applying the evolution matrix many times on some initial state vector. This method is much faster than any of the standard techniques for solving a set of linear equations, especially when the number of variables is very large. The next step is to calculate the average upward growth proba-
bility, according to Eq. \( \text{(1.4)} \), and the average density, according to Eq. \( \text{(1.3)} \). Our computer resources enabled us to conduct the enumeration only up to a finite order \( O_{\text{max}} \) that depends on \( N \). As explained above, for \( N = 2 \) and \( N = 3 \) there exists a finite number of configurations, and higher order approximations are irrelevant. One may be surprised that we are able to reach higher order approximations, and the average density, according to Eq. \( \text{(1.4)} \), and the average density, according to Eq. \( \text{(1.4)} \), are presented in Table I, together with the number of configurations \( N_c \). The Table also presents the extrapolation and simulation results.

D. The extrapolation of the order of approximation to infinity, \( O \to \infty \)

Very good accuracy (about \( 10^{-4} \)) is also obtained for \( N = 8 \), even though \( O_{\text{max}} = N - 2 = 6 \). However, for \( N \geq 9 \) the results are not very accurate, because the maximal available order is only \( O = 5 \) for \( N = 9, 10 \) and \( O = 4 \) for \( N = 11, 12 \). In spite of that, we are able to arrive at a more precise estimation for \( N = 9, 10 \) by extrapolating \( O \to \infty \). The extrapolation does not improve the accuracy of the cases \( N = 11, 12 \) to a satisfactory level. Our aim is to deduce the value of \( \rho(N) \approx \lim_{O \to \infty} \rho_c(N, O) \) from the limited range of available values for \( O \). We start by noting that our data practically reached asymptotia for \( N = 4, 5, 6 \). We detect that the differences, \( \rho_c(O, N) - \rho_c(O + 1, N) \), decay exponentially and thus conclude that the function \( f = \ln[\rho_c(N, O)/\rho(N) - 1] \), is very close to being linear. Substituting the parameterization \( f = \beta - \alpha O/N \) we are able to extract the three unknowns, \( \alpha, \beta, \) and \( \rho(N) \) using at least three data points. For \( N = 6 \) and \( O = 4, 5, \) and 6, we find that \( \beta = 0.03 \) and \( \alpha = 12.31 \). The value of \( \rho(6) \) turns out to be very close to the highest available approximation \( \rho_c(6, 8) \).

Scaling theory would imply that, for large \( N \) and \( O, f \) should become a universal function, which depends only on the scaled ratio \( x = O/N \) (without an additional dependence on \( N \)). Following this expectation, we thus conjecture the general relation

\[
\rho_c(N, O) = \rho(N) \left[ 1 + e^{f(O/N)} \right], \tag{2.29}
\]

with \( f(x) \approx -12.3x \), for \( N, O \gg 1 \).

To test this conjecture, we estimated \( \rho(N) \), for \( N \geq 4 \), via

\[
\rho(N) \approx \frac{\rho_c(N, O_{\text{max}})}{1 + e^{f(O_{\text{max}}/N)}}. \tag{2.30}
\]

We have then used this estimate to calculate \( \rho_c(N, O)/\rho(N) \) for \( O < O_{\text{max}} \). The resulting values are shown in Fig. \( \text{12} \) together with the line \( f(x) = -12.3x \). Clearly, all the values for \( O/N \geq 0.4 \) are consistent with our conjectured form for \( f(x) \).

The values of \( \rho(N) \), as deduced using Eq. \( \text{(2.30)} \), are listed in Table I. Clearly, they all agree with the values from the simulations, except for small deviations that appear for \( N = 9 \) and 10. In the cases \( N = 11, 12 \) the deviations are relatively large, because \( O_{\text{max}} \) is too small, and hence the extrapolation results are not specified.

