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LETTER TO THE EDITOR

A renormalisation group approach to the scaling structure of diffusion-limited aggregation

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Abstract. A renormalisation group method is presented to analyse the scaling structure of the growth probability in diffusion-limited aggregation. The recursion relation for the growth probability is derived under the renormalisation transformation. The growth probability assigned to each growth bond is represented by a random multiplicative process. The scaling of the highest growth probability is derived and the fractal dimension is found. A hierarchy of generalised dimensions $D(q)$ is calculated to describe the growth probability. The partition of $(q-1)D(q)$ into a density of singularities $f(q)$ with singularity strength $\alpha(q)$ is made and the $\alpha-f$ spectrums are found.

Recently, considerable attention has been focused on the problem of geometrical structure in aggregation and growth models (Family and Landau 1986, Pynn and Skjeltorp 1985, Pietronero and Tosatti 1986, Stanley and Ostrowsky 1986). There are a number of different types of growth process ranging from diffusion-limited aggregation (Witten and Sander 1981) to the clustering of clusters (Meakin 1983a, Kolb *et al* 1983). The structure of the aggregates strongly depends on the dynamics of the growth process. It is well known that they have a strong measure of self-similarity, which is characterised by the fractal dimension D (Mandelbrot 1982). Several analytical attempts, including mean-field theories (Muthukumar 1983, Tokuyama and Kawasaki 1984) and position space renormalisation group methods (Gould *et al* 1983), have been made to derive the fractal dimension. It is clear, however, that an aggregate cannot be fully characterised by its fractal dimensionality. Diffusion-limited aggregation (DLA) and percolating clusters have the same fractal dimension in three dimensions, yet they have completely different structures. The essential properties of kinetic aggregation processes are fully described by the growth probability distribution for perimeter bonds (or sites) of these aggregating clusters (Halsey *et al* 1986, Amitrano *et al* 1986). Halsey *et al* and Amitrano *et al* show that a hierarchy of generalised dimensions should be used to characterise the growth probability.

In this letter, we present a renormalisation group method for the scaling structure of the growth probability in diffusion-limited aggregation. We derive the recursion relation for the growth probability under a renormalisation transformation. At the fixed point the growth probability is represented by a random multiplicative process. We find the set of generalised dimensions $D(q)$ for the growth probability. The fractal dimension is also found from the scaling of the highest growth probability.

Let us consider a renormalisation procedure for DLA. Cover all the space of the square lattice by cells of edge b ($= 2$), each containing $2b^2$ bonds; an example for $b = 2$ is shown in figure 2(a). After a renormalisation transformation these cells play the

role of 'renormalised' bonds. We distinguish between three types of bonds on the lattice: (a) break bonds which construct the aggregate, (b) growth bonds which are on the perimeter of the aggregate and can be successively grown, and (c) unbroken bonds which surround the aggregate, except for the growth bonds. If the cell can be connected vertically to the break bonds then the renormalised vertical bond is considered to be broken (figure 1(a)). If the cell cannot be connected vertically to the break bonds and contains the break bonds, then the cell is vertically renormalised with the growth bond (figure 1(b)). When the cell is constructed by unbroken bonds only, the cell is replaced with the renormalised unbroken bond (figure 1(c)). If one considers whether or not the cell is horizontally connected, then we see that the cell is horizontally renormalised. Part of the surface layer of the aggregates is shown in figure 2. After renormalisation, the lattice on the left-hand side is transformed to the renormalised lattice on the right-hand side. We note that if a renormalised unbroken bond is nearest neighbour with the renormalised break bond, then it is transformed to the renormalised growth bond. The cells are renormalised as the growth bonds, which are nearest neighbours to the cell with spanning clusters and are not spanned with break bonds.

