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Aggregation processes with catalysis-driven monomer birth/death*

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We propose two solvable cluster growth models, in which an irreversible aggregation spontaneously occurs between any two clusters of the same species; meanwhile, monomer birth or death of species A occurs with the help of species B. The system with the size-dependent monomer birth/death rate kernel $K(i,j) = Jij^v$ is then investigated by means of the mean-field rate equation. The results show that the kinetic scaling behaviour of species A depends crucially on the value of the index v. For the model with catalysis-driven monomer birth, the cluster-mass distribution of species A obeys the conventional scaling law in the $v \leq 0$ case, while it satisfies a generalized scaling form in the $v > 0$ case; moreover, the total mass of species A is a nonzero value in the $v < 0$ case while it grows continuously with time in the $v \geq 0$ case. For the model with catalysis-driven monomer death, the cluster-mass distribution also approaches the conventional scaling form in the $v < 0$ case, while the conventional scaling description of the system breaks down in the $v \geq 0$ case. Additionally, the total mass of species A retains a nonzero quantity in the $v < 0$ case, but it decreases to zero with time in the $v \geq 0$ case.

Keywords: kinetic behaviour, cluster growth, scaling law, rate equation
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1. Introduction

Cluster growth is an important phenomenon in many fields of science and technology, such as colloid growth, polymerization biology, aerosol formation, star formation and so on.[1−5] The general mechanism for cluster growth is a binary coalescence scheme, $A_i + A_j \rightarrow A_{i+j}$. Here, A_i denotes a cluster consisting of i monomers, and two clusters A_i and A_j can bond spontaneously to form a large cluster A_{i+j}.[6−9] In recent years, considerable interest has been aroused in a variety of aggregations, exchange-driven (migration-driven) cluster growth,[10−15] catalysis-driven aggregation,[16−19] and other reaction mechanisms.[20] Ispolatov *et al* introduced several exchange-driven growth models for the individual wealth redistribution in economical interactions.[12] Leyvraz and Redner proposed an irreversible migration-driven cluster growth model for the evolution of city populations.[13] Krapivsky and Ben-Naim investigated the kinetics of exchange-driven growth with homogeneous exchange kernels.[14] Ke and Lin proposed several catalysis-driven aggregation models and found that the kinetic behaviours of such systems were quite different from those for the ordinary aggregation.[16] These studies gave a complete description of the problem in the approximate scaling regime and found that overall range of possible behaviours and the emergence of self-similar mass distributions were as if those happened in ordinary aggregation processes. However, most of these studies are devoted to the cluster growth driven by one of the above-mentioned mechanisms or several, and there are few studies concerning cluster growth driven by monomer birth/death. Ke and Lin investigated the kinetic behaviour of the growth of clusters through monomer birth and death.[20] They found that in a symmetrical system the cluster-mass distribution approached the conventional scaling form in some cases, while the system could undergo a gelation-like transition in other cases.

Motivated by these studies, we propose an irreversible aggregation model with catalysis-driven birth/death, which may give rise to rich kinetic behaviours of cluster growth. In our model, there are two distinct types of species in the system, A and B species. Irreversible aggregation reaction occurs be-

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tween any two clusters of species A: $A_i + A_j \xrightarrow{K(i,j)} A_{i+j}$, where $K(i,j)$ is the rate of the two clusters A_i and A_j bonding together to form A_{i+j}. Meanwhile, a cluster of species A can produce/lose a monomer with the help of a cluster of species B according to the catalysis-driven birth/death scheme, $A_i + B_j \to A_{i+1} + B_j$ or $A_i + B_j \to A_{i-1} + B_j$. On the other hand, the clusters of species B also coagulate spontaneously according to the binary scheme, $B_i + B_j \to B_{i+j}$. According to this work, we find that the cluster-mass distribution of species A obeys the conventional or generalized scaling law in some cases, while the scaling law may break down in other cases.