E. An enumeration based estimate of the fractal dimension \( D \)

In the previous section, we obtain very accurate estimates of the asymptotic (\( O \to \infty \)) average steady-state densities \( \rho(N) \). In this section, we extrapolate the latter densities in the limit \( N \to \infty \), in order to find the fractal dimension \( D \). Consider a \( N^d \) segment in the steady state regime of growth. Assuming that the structure is a self similar fractal, which has no characteristic length scale other than \( N \), we expect that the average mass of the segment would be proportional to \( N^D \), and that the density would be proportional to \( N^{D-d} \). In principle however, one expects some corrections to scaling as in Eq. \( \text{(1.3)} \). Taking only the first correction term of that equation into account we get an approximation that depends on four parameters: \( D, A, B \) and \( \theta \):

\[
\rho_a(N) = AN^{D-d} \left( 1 + \frac{B}{N^\theta} \right), \tag{2.31}
\]

where the subscript \( a \) denotes that this is an approximation. Using the four data points with \( 7 \leq N \leq 10 \), a fit to Eq. \( \text{(2.31)} \) yields \( D = 1.64, \log(A) = -0.63, B = 1.31 \) and \( \theta = 1.48 \). The calculation of the parameters can also be based on more than the minimal four points, using a least mean square error method. We choose to minimize the logarithmic (or relative) errors \( \Delta \rho/\rho \) rather than the errors in the densities \( \Delta \rho \), because we find them to be more uniformly distributed. The results of the fit using the six data points with \( 5 \leq N \leq 10 \) yields \( D = 1.74 \pm 0.06, \log(A) = -1.0 \pm 0.3, B = 1.5 \pm 0.6, \) and \( \theta = 0.80 \pm 0.13 \). The error estimates are evaluated using a confidence level of 0.95. Since the fit yields a value for \( \theta \) that is close to 1, we also try a three parameter fit, fixing \( \theta = 1 \). Using the three rightmost data points, for \( N = 8, 9 \) and 10, gives \( D = 1.68, \log(A) = -0.79, \) and \( B = 1.16 \). Using more points with \( 5 \leq N \leq 10 \), we get

\[
D = 1.68 \pm 0.01
\]

\[
\log(A) = -0.784 \pm 0.016
\]

\[
B = 1.12 \pm 0.05. \tag{2.32}
\]

Finally, an alternative four parameter form, including only “analytic” corrections, is
\[ \rho_a(N) = AN^{D-d} \left(1 + \frac{B}{N} + \frac{C}{N^2}\right). \] (2.33)

This time the results for \(7 \leq N \leq 10\) are \(D = 1.65\), \(\log(A) = -0.68\), \(B = 0.55\) and \(C = 1.10\), and the least mean square calculation for \(5 \leq N \leq 10\) yields \(D = 1.70 \pm 0.02\), \(\log(A) = -0.87 \pm 0.08\), \(B = 1.5 \pm 0.4\), and \(C = -0.5 \pm 0.4\).

We thus conclude that the fractal dimension of cylindrical DLA is \(D \approx 1.68 \pm 0.01\), close to the results of earlier numerical work \([6]\).

### III. SIMULATION

As mentioned, our analytical enumeration results are confirmed by simulations. In this section we describe how our simulations were conducted, with special attention to the boundary Green’s function \(g_N(n)\), which is given a new probabilistic meaning. We also discuss the accuracy of the results, and finally, we try to fit the results to some approximations as in the end of the previous section and obtain some more estimates of the fractal dimension.

Our simulation is performed on a lattice, which is represented by a 2D array variable. Each of the variables in the array can assume one of two possible values, 1 or 0, that determine whether the relevant site is occupied by an aggregate particle or not, respectively. The size of the array is \((14N) \times N\), i.e., its width is \(N\) and it is composed of 14 blocks of \(N \times N\) sites stacked one on top of the other. The number 14 is quite arbitrary and could be chosen differently. In principle, the lattice should be tall enough to allow the aggregate to arrive at a steady state, and also to allow a margin at the top, because the average density of the aggregate is lower near the growing front. Each time a new cluster is initialized, the lattice array is cleared so that all of its variables are set to 0, except for the bottom row, which is set to 1. This means that the initial shape of the aggregate is a horizontal line at the bottom of the lattice. A random walker is characterized by the coordinates \((m, n)\) of its position. In each simulation step a direction is chosen randomly and the particle is advanced in that direction. If the particle happens to go into a site that is nearest neighbor to the aggregate then it sticks, i.e., the value of the relevant lattice variable is updated from 0 to 1. Then the next random walker is released, and so on.