In DLA the growth probability \mathbb{P}_i at the growth bond i is given by $\mathbb{P}_i \sim E_i$ where E_i is the local electric field at the growth bond. Consider the electrostatic problem for cells which can be renormalised as the growth bond. The electric fields on the growth bonds within the cell are determined by the conductance of the cell. For example, in the configuration labelled by (11) (see figure 3), the electric fields $E_{11,1}$, $E_{11,2}$ and $E_{11,3}$ of growth bonds 1, 2 and 3 are given by

$$E_{11,1} = E_{11,2} = 1/(1+2\sigma_n) \quad E_{11,3} = 1 \quad (1)$$

where the unit voltage is vertically applied and σ_n indicates the conductance of the growth bond at the n th renormalisation. At the $(n+1)$ th stage the conductance $\sigma_{11,n+1}$ of the cell with configuration (11) is renormalised as follows:

$$\sigma_{11,n+1} = \sigma_n + 1/(1+0.5/\sigma_n). \quad (2)$$

The growth probabilities $p_{11,1}$, $p_{11,2}$ and $p_{11,3}$ of growth bonds within the cell (11) are given by

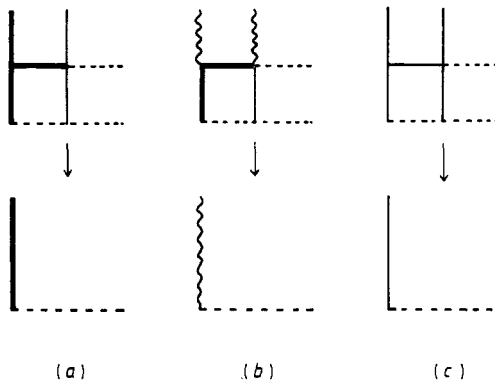


Figure 1. Illustration of the renormalisation of a $b=2$ cell for DLA on the square lattice. The renormalisation procedure in the vertical direction is shown. There are three types of bond: break bonds indicated by bold lines, growth bonds indicated by wavy lines and broken bonds indicated by light lines. Examples of the distinct configurations are shown in (a), (b) and (c), which are renormalised as break, growth and unbroken bonds, respectively. The broken lines represent bonds irrelevant to the renormalisation in the vertical direction.

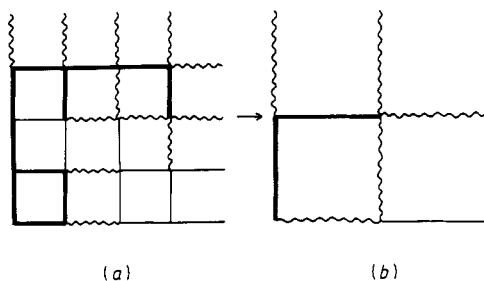


Figure 2. An example of the renormalisation of a part of the surface layer of an aggregate. The lattice on the left-hand side is renormalised to that on the right-hand side, according to the rules of renormalisation.

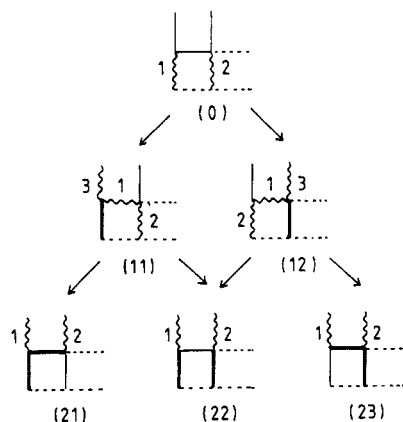


Figure 3. All configurations of the cell that it is possible to renormalise as the growth bond. Configurations (11) or (12) are obtained by adding a break bond onto the growth bonds 1 or 2 in configuration (0). Furthermore, by adding a break bond to configuration (11), configurations (21) or (22) occur.

$$p_{11,1} = p_{11,2} = E_{11,1}/(1 + 2E_{11,1}) \quad p_{11,3} = 1/(1 + 2E_{11,1}). \quad (3)$$