This model may mimic some biological and social processes such as the growth of a bacteria population, economical interactions and city formation. For example, the merging of two separate companies to form a single larger company can be regarded as an aggregation process; meanwhile, a company may correspondingly hire or dismiss employees due to some external factors (such as the market demand of its products). Similarly, city population growth is driven by the merging of small population districts as well as the birth/death of the population. Additionally, irreversible aggregation processes with catalysis-driven monomer birth/death also occur in some chemical systems. For instance, the polymerization of polymers is an irreversible aggregation process and the polymers may grow or be partially annihilated in the presence of a certain catalyst. On the other hand, it is also believed that such cluster growth systems are of interest for the study of the scaling properties of their evolution behaviours.

The rest of this paper is organized as follows. In Section 2, we propose a catalysis-driven birth model and investigate the scaling solution of the cluster-mass distribution by means of the mean-field rate equation. In Section 3, we then investigate the kinetic behaviour of a catalysis-driven death model. Finally, a summary is given in Section 4.

2. Aggregation processes with catalysis-driven monomer birth

We study our model in the mean-field limit. The mean-field approximation neglects the spatial correlations and, therefore, typically holds in the case in which the dimension of the system is larger than the critical dimension $d_c = 2$.[8] The mean-field rate equation assumes that the reaction proceeds at a rate proportional to the reactant concentrations. At time t, the concentrations of k-mers of species A and B are denoted by $a_k(t)$ and $b_k(t)$, respectively. We assume that the birth rate kernel is time-independent and depends only on the size of cluster, i.e. $K(i,j) = Jij^v$. Here J is a constant coefficient which denotes the rate of the catalyzed reaction between the monomer clusters of species A and B, and v represents the degree of the dependence of a B cluster's catalytic ability on its mass. It seems that the overall rate of catalyzed reactions between species A and B may vary as a power law in some scale factor (see Ref. [16] and references therein). The self-coagulation rates I_1 and I_2 of species A and B are assumed to be constant. The rate equations for the aggregation processes with catalysis-driven monomer birth then read

$$\begin{aligned}\frac{\mathrm{d}a_k}{\mathrm{d}t} &= \frac{1}{2}I_1\sum_{j=1}^{\infty}a_i a_j - I_1 a_k\sum_{j=1}^{\infty}a_j \\ &\quad + J(k-1)a_{k-1}\sum_{j=1}^{\infty}j^v b_j - Jka_k\sum_{j=1}^{\infty}j^v b_j, \\ \frac{\mathrm{d}b_k}{\mathrm{d}t} &= \frac{1}{2}I_2\sum_{j=1}^{\infty}b_i b_j - I_2 b_k\sum_{j=1}^{\infty}b_j. \end{aligned} \tag{1}$$

We consider the simplest but important case, in which there only exist monomer clusters of species A and B at $t = 0$ and their concentrations are equal to A_0 and B_0, respectively. Then the initial condition is

$$a_k(0) = A_0\delta_{k1}, \quad b_k(0) = B_0\delta_{k1}. \tag{2}$$

Under the monodisperse initial condition (2), the rate equations (1) can be solved with the help of ansatz[21]

$$a_k(t) = A(t)[a(t)]^{k-1}, \quad b_k(t) = B(t)[b(t)]^{k-1}. \tag{3}$$

Inserting Eqs.(3) into Eqs.(1), we can transform Eqs.(1) into the following differential equations:

$$\begin{aligned}\frac{\mathrm{d}a}{\mathrm{d}t} &= \frac{I_1}{2}A + JM_{Bv} - JaM_{Bv}, \\ \frac{\mathrm{d}A}{\mathrm{d}t} &= -\frac{I_1A^2}{1-a} - JAM_{Bv}, \end{aligned} \tag{4}$$

$$\frac{\mathrm{d}b}{\mathrm{d}t} = \frac{I_2B}{2}, \quad \frac{\mathrm{d}B}{\mathrm{d}t} = -\frac{I_2B^2}{1-b}, \tag{5}$$

with the shorthand notation $M_{Bv}(t) = \sum_{j=1}^{\infty}j^v b_j(t)$. Correspondingly, the initial condition of Eqs.(4) and (5) becomes

$$a = 0, \quad b = 0, \quad A = A_0, \quad B = B_0 \quad \text{at} \quad t = 0. \tag{6}$$