#### A. The role of the Green’s function

In principle, each new random walker should be released far above the aggregate, near the upper distant boundary. In practice, nothing can happen to the random walker (it cannot stick) until it crosses the bold line in Fig. [3]. This line is drawn between the highest row where a random walker can stick \((m = 1)\) and the row above it \((m = 2)\), and thus it differentiates between the active zone below the line, with \(m \leq 1\), and the inactive zone above it, with \(m > 1\). The projection of the path of the random walker on the vertical axis (its \(m\) coordinate) is also a random walk, only in one dimension (1D). Usually in 1D there is a probability of 1/2 to go up and the same probability to go down, but in our case, there is a probability of 1/4 to go in either direction, and a probability of 1/2 to stay at the same row. Nevertheless, this motion is still equivalent to a random walk, however the effective time step is longer. A quality of 1D random walks is that there is a probability of 1 to arrive at any site (no matter how far) within a finite time. Therefore, there is a probability 1 that eventually the random walker would cross the line from the inactive zone into the active zone. The random walker is equally probable to cross this line at any of the \(N\) sites, so instead of waiting for a long time, it is more efficient to start the simulation by inserting the random walker in a random site just below the line in the active zone.

But what happens if the path of the random walker happens to cross the line into the inactive zone? Once more we apply the same reasoning and claim that ultimately the random walker would re-cross the line downwards at some point with probability 1. Unlike the initial insertion, this time the distribution of the reentry point is not uniform. It is quite easy to see for example, that there is a greater chance for the particle to reenter at the exact same site from which it exited than for it to reenter at a site that is far away. Let us denote by \(\Psi(m, n; n')\) the probability that if the particle is at some initial site \((m, n)\) in the inactive zone \((m > 1)\), it will cross the line for the first time at \((m' = 1, n')\). In the next time step the random walker moves to one of its nearest neighbors with equal probability. Therefore \(\Psi(m, n; n')\) must be equal to the average of \(\Psi\) on all the nearest neighbors. This implies that \(\Psi\) satisfies the Laplace equation (in the coordinates \(m\) and \(n\)),

\[
\nabla^2 \Psi(m, n; n') = 0. \tag{3.1}
\]

The boundary conditions for \(\Psi\) at the lower boundary are

\[
\Psi(m = 1, n; n') = \begin{cases} 
1 & , \quad n = n' \\
0 & , \quad \text{otherwise}
\end{cases}. \tag{3.2}
\]

This is true because if the random walker is already in the row \(n' = 1\) then it already passed the line between \(m = 1\) and \(m = 2\) and so it stops before it starts. The boundary conditions at the top are \(\Psi = \text{const.}\), or equivalently

\[
\lim_{m \to \infty} \frac{\partial \Psi}{\partial m} = 0. \tag{3.3}
\]

These are the exact same conditions satisfied by the Green’s function \([16]\), and so the theorem about the uniqueness of the solution of the Laplace equation with boundary condition assures that \(\Psi\) is equal to the Green's function.
function, and especially at the first row above the line
\( m = 1 \),
\[
\Psi(1, n; n') = g_N(n - n'). \tag{3.4}
\]

This means that each time the random walker attempts
to cross the line to the inactive zone, it can be returned to
the active zone immediately. The distance of the reentry
point from the exit point should be chosen randomly from
the distribution defined by the Green’s function \( g_N(n) \).
This policy saves a lot of simulation time in comparison
with the alternative option of letting the random walker
wander freely until it finally sticks, or until it passes some
arbitrary critical distance from the aggregate. We note
in passing that the discussion in this section proves Eq.
(1.12) in an alternative, probabilistic approach, simply
due to the fact that \( g_N(n) \) is a probability function.

