# Assortative exchange processes

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In exchange processes clusters composed of elementary building blocks, monomers, undergo binary exchange in which a monomer is transferred from one cluster to another. In assortative exchange only clusters with comparable masses participate in exchange events. We study maximally assortative exchange processes in which only clusters of equal masses can exchange monomers. A mean-field framework based on rate equations is appropriate for spatially homogeneous systems in sufficiently high spatial dimension. For diffusion-controlled exchange processes, the mean-field approach is erroneous when the spatial dimension is smaller than critical; we analyze such systems using scaling and heuristic arguments. Apart from infinite-cluster systems we explore the fate of finite systems and study maximally assortative exchange processes driven by a localized input.

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## I. INTRODUCTION

Exchange processes underlie numerous natural phenomena such as droplet growth via evaporation and recondensation [1], island growth [2], and phase ordering [3–5], and they have used in modeling of hydrodynamics of granular particles [6–8] and asymmetric dark matter [9]. Exchange processes have been applied to social sciences, e.g., to modeling segregation of heterogeneous populations [10], studying wealth distributions through asset exchange models [11–16], and mimicking growth of urban populations [17] and aggregation behaviors in job markets [18]. Exchange processes also proved useful as toy microscopic models which are simple enough to allow the derivation of the macroscopic "hydrodynamic" equations and explore other fundamental aspects of nonequilibrium statistical mechanics (see Refs. [19–24] and references therein).

In mass exchange processes, clusters interact by transferring mass from one to another. Cluster are usually assumed to be composed of an integer number of elemental building blocks ("monomers"). We denote by $A_j$ a cluster of "mass" $j$, that is, a cluster composed of $j$ monomers. Clusters are labeled solely by their masses; other characteristics (e.g., their shape) are ignored. We assume that in each exchange event, a monomer is transferred from one cluster to another. Symbolically, the mass exchange process is represented by the reaction scheme

$$A_i \oplus A_j \xrightarrow{K_{i,j}} (A_{i\pm1}, A_{j\mp1}). \tag{1}$$

A cluster disappears when its mass vanishes. Thus in an exchange involving a monomer the number of clusters may decrease; it certainly decreases in an exchange between two monomers (one monomer disappears and another becomes a dimer).

Exchange processes characterized by symmetric migration rates $K_{i,j}$ have been most investigated, e.g., models with homogeneous rates $K_{i,j} = i^a j^b + i^b j^a$ have been studied through asymptotic and scaling analyses (see, e.g., Refs. [25–27]). Even in the simplest situation when the system is spatially uniform and remains well mixed throughout the evolution, one needs to solve an infinite set of coupled nonlinear differential equations. This is usually impossible even for simple migration rates. The exchange processes characterized by generalized product kernels $K_{i,j} = (ij)^\lambda$ are exceptional since the governing equations can be linearized, and the models with $\lambda = 0, 1, 2$ have been solved exactly; see Refs. [26–28]. Spatially homogeneous exchange processes have been studied [25–27], and, e.g., for exchange rates $K_{i,j} = (ij)^\lambda$ it was shown [26] that an algebraic $t^{1/(3-2\lambda)}$ growth of the typical mass occurs when $\lambda < \frac{3}{2}$; when $\lambda > \frac{3}{2}$, an infinite cluster containing a finite fraction of the entire mass is formed at a finite "gelation" time, and when $\lambda > 2$ this time vanishes. Exchange processes driven by input of monomers have been investigated in Ref. [29].

In assortative exchange processes, interactions between clusters with disparate masses are suppressed. In this paper we study the maximally assortative processes in which exchange can occur only between clusters of the same mass. The matrix of migration rates becomes diagonal, $K_{i,j} = K(i)\delta_{i,j}$, and the set of reaction channels (1) narrows to

$$A_m \oplus A_m \xrightarrow{K(m)} (A_{m-1}, A_{m+1}). \tag{2}$$

The reaction scheme (2) is rather abstract. A natural physical realization of the maximally assortative processes is based on diffusing clusters and postulates that a collision between equal-mass clusters may result in mass exchange. More precisely, the simplest maximally assortative diffusion-controlled exchange process is the point-cluster process defined as follows:

(1) Each clusters occupies a single lattice site of a $d$-dimensional lattice.

(2) Clusters hop to neighboring sites, and the hopping rates are mass-independent.