From Eqs.(5) one derives the exact solutions of $b(t)$ and $B(t)$ respectively as follows:

$$b(t) = \frac{I_2 B_0 t}{I_2 B_0 t + 2}, \quad B(t) = \frac{4B_0}{(I_2 B_0 t + 2)^2}. \quad (7)$$

The exact solution $b_k(t)$ for species B is then obtained,

$$b_k(t) = \frac{4B_0}{(I_2 B_0 t + 2)^2}\Big(1 - \frac{2}{I_2 B_0 t + 2}\Big)^{k-1}. \quad (8)$$

In the region of $k \gg 1$ and $t \gg 1$, Eq.(8) can be approximately rewritten as

$$b_k(t) \simeq 4B_0^{-1} I_2^{-2} t^{-2} \exp(-x), \quad x = (2/I_2 B_0) k t^{-1}. \quad (9)$$

Equation (9) shows that the cluster-mass distribution of species B approaches the conventional scaling form,

$$c_k(t) \simeq t^{-w} \Phi[k/S(t)], \quad S(t) \propto t^z, \quad (10)$$

where $c_k(t)$ denotes the concentration of k-mers and $S(t)$ is the characteristic mass of such an aggregation system. In this system, the scaling exponents for species B are $w = 2$ and $z = 1$. The total number and the total mass of species B are readily obtained respectively as follows:

$$N_B(t) = \sum_{j=1}^{\infty} b_j(t) \simeq 2 I_1^{-1} t^{-1},$$

$$M_B(t) = \sum_{j=1}^{\infty} j b_j(t) = B_0. \quad (11)$$

The results show that the total mass of species B is conserved and the total number decays as t^{-1}. So species B behaves as if it were in the single-species irreversible aggregation case.

We then turn to determine the cluster-mass distribution of species A. Under the initial condition (6), from Eqs.(4) one can obtain

$$A(t) = A_0 [1 - a(t)]^2 E(t) \quad (12)$$

with the shorthand notation

$$E(t) = \exp\Big[J \int_0^t M_{Bv}(t') \mathrm{d}t'\Big].$$

Substituting Eq.(12) into Eq.(4), we can deduce the following equation:

$$\frac{\mathrm{d}(1-a)}{\mathrm{d}t} = -\frac{I_1}{2} A_0 (1-a)^2 E(t) - J M_{Bv} (1-a). \quad (13)$$

Equation (13) can be straightforwardly solved to yield

$$a(t) = 1 - (1 + I_1 A_0 t/2)^{-1} [E(t)]^{-1}. \quad (14)$$

In the long-time limit, we determine $M_{Bv}(t)$ as follows:

$$M_{Bv}(t) \simeq \begin{cases} \Gamma(1+v) B_0^v \Big(\dfrac{2B_0}{2 + I_2 B_0 t}\Big)^{1-v}, & \text{for} \quad v > -1, \\ \dfrac{4 \ln(I_2 B_0 t/2 + 1)}{I_2 t (I_2 B_0 t + 2)}, & \text{for} \quad v = -1, \\ \dfrac{4B_0}{(I_2 B_0 t + 2)^2} \displaystyle\sum_{j=1}^{\infty} j^v, & \text{for} \quad v < -1, \end{cases} \quad (15)$$

where the Gamma function $\Gamma(1+v) = \int_0^\infty x^v \mathrm{e}^{-x} \mathrm{d}x$. By using Eq.(15) we then investigate the evolution behaviours of species A in three different cases as follows.

