Scaling structure in a simple growth model with screening: forest formation model

LETTER TO THE EDITOR

Scaling structure in a simple growth model with screening: forest formation model

Takashi Nagatani

College of Engineering, Shizuoka University, Hamamatsu 432, Japan and Center for Polymer Studies and Department of Physics, Boston University, Boston, MA 02215, USA

Abstract. A simple growth model with screening is presented to mimic the forest formation. The tree grows independently if it is not screened by other trees but the growth of the tree stops when it is screened by other trees. The height distribution of trees is found to scale as $h^{-\gamma}$ ($1 < \gamma < 2$) by computer simulations. It is shown that the pattern of the forest is a self-affine fractal. The scaling exponent γ is also calculated by using a Monte Carlo renormalization-group method. The values of the exponent γ agree with those of the simulation.

Recently there has been increasing interest in a variety of non-equilibrium aggregation and deposition models such as the diffusion-limited aggregation (DLA) model and the ballistic deposition. Much of this interest stems from the fact that in addition to their connection with processes of fundamental practical importance, such as thin-film growth and crystal growth, these models exhibit non-trivial scaling behaviour (Witten and Sander 1981, Family and Landau 1984, Herrmann 1986, Julien and Botet 1987, Stanley and Ostrowsky 1988, Feder 1988, Vicsek 1989). A variety of computer simulations have been carried out to investigate the relationships between the cluster geometry and growth mechanisms. The structure of the aggregates strongly depends on the dynamics of the growth process. The most simple growth models are the ballistic deposition and the diffusion-limited aggregation. The ballistic deposition model provides a basis for understanding deposition processes used to prepare a wide variety of thin-film devices. The diffusion-limited aggregation model presents a prototype of the pattern formation of diffusive systems including the electrochemical deposition, crystal growth, viscous fingering and dielectric breakdown.

Very recently, Meakin (1988) and Krug and Meakin (1989) investigated numerically and analytically the microstructure (columnar morphology) and surface scaling structure in ballistic deposition at oblique incidence. They found the static and dynamic surface exponents by idealizing the columnar structure as an array of rods and mapping the problem onto a system of coalescing Brownian particles. They took into account only the mutual screening of neighbouring rods: if the tip of the jth rod is screened by the $(j+1)$th, the corresponding particles coalesce and continue to grow as one. They have not performed the direct simulation for the idealized system.

In this letter, we present a simple growth model with screening. The model is a generalized one of the idealized ballistic model at oblique incidence. The model is

described by the governing equation

$$\frac{\partial h_i}{\partial t} = \theta(h_i - h_{i+1} + \Delta h)\theta(h_i - h_{i+2} + 2\Delta h)\ldots\theta(h_i - h_{i+n} + n\Delta h)\ldots h_i^\alpha \xi_i(t) \tag{1}$$

where h_i is the height of a tree on the site i, $\theta(x)$ is the step function, Δh is the slope of the inclined light and $\xi_i(t)$ is white noise in space and time with non-zero mean. Imagine the forest formation. The tree is assumed as a stick. The tree is assumed to grow only in the light of sun. The sunlight streams in on the right-hand side. Each tree grows independently and randomly with a height dependent growth rate h_i^α only if the tree is not screened by other trees. When the tree is screened by other trees, the tree does not grow. Figure 1 shows the model. If the tip of the tree is screened by other trees, the tip of the tree becomes inactive. The tree screened by other trees is represented by the broken line. The inactive tip of trees is indicated by the triangle. The tip of trees not screened by other trees is indicated by the circle. The tip is active. The active tree is indicated by the full line. Δh is the slope of the sunlight. $\theta(h_i - h_{i+1} + \Delta h)$, $\theta(h_i - h_{i+2} + 2\Delta h)$ and $\theta(h_i - h_{i+n} + n\Delta h)$ represent respectively the screening effects of the trees on the sites $i+1$, $i+2$ and $i+n$ to the tree on the site i. If the height of the tree on the site $i+n$ is greater than $h_i + n\Delta h$, the tree on the site $i+n$ screens the sunlight to the tree on the site i. The screening effect is given by $\theta(h_i - h_{i+n} + n\Delta h)$. The growth rate of each tree is given by h_i^α if the tree is not screened by the other trees. In the case of $\alpha = 0$, the idealized ballistic model at oblique incidence, which was devised by Krug and Meakin (1989), is reproduced. In our model, the mutual screening not only of neighbouring sticks but also all rods on the right-hand side is taken into account. The pattern of the forest formation obtained by the simulation with use of (1) is shown in figure 2 for $\alpha = 0$, $\Delta h = 0.5$ and $L = 400$, where L is the width of the system, and the lateral boundary condition is periodic.

