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LETTER TO THE EDITOR

Improved kinetic renormalisation group approach to diffusion-limited aggregation

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Abstract. An improved kinetic renormalisation group approach to diffusion-limited aggregation is presented. This approach is based on the growth process itself and accounts for the dispersity in the growth probabilities. It yields the multifractal spectrum D(q) with better values at smaller q. On the 2D square lattice we find $D_f = 1.694$ for the fractal dimension of the cluster and that of its interface, and D(1) = 1.01 for the information dimension. The former agrees with the simulation results ($D_f \approx 1.70$) and the latter compares very well with the exact value D(1) = 1.

The analytical calculation of the multiscaling dimensions of diffusion-limited aggregates (DLA) and especially their fractal dimension, is still a formidable challenge [1, 2]. This growth process (contrary, say, to that of the Eden model) is highly unstable: deviations from homogeneity are strongly enhanced thus leading to ramified dendritic-like structures. The existence of rigorous field-theoretic and stochastic equations [3, 4] may not be enough to derive a systematic momentum-space renormalisation group (RG) approach (as opposed to the Eden model [5]) since no known regularisation process may control these strong instabilities.

The real-space RG approach may provide an alternative route because it is not based on an expansion around a solvable limit. Rather, one may look for self-consistent relations between probabilities of configurations directly inside this 'strongly chaotic' regime. The first steps in that direction were suggested by Gould *et al* [6], Nakanishi and Family [7] and Montag *et al* [8]. These works followed closely the real-space RG to static clustering models.

Important progress was made in more recent works: Pietronero *et al* [9] introduced a fixed-scale transformation based on the inherent multiplicative randomness of the growth process, and obtained an estimate for the 2D fractal dimension $D_f = 1.64$. Nagatani, in a series of papers [10], introduced an RG approach to compute the growth probabilities on the cluster surface from which he obtained the multifractal spectrum. To derive his estimate for the fractal dimension, however, he had to rely on the Turkevich-Scher [11] relation $D_f = 1 + D(\infty)$, the validity of which has been questioned by Halsey [12].

Following some of Nagatani's ideas, we have introduced in a previous work [13] (hereafter denoted I) a new kinetic renormalisation group (κRG) approach. In this approach recursion relations for the physical parameters of the cluster, its mass and

that of its interface were derived. We were able to show that the bulk and surface have the same fractal dimension and obtained its value $D_f = 1.73$ and 2.494 for 2D and 3D respectively. In addition a correction-to-scaling exponent D_i was derived from the subleading eigenvalue. The multifractal spectrum D(q) and $f-\alpha$ curves were also obtained. As expected the best results were obtained for larger values of q while for small q (in the regions with small growth probabilities) the agreement with the simulations was not so good.

In the present letter we present an important step forward to an improved KRG approach which accounts better for the dispersity in the growth probabilities on different surface sites. The KRG approach is based on the combined time and length scale invariance of the DLA cluster which is used to obtain the relation between the probabilities for configurations on consecutive scales directly from the growth process itself. Indeed, given a cluster configuration at time t, probabilities for the configuration at time t+1 (with one more particle) are completely defined from the growth probabilities on the surface sites. The KRG approach uses the fact that the growth probability distribution remains invariant and is the same at t+1 as it was at t. In practice we can only find the recursion relations between probabilities of the configurations of small cells, like the one we choose here depicted in figures 1 and 2.

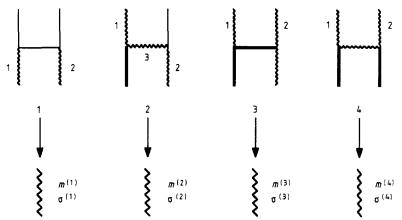


Figure 1. All possible configurations which are renormalised to the vertical perimeter bonds for the square lattice.

Three types of bonds are defined at each order n of the transformation: bulk bonds representing the particles on the cluster with mass M_n (bold lines in figures 1 and 2); perimeter bonds, with mass m_n (wavy lines), representing the surface of the aggregate on which the next potential growth may occur; massless empty bonds for the rest (thin lines).

As a particle is added to the cluster one perimeter bond turns into a bulk bond and all its unoccupied neighbours become growth bonds. The following rules guide the transformation. If the cell is connected from top to bottom by bulk bonds it will be renormalised into a bulk bond; if the cell is completely empty it will be renormalised to an empty bond; all other configurations are renormalised into a perimeter bond.