2.1. $v < 0$ case

In this case, Eq.(14) reduces to the following approximate solution of $a(t)$ at large times:

$$a(t) \simeq 1 - C_1 t^{-1}, \quad (16)$$

where

$$C_1 = (2/I_1 A_0) \exp\Big[-\int_0^\infty J M_{Bv}(t) \mathrm{d}t\Big].$$

Then we obtain the approximate scaling solution of $a_k(t)$ at large times,

$$a_k(t) \simeq 2 I_1^{-1} C_1 t^{-2} \exp(-x), \quad x = C_1 k t^{-1}. \quad (17)$$

Equation (17) shows that for this case, the cluster-mass distribution of species A also approaches to the conventional scaling form (10) with the scaling exponents $w = 2$ and $z = 1$.

In the long-time limit, the total number $N_A(t)$ and the total mass $M_A(t)$ of species A can be respec-

tively expressed as

$$N_A(t) = \sum_{j=1}^{\infty} a_j(t) \simeq 2I_1^{-1}t^{-1},$$
$$M_A(t) = \sum_{j=1}^{\infty} ja_j(t) \simeq A_0\exp\Big[\int_0^{\infty} JM_{Bv}(t)\mathrm{d}t\Big]. \quad (18)$$

The results imply that the total number of species A decays linearly with time, while the total mass grows slowly with time and reaches a quantity larger than its initial mass at the end.

2.2. $v = 0$ case

In this case, from Eq.(13) we derive the following exact solution:

$$a(t) = 1 - \frac{1}{(1 + I_1A_0t/2)(1 + I_2B_0t/2)^{2J/I_2}}, \quad (19)$$

and then obtain the approximate solution of $a_k(t)$ at large times,

$$a_k(t) \simeq 2I_1^{-1}C_2t^{-(2+2J/I_2)}\exp(-x),$$
$$x = C_2kt^{-(1+2J/I_2)}, \quad (20)$$

where $C_2 = 2(I_1A_0)^{-1}(I_2B_0/2)^{-2J/I_2}$. In this case, the cluster-mass distribution $a_k(t)$ also takes the conventional scaling form (10) with the scaling exponents $w = 2 + 2J/I_2$ and $z = 1 + 2J/I_2$. It is different from the form in the above $v < 0$ case in that the scaling exponents for this case are nonuniversal constants, and they are dependent on the rate kernel of the self-coagulation of species B as well as the rate kernel of the catalysis reaction.

Moreover, in the long-time limit, the total number $N_A(t)$ and the total mass $M_A(t)$ can be determined respectively by

$$N_A(t) \simeq 2I_1^{-1}t^{-1},$$
$$M_A(t) \simeq A_0(I_2B_0/2)^{2J/I_2}t^{2J/I_2}, \quad (21)$$

which show that the total number of species A decays linearly with time and the total mass grows as t^{2J/I_2}. Obviously, the total mass diverges in the $t \to \infty$ limit.

2.3. $v > 0$ case

From Eqs.(14) and (15) we deduce

$$a(t) \simeq 1 - (2/I_1A_0)t^{-1}\mathrm{e}^{-C_3t^v}, \quad (22)$$

where $C_3 = J\Gamma(v)B_0^v(2/I_2)^{1-v}$. The approximate solution of $a_k(t)$ at large times is then obtained as

$$a_k(t) \simeq 4I_1^{-2}A_0^{-1}t^{-2}\mathrm{e}^{-C_3t^v}\exp(-x),$$
$$x = 2(I_1A_0)^{-1}kt^{-1}\mathrm{e}^{-C_3t^v}. \quad (23)$$