B. Analyzing the statistics

A single cluster is completed as soon as the first parti-
cle sticks in the top row of the lattice. Then, the number
of particles in each row is counted and stored in a (1D)
array variable that represents the average density profile
as a function of height. Then the lattice array is cleared
and a new aggregate is started. In contrast, the density
profile array is not cleared, and it accumulates data for
each new cluster so that after many iterations it con-
verges to the average density, when normalized by the
number of iterations \( N_i \).

An example of a density profile is shown in Fig. 14,
where \( N = 10 \) and \( N_i \approx 2 \times 10^7 \). Three distinct regions
are visible in the graph: On the left part there is a fast
decay from an initial density of 1 to a plateau. These
graphs always start from a density of 1, because the ini-
tial conditions for growth are that the bottom row of the
lattice is completely occupied. The decay to the plateau
shows the convergence to the steady state stage of the
growth. It seems that the steady state settles roughly at
a height that is equal to the width, i.e., about 10. The
middle section of the graph seems to be a flat plateau of
constant density. In fact, there are small statistical fluc-
tuations due to the randomness of the simulations, which
are invisible because they are on the order of \( 10^{-4} \), beca-
use there are 10 blocks of \( N \times N \) is the steady
state region. This error estimate is based on the expected
dependence on the number of blocks, but there could be
some numerical factor missing.

An alternative way of measuring \( \rho(N) \) is by measuring
\( \langle \rho_{up} \rangle^* \) directly and using Eq. \( (3.3) \). After the aggre-
gate reaches a height of \( 2N \) we assume that it is in the
steady state and we start gathering statistics. In particu-
lar, we count the number of upward growth events, when
the random walker sticks above all the particles in the
aggregate. Our results show very good correspondence
between the two different ways; The typical relative dif-
fERENCE is on the order of \( 10^{-6} \).

The simulations were carried out for the following val-
ues of \( N: 2, 3, \ldots, 12, 16, 24, 32, 48, 64, 96 \) and 128. We
did not go beyond that because our computer resources
did not suffice to iterate a large enough number of clus-
ters to obtain a relative accuracy of around \( 10^{-4} \) or better,
as obtained for the other cases.

We now proceed to fit the results for the 10 available
data points with \( 128 \geq N \geq 10 \) in a similar way to
Sec. II E. The difference is that now we use the error
estimates \( \sigma_i \) to give weights to the different data points,
because not all the accuracies are the same. This way
the fit will allow greater residuals for data points with
larger error estimates. Our first attempt is to fit the four parameter approximation of Eq. \( (2.31) \). The re-
results are
\[
D = 1.673 \pm 0.002, \quad \log(A) = -0.770 \pm 0.0013, \\
B = 1.03 \pm 0.06, \quad \theta = 0.96 \pm 0.06. 
\]

The resulting error estimates seem a bit too optimistic,
perhaps also because of the presence of some systematic
errors that are not taken into account. The simulation
results are shown in Fig. 13 on log-log scales as plus
signs, along with the latter three-parameter fit, shown

\[
D = 1.671 \pm 0.001, \\
\log(A) = -0.762 \pm 0.003, \\
B = 1.071 \pm 0.015. \tag{3.5}
\]
as a dashed line. The figure also shows the enumeration results as circles. Since the differences are hardly noticeable, we display the relative (logarithmic) residuals $v_i \equiv (\rho(N_i) - \rho_c(N_i)) / \rho(N_i)$ separately in Fig. 10 on semi-log scales, in comparison with the relative error estimates $\pm \sigma_i$. The maximal relative residual is $1.3 \times 10^{-4}$. This is consistent with the order of magnitude of the estimated a priori errors.

A factor that indicates the compatibility between the a priori error estimates $\sigma_i$ and the a posteriori residuals $v_i$ is,

$$
\chi^2 = \frac{1}{N_d} \sum_i \left( \frac{v_i}{\sigma_i} \right)^2,
$$

where $N_d$, the number of degrees of freedom, is equal to the number of data-points minus the number of unknown parameters. The value of $\chi^2$ should be close to 1. In the latter fit we get $\chi^2 = 0.9$, whereas $\chi^2 = 0.3$ in the former. The results of the fit imply that the three parameter approximation is sound.