Figure 3 shows the mass scaling against the height for $\Delta h = 0.5$, 1 and 2 in the log–log plot ($\alpha = 0$ and $L = 3000$). The mass scaling depends weakly on the slope of sunlight. For $1 \ll h \ll L$, the mass scales as

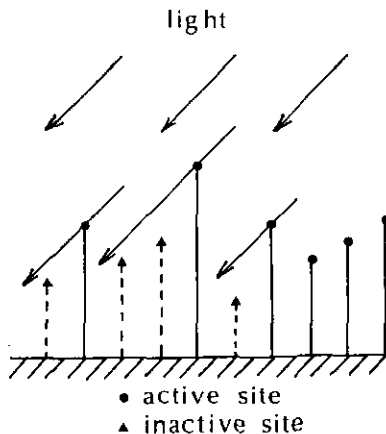$$M(h) \approx h^\beta \tag{2}$$

Figure 1. Illustration of the simple growth model with screening. The sunlight streams in on the right-hand side. Each tree grows independently and randomly if the tree is not screened by other trees. If it is screened by other trees, its growth stops. The screened and the unscreened trees are indicated by the broken and the full lines.
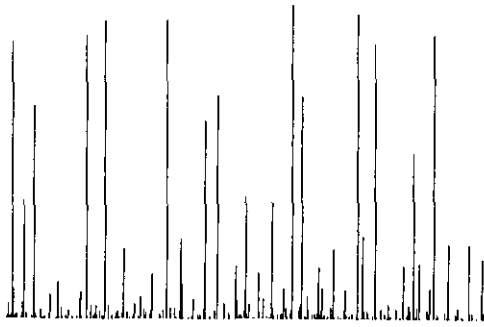
Figure 2. The pattern obtained by simulation for $\alpha = 0$, $\Delta h = 0.5$ and $L = 400$.
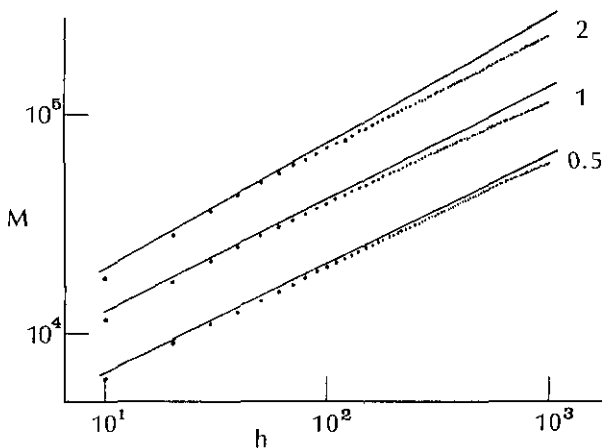

Figure 3. The mass scaling against the height for $\Delta h = 0.5$, 1 and 2 ($\alpha = 0$ and $L = 3000$) in the log-log plot.

with $\beta = 0.45 \pm 0.03$ ($\Delta h = 0.5$), $\beta = 0.55 \pm 0.03$ ($\Delta h = 1$), $\beta = 0.69 \pm 0.03$ ($\Delta h = 2$). The height distribution of trees is related with the mass as follows:

$$M(h) = \int_0^h hf(h)\, dh \tag{3}$$

where $f(h)$ is the height distribution of trees. If one assumes

$$f(h) \approx h^{-\gamma} \tag{4}$$

the height distribution exponent γ is given by

$$\gamma = 2 - \beta. \tag{5}$$

The above scaling structures of the mass and the height distribution have not been found in the idealized ballistic model by Krug and Meakin (1989). In their model, only mutual screening of neighbourhood sticks was taken into account. However, the screening effect of all sticks on the right-hand side was not taken into account. The scaling structure of the height distribution is due to the screening effect of all sticks.

Figure 4 shows the mass scaling against the height for $\alpha = -1, -0.5, 0, 0.5, 1.2$ in the log-log plot ($\Delta h = 0.5$, $L = 300$). Table 1 shows the exponents α, β and γ. If $\alpha < 0$,
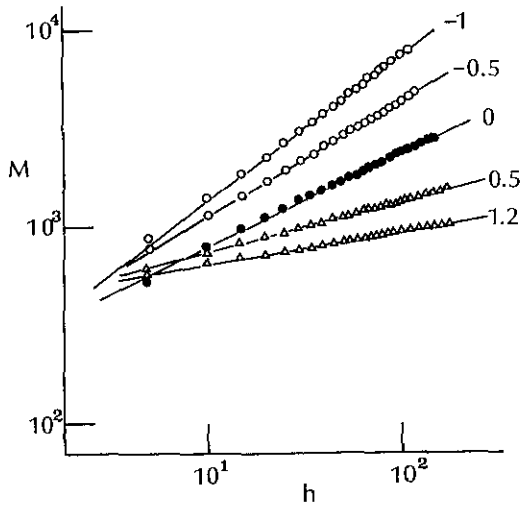
Figure 4. The dependence of the mass scaling against the height upon α in the log-log plot for $\alpha = -1$, -0.5, 0, 0.5, 1.2 ($\Delta h = 0.5$ and $L = 300$).

Table 1. Mass exponent β and height distribution exponent γ for α ($\Delta h = 0.5$, $L = 300$). The errors of the exponents β and γ are about ± 0.03.