In general, the conductance $\sigma_{\alpha,n+1}$ of the cell with a particular configuration α is given by

$$\sigma_{\alpha,n+1} = f_{\alpha}(\sigma_n). \quad (4)$$

One can enumerate all configurations of the cell. The $(n + 1)$ th renormalised conductance σ_{n+1} will be assumed to be given by the configurational average

$$\sigma_{n+1} = \sum_{\alpha} C_{\alpha}(\sigma_n) \sigma_{\alpha,n+1} \quad (5)$$

where the $C_{\alpha}(\sigma_n)$ represents the probability of a particular configuration α and the sum ranges over all the configurations. The relationships (4) and (5) present the renormalisation group $\sigma_{n+1} = R(\sigma_n)$. Its fixed point σ^* is given by

$$\sigma^* = R(\sigma^*). \quad (6)$$

At the fixed point, the growth probability on the growth bond i within the cell α is represented by a function of σ^* :

$$p_{\alpha,i}^* = g_{\alpha,i}(\sigma^*). \quad (7)$$

After renormalisation, the growth probability $P_i(L)$ on any growth bond i is given by

$$P_i(L) = p_{\beta,i} P_{\beta}(L/b) \quad (8)$$

where L represents the size of the system, b is the scale factor and $p_{\beta,i}$ indicates the growth probability of the growth bond i within the cell β . After many repeated renormalisations, $p_{\beta,i}$ approaches the value $p_{\beta,i}^*$ at the fixed point, given by (7). The recursion relation (8) is not the scaling relation but represents a random multiplicative process. The relationship (8) is the most important feature of our approach, characterising the scaling structure of DLA. From relation (8) we can construct an infinite hierarchy of generalised dimensions $D(q)$:

$$D(q) \equiv -(q-1)^{-1} \log\left(\sum_i \mathbb{P}_i^q\right) (\log L)^{-1}. \tag{9}$$

In the limit of L sufficiently large, it is given by

$$D(q) \sim -(q-1)^{-1} \sum_{\alpha} C_{\alpha}^* \left[\log\left(\sum_{i_{\alpha}} p_{\alpha,i_{\alpha}}^{*q}\right) \right] (\log b)^{-1} \tag{10}$$

where the C_{α}^* indicates the probability of configuration α at the fixed point and the second sum ranges over the growth bonds within the cell α .

From relation (8) the highest growth probability \mathbb{P}_{\max} scales as

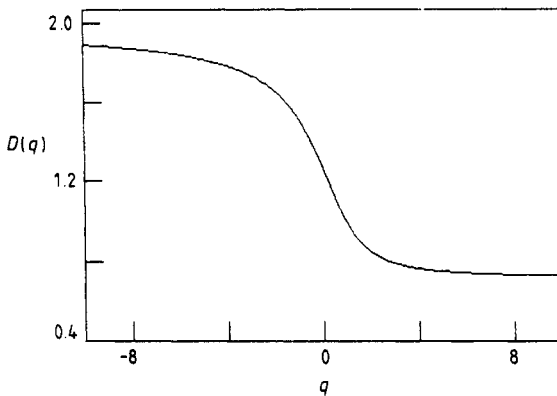


Figure 4. $D(q)$ plotted against q for DLA.

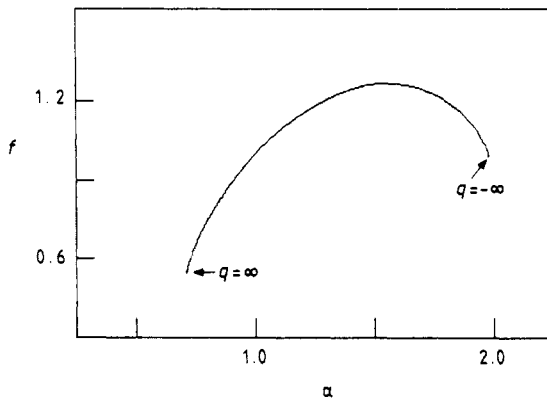


Figure 5. The plot of f against α for the $D(q)$ of figure 4. Note that $q = \infty$ corresponds to $D(\infty) = d_f - 1$ and $d_f = 1.711 \dots$

$$\mathbb{P}_{\max} \sim \left(\prod_{\alpha} (p_{\alpha, \max}^*)^{C_{\alpha}^*} \right)^{L/b} \tag{11}$$

where $p_{\alpha, \max}$ represents the highest growth probability in the cell with configuration α . If one assumes the scaling $\mathbb{P}_{\max} \sim L^{1-d_f}$ (Turkevich and Scher 1985), the fractal dimension d_f is given by

$$d_f = 1 - \sum_{\alpha} C_{\alpha}^* (\log p_{\alpha, \max}^*) / \log b. \tag{12}$$