(3) When a cluster hops to a site containing a cluster with the same mass, an exchange (2) instantaneously occurs.

To give a flavor of our findings we present a few basic results for this simplest diffusion-controlled maximally assortative exchange process. Imagine that each site is initially occupied by a single monomer, so the initial density of monomers,

 

i.e., the number of monomers per site, is $c_1(0) = 1$. We shall show that the density of monomers decays according to

$$c_1 \sim \begin{cases} t^{-5/8} & d = 3 \\ t^{-5/8}(\ln t)^{5/8} & d = 2\,. \\ t^{-7/18} & d = 1 \end{cases} \tag{3}$$

The temporal behavior changes at $d = d_c = 2$, which is the critical dimension for our diffusion-controlled maximally assortative exchange process. In three dimensions and generally above the critical dimension, $d > 2$, one can employ a mean-field description of (2) with rates $K(m) = 1$ reflecting that the hopping rates are mass-independent. At the critical dimension there is a logarithmic correction to the mean-field behavior; below the critical dimension the decay is slower than the mean-field prediction (similarly to other diffusion-controlled processes; see Ref. [28]). It is often useful to treat $d$ as a continuous parameter. The decay exponents are universal when $d > d_c = 2$ and become dimension-dependent below the critical dimension. In Sec. III we show that when $d < d_c$ the density of monomers decays as

$$\frac{c_1}{n_0} \sim [n_0(Dt)^{d/2}]^{-\frac{3d+4}{(d+2)^2}}. \tag{4}$$

Here we write the answer in the dimensionally correct form, which demonstrates the dependence on the diffusion coefficient $D$ and the initial density $n_0$; the latter is defined via $c_m(0) = n_0\delta_{m,1}$ if the system is initially composed of monomers. (Hereinafter we denote by $c_m$ the density of clusters of mass $m$.)

We shall further show that the cluster density

$$N(t) = \sum_{m\geqslant 1} c_m(t) \tag{5}$$

decays according to

$$N \sim \begin{cases} t^{-1/4} & d = 3 \\ t^{-1/4}(\ln t)^{1/4} & d = 2\,. \\ t^{-1/6} & d = 1 \end{cases} \tag{6}$$

More generally, below the critical dimension, $d < 2$, the cluster density decays as

$$\frac{N}{n_0} \sim [n_0(Dt)^{d/2}]^{-\frac{1}{d+2}}. \tag{7}$$

The outline of the paper is as follows. In Sec. II we study the maximally assortative exchange processes in the framework of mean-field rate equations. First we probe the asymptotic behaviors of the process with mass-independent migration rates, $K(m) = 1$, and then extend the results to a one-parameter family of rates varying algebraically with mass, $K(m) = m^a$. Such rates are particularly suitable for scaling techniques which we employ. In Sec. III we discuss the behavior of the simplest diffusion-controlled maximally assortative exchange process in which each cluster occupies a single lattice site (the point cluster process) and hops with mass-independent rate. The critical dimension is $d_c = 2$ for such exchange processes, and we analyze asymptotic behaviors of these processes in one and two dimensions. Maximally assortative exchange processes with a finite mass generically do not condense in a single cluster but reach a nontrivial final state with numerous clusters with different masses. In Sec. IV we describe these final states. Diffusion-controlled maximally assortative exchange processes driven by a localized input of monomers are investigated in Sec. V. In the last Sec. VI we discuss approaches which may lead to the progress in understanding of maximally assortative exchange processes with quickly growing rates where scaling is violated. Technical details are relegated to the appendices.

## II. MEAN-FIELD ANALYSIS

In this section we analyze maximally assortative exchange processes using the rate equations approach. This framework is applicable if the initial state is spatially homogeneous and if the system remains well mixed throughout the evolution.

The rate equations governing the evolution of the maximally assortative exchange process (2) with arbitrary migration rates $K(m)$ read

$$\frac{dc_m}{dt} = K(m+1)c_{m+1}^2 - 2K(m)c_m^2 + K(m-1)c_{m-1}^2. \tag{8}$$

The density of monomers obeys $\dot{c}_1 = K(2)c_2^2 - 2K(1)c_1^2$, which is consistent with the first equation (8) after setting $c_0 \equiv 0$, or introducing an extra rate $K(0) = 0$. One can verify that Eqs. (8) agree with mass conservation:

$$\sum_{m\geqslant 1} mc_m(t) = 1. \tag{9}$$

Hereinafter we set the conserved mass density $M$ to unity; this can always be done by rescaling: $c_m \to Mc_m$.