It is obvious that for this case, the conventional scaling form (10) breaks down and the cluster-mass distribution scales according to the stretched exponential correction form. The conventional scaling form (10) can be generalized to

$$c_k(t) \simeq [g(t)]^{-w_1}[f(t)]^{-w_2}\Phi[k/S(t)],$$
$$S(t) \propto [g(t)]^{z_1}[f(t)]^{z_2}, \quad (24)$$

where $g(t)$ and $f(t)$ are increasing time functions. Let $g(t) = t$ and $f(t) = \exp(t^v)$, and one will be able to obtain the scaling exponents, $w_1 = 1$, $w_2 = 1$, $z_1 = 1$ and $z_2 = C_3$. The scaling exponent z_2 is dependent on the details of the reaction events. We also obtain the total number $N_A(t)$ and the total mass $M_A(t)$ in the long-time limit respectively:

$$N_A(t) \simeq 2I_1^{-1}t^{-1}, \quad M_A(t) \simeq A_0\exp(C_3t^v). \quad (25)$$

As in the above two cases, the total number of species A also decays as t^{-1}. The total mass grows stretched exponentially with time and diverges at $t \to \infty$. Especially, $M_A(t) \propto \exp(C_3t)$ in the $v = 1$ case. In this case, the monomer birth process dominates over the irreversible aggregation process. The results are qualitatively in agreement with the (population) growth of a biological system.[22]

3. Aggregation processes with catalysis-driven monomer death

In this section, we investigate the kinetics of aggregation processes with catalysis-driven monomer death. The concentrations of k-mers of species A and B at time t are also denoted by $a_k(t)$ and $b_k(t)$, respectively. The rate kernel also takes the form $K(i, j) = Jij^v$ and the self-coagulation rates of species A and B are constants I_1 and I_2 respectively. Then the rate equations for this system are expressed as

$$\frac{\mathrm{d}a_k}{\mathrm{d}t} = \frac{1}{2}I_1\sum_{j=1}^{\infty} a_ia_j - I_1a_k\sum_{j=1}^{\infty} a_j + J(k+1)a_{k+1}\sum_{j=1}^{\infty} j^vb_j - Jka_k\sum_{j=1}^{\infty} j^vb_j, \quad (26)$$

$$\frac{\mathrm{d}b_k}{\mathrm{d}t} = \frac{1}{2}I_2\sum_{j=1}^{\infty} b_ib_j - I_2b_k\sum_{j=1}^{\infty} b_j. \quad (27)$$

Obviously, the governing rate equation (27) for species B is the same as that in the above section and thus the cluster-mass distribution of species B in this model also takes the form (8). Under the monodisperse initial condition (2), with the help of ansatz (3) we recast Eq.(26) into the following equations:

$$\frac{\mathrm{d}a}{\mathrm{d}t} = \frac{1}{2}I_1 A + JM_{Bv}a^2 - JM_{Bv}a,$$
$$\frac{\mathrm{d}A}{\mathrm{d}t} = -\frac{I_1 A^2}{1-a} + JAM_{Bv}(2a-1). \tag{28}$$

From Eqs.(28) one can deduce

$$A(t) = A_0(1-a)^2 F(t), \tag{29}$$

with the shorthand notation

$$F(t) = \exp\Big[-J\int_0^t M_{Bv}(t')\mathrm{d}t'\Big].$$

Substituting Eq.(29) into Eqs.(28), we can rewrite the differential equation of $\mathrm{d}a/\mathrm{d}t$ as

$$\frac{\mathrm{d}(1-a)}{\mathrm{d}t} = -[(I_1A_0/2)F + JM_{Bv}] \times (1-a)^2 + JM_{Bv}(1-a). \tag{30}$$

From Eqs.(30) we derive the implicit solution of $a(t)$ as follows:

$$a(t) = 1 - \frac{2}{I_1A_0tF(t)+2}. \tag{31}$$

By solving Eq.(31) one can then investigate the behaviour of the cluster-mass distribution of species A in several different cases.