In order to find the local growth probabilities on each bond we use the equivalence between the DLA problem and that of the dielectric breakdown [14]. The growth probability in the frontier is proportional to the (normalised) voltage drop, or local

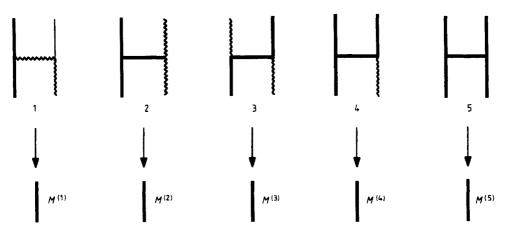


Figure 2. All possible configurations which are renormalised to the vertical bulk bonds for the square lattice.

electric field, in the latter. In order to compute their distribution each perimeter bond is assigned a conductance σ (it is chosen to be 1 on empty bonds and is obviously infinite on the conducting bulk bonds).

In I, all perimeter bonds were considered equivalent with the same mass m_n and the same conductance σ_n . In the upgraded version of the KRG presented here, this constraint is released. The different configurations in figure 1 will be renormalised into perimeter bonds with different masses and different conductances. Similarly, the configurations in figure 2 will yield bulk bonds with different masses (they all have infinite conductances). We therefore allow the RG flow to take place in a much larger parameter space and assign to the conductances their fixed-point values rather than arbitrary values. In the following, Greek superscripts denote different cell configurations and the Roman subscripts the different bonds of the cell.

To find the conductances and growth probabilities for each bond in figure 1, we solve the equivalent Kirchoff problem with zero voltage at the bottom of the cluster and unit voltage at the top. Let us take configuration 2 of figure 1 as an example. If we denote σ_1 , σ_2 , and σ_3 as the conductances of the respective bonds and $E_1^{(2)}$, $E_2^{(2)}$, and $E_3^{(2)}$ as the potential drops on them, we have

$$E_1^{(2)} = 1 \tag{1a}$$

$$E_2^{(2)} = E_3^{(2)} = 1/(1 + \sigma_2 + \sigma_3). \tag{1b}$$

The cell conductance in configuration 2 will thus be

$$\sigma_n^{\prime(2)} = \sigma_1 + (\sigma_2 + \sigma_3) / (1 + \sigma_2 + \sigma_3).$$
⁽²⁾

From the potential drops, we can find the growth probabilities on these bonds, proportional to the potential drops:

$$p_1^{\prime(2)} = (1 + \sigma_2 + \sigma_3)/(3 + \sigma_2 + \sigma_3)$$
(3a)

$$p_2^{\prime(2)} = p_3^{\prime(2)} = 1/(3 + \sigma_2 + \sigma_3). \tag{3b}$$

Next we have to find the weights $C^{(\alpha)}$ (namely their relative occurrence) of the different cell configurations in figure 1 (and, similarly, the weights $W^{(\alpha)}$ of those in

figure 2). The weights are not independent since, e.g., configuration 3 is obtained from configuration 2 by adding a particle on bond 2 and therefore

$$C^{(3)} = C^{(2)} p_2^{\prime(2)}. \tag{3c}$$

Similar relations between the rest of the $C^{(\alpha)}$ and the requirement $\sum_{\alpha=1}^{4} C^{(\alpha)} = 1$ allow us to express them in terms of the $p_i^{\prime(\alpha)}$, e.g. in terms of $\sigma^{\prime(\alpha)}$. The values of the renormalised conductances $\sigma^{\prime(\alpha)}$, on the other hand, depend on the $C^{(\alpha)}$. To compute the renormalised conductance $\sigma^{\prime(\alpha)}$, we recall that σ_1 , σ_2 and σ_3 may assume any of the four $\sigma^{(\alpha)}$ values, each with a probability $C^{(\alpha)}$. Summing over all $4^3 = 64$ possible assignments of the four $\sigma^{(\alpha)}$ to three conductances in configuration 2 of figure 1, we find the renormalised $\sigma^{\prime(2)}$ in terms of the $\sigma^{(\alpha)}$ and $C^{(\alpha)}$.

In a similar way expressions for all $\sigma'^{(\alpha)}$ are obtained. We then use equations similar to (3a, b) to find expressions for the $p'^{(\alpha)}_i$ from which we derive expressions for the $C^{(\alpha)}$ using relations like (3c).

The fixed-point value for $\sigma^{(\alpha)}$ and $C^{(\alpha)}$ are then found by solving their system of coupled non-linear equations. We find

$$\sigma^{(1)*} = 1.431 \qquad \sigma^{(2)*} = 3.817 \qquad \sigma^{(3)*} = 5.954 \qquad \sigma^{(4)*} = 5.954 \qquad (4a)$$

$$C^{(1)*} = 0.447$$
 $C^{(2)*} = 0.447$ $C^{(3)*} = 0.053$ $C^{(4)*} = 0.053.$ (4b)

These fixed-point values are a major step forward with respect to our earlier work where we have arbitrarily assigned $\sigma^{(\alpha)} \equiv 1$ (and the $C^{(\alpha)}$ were calculated based on these values).