Let us consider the configurational probability $C_{\alpha}(\sigma_n)$ with which a particular configuration α appears. Figure 3 shows all the configurations of the cell that it is possible to renormalise as the growth bond. The distinct configurations are labelled by α ($\alpha = 0, 11, 12, 21, 22, 23$) in figure 3. Configurations (11) or (12) are constructed by adding a break bond to configuration (0). The probability with which a break bond adds onto growth bond 1 or 2 in configuration (0) is given by $p_{0,1}$ or $p_{0,2}$. In addition, by adding a break bond to configuration (11), configurations (21), (22) or (23) occur. The configurational probabilities C_{α} are given by

$$\begin{aligned} C_{11} &= C_0 p_{0,1} & C_{12} &= C_0 p_{0,2} & C_{21} &= C_0 p_{0,1} p_{11,1} \\ C_{22} &= C_0 (p_{0,1} p_{11,2} + p_{0,2} p_{12,2}) & C_{23} &= C_0 p_{0,2} p_{12,1}. \end{aligned} \tag{13}$$

The configurational probability C_0 is determined from the normalisation condition:

$$\sum_{\alpha} C_{\alpha} \equiv 1. \tag{14}$$

In general, the probability that a given growth cluster configuration of n bonds occurs is given by the product of growth probabilities of adding a break bond at each step. The configurational probability $C_{\alpha}(\sigma_n)$ is determined by the growth probabilities $p_{\alpha,i}$ of the cells. Equations (4), (5), (7) and (13) are simultaneously solved. For $b = 2$ we obtain

$$\begin{aligned} p_{0,1}^* &= p_{0,2}^* = 0.5 & p_{11,1}^* &= p_{11,2}^* = 0.110 \dots & p_{11,3}^* &= 0.779 \dots \\ p_{21,1}^* &= p_{21,2}^* = p_{11,1}^* \\ p_{21,3}^* &= p_{11,3}^* \\ p_{21,1}^* &= p_{21,2}^* = p_{22,1}^* = p_{22,2}^* = p_{23,1}^* = p_{23,2}^* = 0.5. \end{aligned} \tag{15}$$

One can obtain the set of generalised dimensions $D(q)$ via equation (10). The exponents $D(q)$ are plotted in figure 4. From (10) and (12) we find the fractal dimension

$$d_f = D(\infty) + 1 = 1.711 \dots \tag{16}$$

in good agreement with the off-lattice result (Meakin 1983b). The information dimension $D(1)$ is given by $D(1) = 0.991 \dots$. This value is very close to the exact value of the harmonic measure. The scaling exponent $D(0)$ of the number of growth bonds in the surface layer is also given by $D(0) = 1.263 \dots$. This value is in poor agreement with the result of Amitrano *et al* (1986). The partition of $D(q)$ into a density of singularities $f(q)$ into singularity strength $\alpha(q)$ is introduced:

$$D(q) = (q - 1)^{-1} \{ q\alpha(q) - f(q) \}.$$

We display the relation between α and f in figure 5. The α - f spectrum has a convex shape. This curve agrees with the result of Amitrano *et al* for comparatively large values of q , but is poor for smaller values of q . This poor result contributes to the small-size cell of the renormalisation transformation.

In summary, we present the renormalisation group method to derive the set of generalised dimension in relation to the cluster structure of surface layers in diffusion-limited aggregation. Under RG transformation a recursion relation is derived for the growth probability. The growth probability is represented by a random multiplicative process. The multifractal spectrum is found for DLA. Our RG approach to the scaling structure is general and is not limited to the particular cell considered here. To obtain better values, it will be necessary to perform large-cell calculations using a Monte Carlo renormalisation method.

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