3.1. $v < 0$ case

In this case, Eq.(31) reduces to

$$a(t) \simeq 1 - C_4 t^{-1}, \tag{32}$$

where

$$C_4 = 2\exp\Big[\int_0^\infty JM_{Bv}(t)\mathrm{d}t\Big] \Big/ I_1A_0.$$

Thus we obtain the approximate solution of $a_k(t)$ at large times,

$$a_k(t) \simeq 2I_1^{-1}C_4t^{-2}\exp(-x), \quad x = C_4kt^{-1}. \tag{33}$$

Equation (33) shows that the cluster-mass distribution $a_k(t)$ of species A approaches the conventional scaling form (10), with the universal scaling exponents $w = 2$ and $z = 1$. We also determine the total number $N_A(t)$ and the total mass $M_A(t)$ of species A in the long-time limit respectively:

$$N_A(t) \simeq 2I_1^{-1}t^{-1},$$
$$M_A(t) \simeq A_0\exp\Big[-\int_0^\infty JM_{Bv}(t)\mathrm{d}t\Big]. \tag{34}$$

The results show that the total number of species A decays as t^{-1}, while the total mass decreases with time and reaches a quantity smaller than its initial mass at the end.

3.2. $v = 0$ case

In this special case, we have $M_{B0}(t) = 2B_0(2 + I_2B_0t)^{-1}$. Equation (31) reduces to

$$a(t) = 1 - \frac{1}{\frac{1}{2}I_1A_0t\left(\frac{I_2B_0}{2}t+1\right)^{-2J/I_2}+1}. \tag{35}$$

It follows from Eq.(35) that the solution of $a(t)$ is dependent on the ratio of I_2 to $2J$.

When $I_2 > 2J$, Eq.(35) is approximately rewritten as

$$a(t) \simeq 1 - C_5t^{-1+2J/I_2}, \tag{36}$$

where $C_5 = 2(I_2B_0/2)^{2J/I_2}/I_1A_0$. We then obtain the cluster-mass distribution $a_k(t)$ at large times,

$$a_k(t) \simeq 2I_1^{-1}C_5t^{-2+2J/I_2}\exp(-x),$$
$$x = C_5kt^{-(1-2J/I_2)}. \tag{37}$$

Equation (37) shows that the cluster-mass distribution $a_k(t)$ also takes the conventional scaling form (10), with the nonuniversal scaling exponents $w = 2-2J/I_2$ and $z = 1-2J/I_2$. Moreover,

$$N_A(t) \simeq 2I_1^{-1}t^{-1},$$
$$M_A(t) \simeq A_0(I_2B_0/2)^{-2J/I_2}t^{-2J/I_2}. \tag{38}$$

The results indicate that the total number of species A decays linearly as t^{-1}, and the total mass decreases as t^{-2J/I_2}. So, species A will die out finally in this subcase.

When $I_2 = 2J$, we obtain

$$a(t) = \frac{I_1A_0t}{(I_1A_0+I_2B_0)t+2}. \tag{39}$$

In the long-time limit, the approximate solution of $a_k(t)$ is then determined as follows:

$$a_k(t) \simeq 2A_0(I_2B_0)^{-1}(1-C_6)^2t^{-1}C_6^k\exp(-x),$$
$$x = 2(I_1A_0+I_2B_0)^{-1}kt^{-1}, \tag{40}$$

where

$$C_6 = I_1A_0/(I_1A_0+I_2B_0).$$

It is obvious that for this case, the conventional scaling form (10) breaks down and the cluster-mass distribution scales according to a modified scaling form. The conventional scaling form (10) can be generalized to[21]

$$c_k(t) = h^k t^{-w} \Phi[k/S(t)], \quad S(t) \propto t^z. \tag{41}$$

So the cluster-mass distribution $a_k(t)$ takes the modified scaling form (41) with the exponents $w = z = 1$. Moreover, we also determine the total number $N_A(t)$ and the total mass $M_A(t)$ of species A respectively as follows:

$$\begin{aligned} N_A(t) &\simeq 2A_0(I_1A_0 + I_2B_0)^{-1}t^{-1}, \\ M_A(t) &\simeq (2A_0/I_2B_0)t^{-1}. \end{aligned} \tag{42}$$

In the long-time limit, from Eqs.(42) we know that both the total number and the total mass of species A decrease linearly with time. Hence, species A cannot survive at the end.