For the sake of comparison we also try to fit to the other test approximations that were introduced in the previous section. The best fit to the four parameter approximation in Eq. (2.33) is $D = 1.6721 \pm 0.0012$, log($A$) = $-0.766 \pm 0.006$, $B = 1.12 \pm 0.07$ and $C = -0.28 \pm 0.4$. In this approximation, the residuals are not lowered drastically; the maximal relative residual is $1.1 \times 10^{-4}$ and $\chi^2 = 0.2$. The error estimate of fourth parameter $C$ is much greater than the error estimates of the other parameters. The contribution of the term with the $C$ parameter is on the same order of magnitude as the residuals, at least for the data point with large $N$’s. This implies that there may be significant contributions from the noise (the errors) in these data points to the parameter, and therefore its inclusion is redundant.

IV. SUMMARY

In this paper, we continue our endeavour to solve cylindrical DLA analytically, i.e. to calculate the steady state average density $\rho$, as a function of the cylinder width $N$, and to find the fractal dimension $D$. Unlike our previous work, which deals with bond-sticking conditions [14], this work solves for site-sticking conditions. The immediate problem in following our Markovian method is that, except for $N = 2, 3$, there is usually an infinite number of configurations. The case $N = 4$ has an infinite number of configurations, but is still relatively simple. The large variety of possible complex interface shapes for $N \geq 5$ prevents the inclusion of all the configurations and compels the use of an approximation scheme, in which only a finite number of rows $O$ of the growing front near the tip are included. This approximation works because of the exponential decay of the Laplace potential $\Phi$ inside deep fjords. The approximation leaves a finite number of configurations to work with, and thus the computational procedure can be completed.

We find that this is a well controlled approximation, in the sense that any desired numerical accuracy can be achieved provided that a high enough order of approximation $O$ is used. The results are summarized in Table [ ], that shows the computed density $\rho_c$ for various values of $N$ and $O$ along with the number of relevant configuration $N_c$. An evident fact is that $N_c$ grows very rapidly as a function of $O$ and $N$, making it impractical to perform the calculation for wide cylinders. We note that in order to obtain the same relative accuracy it is necessary to use $O \propto N$, e.g., in order to obtain a relative accuracy better than $10^{-4}$ one should use at least $O = N - 1$. This is the case for $N \leq 7$, where the results are very accurate, but not so for $N \geq 8$, where our available computer resources allowed only lower order computations. As discussed in Sec. [11], we are able to improve the estimates in these cases by extrapolating $O \to \infty$, taking advantage of the universal exponential decay of $\rho_c(N, O)/\rho(N)$ with the scaled variable $O/N$. Table [ ] also compares the enumeration estimates with direct measurements from simulations, and finds them to agree within the simulation errors. Once accurate estimates are obtained for $\rho(N)$ for $N \leq 10$, they are fitted to a power-law approximation with a correction to scaling term according to Eq. (2.31). The fit (with $\theta = 1$) gives an estimate of the fractal dimension $D = 1.68 \pm 0.01$.

Besides the range $2 \leq N \leq 10$, simulations are also performed on cylinders with larger $N$’s in the range $10 \leq N \leq 128$. The relative errors of the measurements of $\rho(N)$ are estimated around $10^{-4}$. The simulation data are also fitted to the same approximations. Once again, the three parameter approximation proves most appropriate and the resulting fractal dimension this time is $D = 1.671$. The fact that the enumeration and simulation based estimates of the fractal dimension are very close is a good indication of their accuracy.

The last statement should be taken with some caution in light of evidence that raises doubts concerning self-similarity in radial DLA [12,21,22], or suggesting some very slow crossovers [23]. Indeed, radial DLA is somewhat different than cylindrical DLA, as manifested by the difference between their fractal dimensions: $D = 1.71$ for radial DLA [23] and $D = 1.66$ for cylindrical DLA (this difference is still not fully understood).