Equations (8) have not been solved apart from somewhat pathological models in which for a certain mass $j$ the corresponding rate vanishes, $K(j) = 0$, so only clusters up to mass $j$ are present. In the following we assume, if not stated otherwise, that $K(m) > 0$ for all $m \geqslant 1$ so that the number of interacting cluster species is infinite. The most interesting long time behavior of such models can be probed through asymptotic and scaling analyses. We start with the simplest situation when the migration rates are mass-independent.

### A. Mass-independent rates

For the maximally assortative exchange process with mass-independent rates, $K(m) = 1$, Eqs. (8) reduce to

$$\frac{dc_m}{dt} = c_{m+1}^2 - 2c_m^2 + c_{m-1}^2. \tag{10}$$

This neat infinite system of nonlinear coupled ordinary differential equations (ODEs) appears intractable. The most interesting large time behavior can be established, however, since the typical mass exhibits an unlimited growth when $t \to \infty$, thereby allowing us to employ asymptotic and scaling approaches. The chief idea is to treat $m$ as a continuous variable. If $c(m, t) \equiv c_m(t)$ slowly varies with $m$, the right-hand side in (10) can be replaced by the second derivative to yield a partial differential equation (PDE)

$$\frac{\partial c}{\partial t} = \frac{\partial^2}{\partial m^2} c^2, \tag{11}$$

known as a porous medium equation. (More generally, a nonlinear PDE of the form $u_t = \Delta u^n$, where $n > 1$ and $\Delta$

is the Laplace operator, is known as the porous medium equation; see Ref. [30].)

One then seeks a scaling solution to (11):

$$c(m,t) = t^{-2\beta} F(x), \qquad x = \frac{m}{t^{\beta}}. \tag{12}$$

The scaling form (12) agrees with mass conservation, and the choice (9) of the initial mass density implies

$$\int_0^\infty dx\, x F(x) = 1. \tag{13}$$

By inserting the scaling form (12) into (11) we find that the scaling form is consistent only when $\beta = 1/4$, and in that case the governing PDE turns into an ODE,

$$4(F^2)'' + xF' + 2F = 0, \tag{14}$$

where $(\cdot)' = d(\cdot)/dx$. Multiplying (14) by $x$ and integrating we get

$$4\,\frac{d}{dx}\left(\frac{F^2}{x}\right) + F = 0, \tag{15}$$

where the integration constant was chosen to be zero to ensure that $F$ vanishes as $x \to \infty$. Rewriting Eq. (15) as a product of two factors, $F[8F'/x + 1 - 4F/x^2] = 0$, we immediately extract the special solution $F(x) = 0$, and then from $8F'/x + 1 - 4F/x^2 = 0$ we find a one-parameter family of solutions

$$F = \frac{1}{12}\sqrt{x}\left(x_0^{3/2} - x^{3/2}\right). \tag{16}$$

The solution is the combination of (16) and $F = 0$. Since the density is non-negative, the scaled mass distribution is given by (16) when $0 \leqslant x \leqslant x_0$, and it vanishes when $x > x_0$. The normalization requirement, $1 = \int_0^{x_0} dx\, xF(x)$, yields $x_0 = (80)^{1/4}$. Hereinafter it proves convenient to use a renormalized scaled mass variable $y = x/x_0$, which in the present case equals $y = m/(80t)^{1/4}$ in terms of the original variables. Collecting previous results we write the scaling solution in the form

$$c_m(t) = t^{-1/2}\, G(y) \tag{17}$$

with

$$G(y) = \frac{1}{3} \times \begin{cases} \sqrt{5y}\,(1 - y^{3/2}) & 0 \leqslant y \leqslant 1 \\ 0 & y > 1 \end{cases}. \tag{18}$$