When $I_2 < 2J$, $a(t)$ takes the following form different from those forms in other cases,

$$a(t) \simeq C_7 t^{1-2J/I_2}, \tag{43}$$

where

$$C_7 = (I_1A_0/2)(I_2B_0/2)^{-2J/I_2}.$$

The cluster-mass distribution of species A can be expressed as

$$a_k(t) \simeq A_0(I_2B_0/2)^{-2J/I_2} C_7^{k-1} t^{k(1-2J/I_2)}. \tag{44}$$

Obviously, the scaling description of the cluster-mass distribution $a_k(t)$ breaks down completely in this case. The total number and the total mass of species A are respectively

$$\begin{aligned} N_A(t) &\simeq A_0(I_2B_0t/2)^{-2J/I_2}, \\ M_A(t) &\simeq A_0(I_2B_0t/2)^{-2J/I_2}. \end{aligned} \tag{45}$$

In the long-time limit, both the total number and the total mass of species A decrease as t^{-2J/I_2}. So species A will die out at the end.

3.3. $v > 0$ case

In the long-time limit, we approximately rewrite Eq.(31) as follows:

$$a(t) \simeq \frac{1}{2} I_1 A_0 t \exp(-C_3 t^v). \tag{46}$$

One can then obtain the cluster-mass distribution of species A,

$$a_k(t) \simeq A_0(I_1A_0/2)^{k-1} t^{k-1} \exp(-C_3 k t^v). \tag{47}$$

Equation (47) shows that for this case, the cluster-mass distribution $a_k(t)$ is not scaled. Moreover, both the total number $N_A(t)$ and the total mass $M_A(t)$ of species A decrease stretched exponentially as $\exp(-C_3t^v)$. In this case, species A will also die out finally.

4. Summary

We have proposed two solvable cluster growth models, in which an irreversible self-aggregation occurs between any two clusters of the same species; meanwhile, monomer birth or death of species A is driven by species B. Based on the mean-field rate equations, we analyse the kinetic scaling properties of the cluster-mass distributions in the systems with the catalysis-driven birth/death rate kernel $K(i,j) = Jij^v$. The results show that the kinetic behaviour of the system depends crucially on the value of index v.

For the model with catalysis-driven monomer birth, the cluster-mass distribution $a_k(t)$ of species A approaches the conventional scaling form (10) in the $v \leq 0$ case, while it obeys the modified scaling law in the $v > 0$ case. The total number of species A decays as t^{-1} for all cases, but the total mass is distinct from each other in different cases. When $v < 0$, the total mass of species A reaches a quantity larger than the initial total mass. When $v \geq 0$, the total mass of species A grows with time and diverges at $t \to \infty$.

For the second model with catalysis-driven monomer death, we also study the cluster-mass distribution, the total number and mass of the clusters of species A. When $v < 0$, the cluster-mass distribution of species A obeys the conventional scaling law, and the total number decays as t^{-1}, and the total mass decreases slowly with time and reaches a quantity smaller than the initial total mass at the end. When $v > 0$, the conventional scaling description of the cluster mass distribution $a_k(t)$ breaks down, and both the total number and the total mass of species A decrease stretched exponentially with time. In particular, there are abundant interesting results in the case of $v = 0$. The kinetic evolution behaviour of species A is related to the relationship between the self-coagulation rate I_2 of species B and the catalysis

reaction rate coefficient J. The cluster-mass distribution $a_k(t)$ takes the conventional scaling form in the $I_2 > 2J$ subcase and the modified scaling form in the $I_2 = 2J$ subcase, but it is not scaled in the $I_2 < 2J$ subcase.

We hope that this model can reveal some unbeknown new mechanisms for cluster growth, or at least it offers a new method of solving some similar problems.

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