We also tried performing the exact calculations for $N = 11$ and 12, but managed to go only up to $O_{\text{max}} = 4$. This was insufficient for extrapolation with an accuracy that is comparable to the rest of the data points. With the aid of stronger computers we think that it would be possible and beneficial to compute a few more data points $\rho(N)$, which would help obtaining more accurate estimates of the fractal dimension. Also, the techniques discussed here could be used to find the fractal dimension of cylindrical DLA in 3D. However, since a much larger number of configurations can be expected, this task would also probably require the aid of a very strong...
computer.

There are a few differences between site-DLA and bond-DLA: The boundary conditions for the Laplace equation are a little bit different; In bond-DLA the potential is set to zero on the aggregate itself, whereas in site-DLA the potential is set to zero on sites that are nearest neighbors of the aggregate. Also, the growth probabilities are computed somewhat differently; In bond-DLA contributions are summed over bonds that go out of a site where sticking may occur, whereas they are summed over bond that go into it in site-DLA. The normalization factor, however, is equal to the width $N$ is both cases. In the case of site sticking conditions there is an effective thickening of branches and thus a narrowing of fjords. Thus, there is a notable decrease in the probability of a random walker to penetrate deep into fjords. This also causes the number of configurations for a particular choice of $N$ and $O$ to be considerably less for site-DLA in comparison to bond-DLA. Therefore, accurate enumeration results can be obtained for larger $N$’s and $O$’s in site-DLA. The extrapolation $O \to \infty$ performed in this paper was not done in Ref. [14], which deals with bond-DLA, because the technique was not developed at that time. When we apply the method to the bond-DLA case, we manage to improve the relative accuracy of the highest available approximations, $\rho_c(N, O_{\text{max}}(N))$ for $N = 6, 7$ by an order of magnitude: from about $1.2 \times 10^{-3}$ to $2 \times 10^{-4}$ for $N = 6$, and from $5 \times 10^{-2}$ to $1.6 \times 10^{-3}$. This extrapolation is based on the data points for $N = 5$. The relative accuracy of $\rho_c(N, O_{\text{max}}(N))$ for $N \leq 5$ is better than $10^{-4}$ and hence, the extrapolation is not necessary. The estimate of the fractal dimension for site-DLA is, $D = 1.68$, to be compared with the bond-DLA enumeration result $D = 1.64$ [4]. In contrast, the difference in the simulation results for the two cases is smaller: $D = 1.67$ for site-DLA and $D = 1.66$ for bond-DLA. Given the uncertainties, our results are consistent with universality with respect to the sticking conditions [3,4].

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FIG. 1. An example of the solution of the Laplace equation $\nabla^2 \Phi(m, n) = 0$, with boundary conditions $\Phi = 0$ on the aggregate, and $\partial \Phi / \partial m = 1$ on the upper distant boundary. Here, the width is $N = 5$ and there are periodic boundary conditions on the sides. The axes indicate the directions of the coordinates $m$ and $n$. These boundary conditions are consistent with bond-sticking conditions.

FIG. 2. The growth probabilities for the aggregate shown in Fig. 1. The growth probability in each perimeter site is proportional to the potential $\Phi$ at that site and to the number of bonds $N_b$ leading from the site into the aggregate (denoted by arrows), e.g., $N_b = 3$ for the site at $(-1, 2)$ and $N_b = 1$ for the site $(0, 2)$, right above it.
FIG. 3. The solution to the Laplace equation near the same aggregate as in Figs. 1 and 2, only with site-sticking conditions. The circles denote the perimeter sites where a random walker might stick. The boundary conditions are that $\Phi = 0$ on these sites, unlike the case of bond-sticking conditions where $\Phi = 0$ on the aggregate itself. The boundary conditions $\partial \Phi / \partial m = 1$ at large $m$ remain unchanged.

FIG. 4. Two different aggregates (represented by the dashed squares) with $N = 2$, having exactly the same set of sites where a random walker may stick (shown in circles), and thus having the same boundary (the bold line) for the Laplace equation, where $\Phi = 0$. 
FIG. 5. The sticking probabilities in each of the circled sites of Fig. 3. They are computed by summing over all of the bonds that go into each site (denoted by arrows), unlike the case of bond-sticking conditions, where contributions are summed over bonds that go out of each site.
FIG. 6. The two possible configurations for $N = 2$. The circles denote the sites where a random walker might stick. Also shown are the possible transitions between them, denoted by arrows, and the relevant matrix elements $E_{i,j}$. The distribution of the potential $\Phi$ over the lattice is demonstrated only for configuration $i = 2$, see text for explanation. The double arrows (⇓, ⇒ and ⇐) show the bonds of the possible access paths, which a random walker can take into the circled sites. The bold double arrow shows the only bond going into site (0, 0). The other three bonds lead into site (1, 1).