Note also simple asymptotic formulas

$$c_1(t) = B_1\, t^{-5/8}, \tag{19a}$$

$$N(t) = B\, t^{-1/4} \tag{19b}$$

for the density of monomers and the total cluster density $N(t) = \sum_{m\geqslant 1} c_m(t)$. The amplitudes in (19a) and (19b) are

$$B_1 = \frac{5^{3/8}}{3\sqrt{2}}, \qquad B = \frac{2 \times 5^{3/4}}{9}.$$

At first sight, the compact shape of the mass distribution seems paradoxical given that the governing equations are parabolic PDEs. Our intuition is based on linear parabolic PDEs for which perturbations propagate with infinite speed preventing the formation of compact solutions. For *nonlinear* parabolic PDEs like the porous medium equation (11), compact solutions may arise [30] as was discovered many years ago [31,32]; see Refs. [33–35] for review and [36,37] for recent examples of such nonlinear parabolic PDEs appearing in the context of lattice gases.

The compactness is a drawback of the continuum approximation. In the realm of the original discrete system (8), the mass distribution is positive for all $m$. The front is extremely steep, however, so the discrepancy between the actual solution of the discrete system and the prediction of the continuum approach, *viz.* $c(m,t) = 0$ in the region $m > m_*(t) = (80t)^{1/4}$, is tiny. To appreciate this we take into account a very sharp decay and simplify (10) in the $m > m_*(t)$ region to $\frac{dc_m}{dt} \simeq c_{m-1}^2$ from which we deduce a double exponential decay:

$$\ln(1/c_m) \propto 2^{m - m_*(t)}. \tag{20}$$

The validity of the scaling approach is physically obvious but hard to justify rigorously. We cannot compare the scaling solution (17) and (18) with exact solutions since such solutions of Eqs. (10) are unknown. As usual, one anticipates that for *localized* initial conditions, i.e., such that $c_m(0)$ vanishes for sufficiently large $m$, the solution approaches to the scaling solution (17) and (18). The same should be valid also for $c_m(0)$ sufficiently quickly decaying with $m$; more complicated behaviors might occur when $c_m(0)$ has a slowly decaying tail.

### B. Homogeneous rates $K(m) = m^a$

Let us now look at the one-parameter family of maximally assortative exchange processes with algebraically varying migration rates $K(m) = m^a$. The governing rate equations read

$$\frac{dc_m}{dt} = (m+1)^a c_{m+1}^2 - 2m^a c_m^2 + (m-1)^a c_{m-1}^2. \tag{21}$$

Note that a rate equation for the cluster density

$$\frac{dN}{dt} = -c_1^2 \tag{22}$$

is independent on the exponent $a$.

#### 1. Scaling approach

Algebraically varying migration rates are physically natural and convenient for analysis since they are compatible with the scaling approach. Thus we immediately focus on the large time behavior, treat again $m$ as a continuous variable, and turn an infinite set of ODEs, Eqs. (21), into a single PDE:

$$\frac{\partial c}{\partial t} = \frac{\partial^2}{\partial m^2}\, m^a c^2. \tag{23}$$

The scaling solution to this PDE has the form (12) with $\beta = (4-a)^{-1}$; the scaled mass distribution obeys

$$(4-a)(x^a F^2)'' + xF' + 2F = 0. \tag{24}$$

Multiplying (24) by $x$ and integrating once we obtain

$$(4-a)\,\frac{d}{dx}\left(\frac{F^2}{x^{1-a}}\right) + F = 0. \tag{25}$$

This equation admits the special solution $F(x) = 0$ and a one-parameter family of solutions

$$G = \frac{x_0^{2-a}}{(3-a)(4-a)}\, y^{\frac{1-a}{2}}\left(1 - y^{\frac{3-a}{2}}\right), \tag{26}$$

where we have used again the renormalized scaled mass variable $y = x/x_0$. The scaled mass distribution is given by (26) when $0 \leqslant y \leqslant 1$, while $G(y) = 0$ for $y > 1$. The parameter $x_0$ is fixed by normalization:

$$x_0 = (4-a)^{2/(4-a)}(5-a)^{1/(4-a)}. \tag{27}$$

Gathering previous results we arrive at

$$\begin{aligned} c_m(t) &= t^{-\frac{2}{4-a}}\, G_a(y), \\ y &= \frac{x}{x_0} = [(4-a)^2(5-a)t]^{-\frac{1}{4-a}}\, m, \end{aligned} \tag{28}$$

The scaled mass distribution reads

$$G_a(y) = C(a) \times \begin{cases} y^{\frac{1-a}{2}}\left(1 - y^{\frac{3-a}{2}}\right) & 0 \leqslant y \leqslant 1 \\ 0 & y > 1 \end{cases}. \tag{29}$$

The amplitude is

$$C(a) = \frac{x_0^{2-a}}{(3-a)(4-a)} \tag{30}$$

with $x_0(a)$ given by (27).