The multifractal dimensions [13, 15, 16], which describe the hierarchy of the DLA cluster, are given by

$$D(q) = -\frac{1}{(q-1)\ln(2)} \ln\left(\sum_{\alpha,i} C^{(\alpha)}(p_i^{(\alpha)})^q\right) \qquad q \neq 1$$
(5a)

$$D(1) = -\frac{1}{\ln(2)} \sum_{\alpha,i} C^{(\alpha)} \ln(p_i^{(\alpha)}) \qquad q = 1.$$
 (5b)

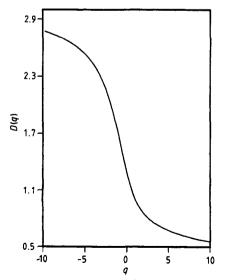


Figure 3. The plot of D(q) against q for the DLA on the square lattice.

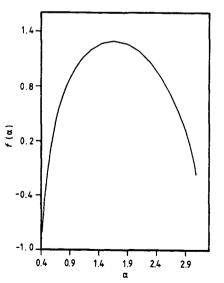


Figure 4. The plot of f against α for the DLA on the square lattice.

The curve D(q) is shown in figure 3. The $f-\alpha$ spectrum, the Legendre transformation of D(q), is also shown in figure 4.

Similarly, we can find the recursion relations between the $W^{(\alpha)}$ and, by solving them, we obtain

$$W^{(1)} = 0.28$$
 $W^{(\alpha)} = 0.18$ for $i = 2-5$. (6)

Having found the $C^{(\alpha)}$ and $W^{(\alpha)}$ we can then find recursion relations of the $m^{(\alpha)}$ and $M^{(\alpha)}$. For example,

$$m^{(2)} = 2(C^{(1)}m^{(1)} + C^{(2)}m^{(2)} + C^{(3)}m^{(3)} + C^{(4)}m^{(4)}) + W^{(1)}M^{(1)} + W^{(2)}M^{(2)} + W^{(3)}M^{(3)} + W^{(4)}M^{(4)} + W^{(5)}M^{(5)}$$
(7a)

for the cell of configuration 2 of figure 1, which has two vertical perimeter bonds and one vertical bulk bond, and which is renormalised to a perimeter bond with mass $m^{(2)}$.

This recursion relation may also be expressed as

$$m^{(2)} = 2\bar{m} + \bar{M} \tag{7b}$$

where $\bar{m} = \sum_{\alpha=1}^{4} C^{(\alpha)} m^{(\alpha)}$, and $\bar{M} = \sum_{\alpha=1}^{5} W^{(\alpha)} M^{(\alpha)}$. Since all renormalised masses only depend on these combinations we rather look at their recursion relations:

$$\begin{pmatrix} \bar{m} \\ \bar{M} \end{pmatrix}_{n} = T \begin{pmatrix} \bar{m} \\ \bar{M} \end{pmatrix}_{n-1}.$$
(8)

The eigenvalues of the matrix \mathbf{T} are

$$\lambda_{\pm} = 2 + W^{(2)} + \frac{C^{(3)}}{2} \pm 2 \left[\frac{1}{8} + \frac{C^{(3)}}{2} + \left(W^{(2)} - \frac{C^{(3)}}{4} \right)^2 \right]^{1/2} = \begin{cases} 3.244 \\ 1.541. \end{cases}$$
(9)

From the largest eigenvalue we find the fractal dimension of both the bulk and the interface of the cluster: $D_f = \ln(\lambda_+)/\ln(2) = 1.694$. The smallest eigenvalue yields a correction-to-scaling exponent $D_i = \ln(\lambda_-)/\ln(2) = 0.624$.

The value of D_f we find above is consistent with the most accurate values extracted from large-scale simulations ($D_f = 1.70 \pm 0.07$). This agreement for D_f is better than that of the value $D_f = 1.727$ obtained by a simplest approach in I. The advantage of this new approach is also apparent if we inspect the information (entropy) dimension: the exact value is D(1) = 1 [17]; here we obtained D(1) = 1.01 compared with D(1) =1.14 in our previous work. Because of the small cell we consider, we still cannot expect a very good agreement at the extremal values of q = 0 and $q = \infty$.

The conceptual improvement of the KRG approach is reflected by an amelioration of the results for the fractal dimension and for a range of smaller values of q (which includes q = 1). With larger cells one may hope to improve the description in both tails of the probability distribution as well.

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