FIG. 7. The possible configurations and the possible transitions between them for $N = 3$. 
FIG. 8. A “potential diagram”: the potentials $\Phi(m, n)$ of configuration $i = 2$, expressed in terms of the variable $x$.  

$\Phi(m, n) = 1 + 2g_3(1)x$ 

$\Phi(m, n) = 1 + [1 - g_3(1)]x$
FIG. 9. The potential diagram for configuration $i = 3$. 
FIG. 10. The only configurations for a cylinder of width $N = 4$: (a) $\Delta m = 2$, (b) $\Delta m > 2$. 
FIG. 11. The four possible configurations for $N = 4$ with $\Delta m = 1$. These configurations are indexed between $i = 2$ and $i = 5$, and the flat configuration with $\Delta m = 0$ is indexed by $i = 1$. 
FIG. 12. Data collapse of $e^f = \frac{\rho_c(N,O)}{\rho(N)} - 1$ vs. $O/N$ for all the data points with $4 \leq N \leq 10$ and $O > 2$, on a semi-log scale. The continuous line shows the linear approximation $f \approx -12.3O/N$. 
FIG. 13. The bold line separates between the upper inactive zone with $m > 1$ and the lower zone with $m \leq 1$. A random walker cannot stick in the inactive zone.
FIG. 14. The density profile as a function of height for a lattice with $N = 10$ averaged over some $N_i \approx 2 \times 10^7$ iterations. The height of the lattice is 140 sites.
FIG. 15. A plot of $\rho(N)$ vs. $N$ on log-log scales. The plus signs denote the simulation results, the dashed line denotes $\rho_a(N)$ - the best fit to the three parameter approximation of Eq. (2.31), with $\theta = 1$. The circles denote the enumeration results.
FIG. 16. The relative residuals $v = (\rho - \rho_a)/\rho$ (the plus signs) vs. $N$ on semi-log scales. The upper and lower triangles show the estimated confidence intervals (errors) of the simulation data, $\pm \sigma$. 
TABLE I. The approximated densities \( \rho_c \) and the number of configurations \( N_c \) for various orders \( O \) and cylinder widths \( N \). The approximated densities from enumeration are compared to simulation results. In addition, the extrapolated density \( \rho(N, O \to \infty) \) is also presented.

| \( N/O \) | simulation | \( O \to \infty \) |
|---|---|---|
| 2 | 0.5732 | 0.5732 |
| 3 | 0.4408 | 0.4408 |
| 4 | 0.3744  | 0.3744  0.3743  0.3750  0.3744  0.3744  0.3744  0.3744  0.3744 |
| 5 | 0.3334  | 0.3334  0.3323  0.3355  0.3336  0.3334  0.3334  0.3334  0.3334 |
| 6 | 0.3049  | 0.3049  0.3025  0.3094  0.3057  0.3050  0.3049  0.3049  0.3049  0.3049  0.3049 |
| 7 | 0.2837  | 0.2837  0.2798  0.2908  0.2857  0.2840  0.2837  0.2837  0.2837  0.2837  0.2837  0.2837  0.2837 |
| 8 | 0.2671  | 0.2671  0.2616  0.2767  0.2707  0.2679  0.2672  0.2672  0.2671  |
| 9 | 0.2536  | 0.2537  0.2467  0.2655  0.2593  0.2551  0.2540  |
| 10 | 0.2424  | 0.2426  0.2341  0.2562  0.2503  0.2450  0.2431  |
| 11 | 0.2329  | 0.2333  0.2483  0.2431  0.2368  |
| 12 | 0.2247  | 0.2139  0.2415  0.2371  0.2300  |

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