α	$(-\infty)$	-1	-0.5	0	0.5	1.2	(∞)
β	(1)	0.743	0.594	0.45	0.25	0.167	(0)
γ	(1)	1.275	1.406	1.55	1.75	1.833	(2)

the growth rate of each tree decreases with increasing height. If $\alpha > 0$, the growth rate increases with the height. In the limit of $\alpha \to -\infty$, the dense pattern appears and $\beta = 1$. In the limit of $\alpha \to \infty$, the pattern becomes a single tree and $\beta = 0$.

We construct the deterministic fractal model by iterating the generator. Figure 5 shows the deterministic model for the height distribution ($\alpha = 0$). Figure 5(a) and figure 5(b) represent respectively the first stage and the second stage of the iteration. The deterministic model is constructed by iterating the generator (figure 5(a)). The vertical line is replaced by shrinking the generator by 25% in height and by 12.5% in width. The pattern is a self-affine fractal. Then the height distribution with the scaling $f(h) \approx h^{-1.5}$ is obtained.

We calculate the scaling exponent β by using a position-space renormalization-group method. First, we consider a small cell renormalization with scale factor $b = 2$. Consider a growth process within the 2×2 cell (see figure 6). Set $\Delta h = 1$. The lateral boundaries are periodic. We assume a self-organized criticality for a state when the height of the tree reaches the upper boundary. Configurations (b) or (c) in figure 6 are obtained by adding a particle to configuration (a). The configurational probabilities p_b and p_c are given by $2^\alpha/(1 + 2^\alpha)$ and $1/(1 + 2^\alpha)$. Configuration (d) is obtained by adding a particle to configuration (c) with probability one. Configurations (b) and (d) are in a self-organized critical state. Then the mass M_2 within the cell is assumed to be given by the mean value

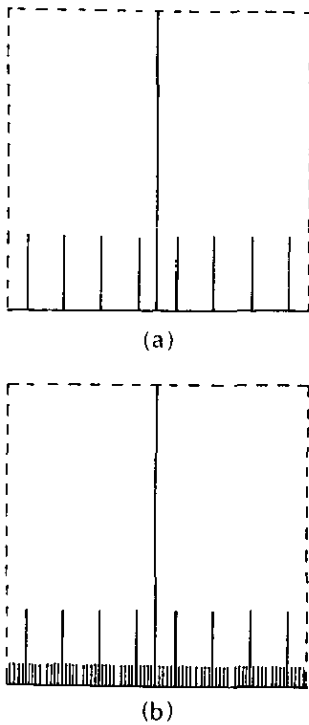$$M_2 = [2^\alpha/(1 + 2^\alpha)]2 + [1/(1 + 2^\alpha)]3. \tag{6}$$

Figure 5. The deterministic fractal model. (*a*) The generator and the first stage. (*b*) The second stage. The vertical line is replaced by shrinking generator by 25% in height and by 12.5% in width.
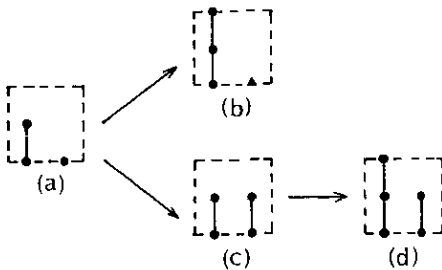

Figure 6. All distinct configurations of the 2×2 cell for small cell renormalization.

The exponent β is given by

$$\beta = \ln M_2/\ln 2 - 1 \tag{7}$$

for $\alpha = 0$, $\beta = 0.322$. For $b = 3$, we obtain $\beta = 0.401$ ($\alpha = 0$ and $\Delta h = 1$). For larger cells, we apply a Monte Carlo renormalization method. Consider a growth process within the $b \times b$ cell. The lateral boundaries are periodic. The growth process continues until a tree connects with the top of the cell. This growth process is repeated 100 times. The total mass within the cell is calculated and is averaged over 100 Monte Carlo realizations. Table 2 shows the values of the mass exponent β ($\alpha = 0$) obtained by a Monte Carlo renormalization method for $\Delta h = 0.5$, 1 and 2. This method gives quick convergence

Table 2. The values of the mass exponent β ($\alpha = 0$) obtained by Monte Carlo renormalization group method for $\Delta h = 0.5$, 1 and 2. Each result is averaged over 100 samples.

b	$\Delta h = 0.5$	$\Delta h = 1$	$\Delta h = 2$
5	0.394	0.513	0.662
7	0.427	0.553	0.674
10	0.439	0.552	0.675
15	0.433	0.555	0.700
20	0.436	0.550	0.694
30	0.432	0.547	0.693
50	0.433	0.551	0.683
	(0.43 ± 0.01)	(0.55 ± 0.01)	(0.68 ± 0.01)

with an increase in the cell size. With relatively small cells, we obtain values in excellent agreement with the large-size simulation result.

In summary, we present a simple growth model with screening to mimic the forest formation. We find that the height distribution of trees shows a power law of height. We give the scaling exponent by computer simulation. Also we calculate the scaling exponent by using a Monte Carlo renormalization method.

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