The density of monomers and the total cluster density exhibit algebraic long time behaviors

$$c_1 = B_1(a)\, t^{-(5-a)/(8-2a)}, \tag{31a}$$

$$N = B(a)\, t^{-1/(4-a)} \tag{31b}$$

with amplitudes

$$B_1(a) = \frac{x_0^{(3-a)/2}}{(3-a)(4-a)}, \quad B(a) = \frac{x_0^{3-a}}{(3-a)^2(4-a)}. \tag{32}$$

These results are applicable when the homogeneity index lies in the range $-\infty < a < 3$. Let us now look at the special values $a = -\infty$ and $a = 3$.

#### 2. *Special cases: $a = -\infty$ and $a = 3$*

When $a = -\infty$, there are only monomers and dimers, and their densities evolve according to

$$\frac{dc_1}{dt} = -2c_1^2, \quad \frac{dc_2}{dt} = c_1^2, \tag{33}$$

from which

$$c_1 = \frac{1}{1+2t}, \tag{34a}$$

$$c_2 = \frac{t}{1+2t}. \tag{34b}$$

The scaling description does not hold in this special case, e.g., the mass attains just two values, and it cannot be treated as a continuous variable.

In contrast, one obtains consistent results by taking the $a \uparrow 3$ limit in (29). The scaled mass distribution becomes

$$c_m(t) = t^{-2} G_3(y), \quad y = \frac{m}{2t} \tag{35}$$

with

$$G_3(y) = \begin{cases} (4y)^{-1}\ln(1/y) & 0 < y < 1 \\ 0 & y \geqslant 1 \end{cases}. \tag{36}$$

Specializing (35) and (36) to $m = 1$ we obtain

$$c_1 \simeq \frac{\ln t}{2t}. \tag{37a}$$

The decay law for the total cluster density also acquires a logarithmic correction:

$$N \simeq \frac{(\ln t)^2}{4t}. \tag{37b}$$

To establish this decay law we use (35) and (36) and find

$$N = \sum_{m \geqslant 1} m c_m(t) \simeq \frac{2t}{t^2}\int_{1/(2t)}^{1} dy\, \frac{\ln(1/y)}{4y}. \tag{38}$$

Computing the integral yields (37b) in the leading order. Note that the integral in (38) diverges in the $y \to 0$ forcing one to keep the lower limit finite. This makes the replacement of the summation by integration somewhat doubtful, but it actually does not cause troubles since the divergence is logarithmic and hence the prediction should be correct. As an independent check one can use the exact rate equation (22) and verify that it is consistent with (37a) and (37b).

#### 3. *Nonscaling regime: $a > 3$*

The scaling solution (28) and (29) becomes ill-defined if $a > 3$. The behavior in this region is nonscaling and hence difficult to probe analytically. Our understanding of this range is incomplete. In Appendix A we present arguments in favor of a rather amusing behavior combining a normal behavior with instantaneous gelation.

## III. EXCHANGE PROCESSES IN LOW SPATIAL DIMENSIONS

Here we probe the behavior of the simplest diffusion-controlled maximally assortative exchange process. First, we recall the definition of the process

(1) Each clusters occupies a single lattice site of a $d$-dimensional lattice.

(2) Clusters hop to neighboring sites, and the hopping rates are mass-independent.

(3) When a cluster hops to a site containing a cluster with the same mass, an exchange (2) instantaneously occurs.

Several clusters can occupy the same site, but all such clusters must have different masses. When a cluster hops to a site that contains another cluster which can participate in an exchange process, the exchange instantaneously occurs; if then another exchange becomes possible, it also occurs instantaneously. Overall, an avalanche of exchanges may happen. (If exchange between clusters of arbitrary masses would be allowed, the resulting diffusion-controlled exchange process would be identical to the diffusion-controlled aggregation process: When a cluster $A_i$ hops to a site with cluster $A_j$, an avalanche of exchanges occur till eventually a single cluster $A_{i+j}$ is formed; this happens instantaneously, so the process is indeed a merging event $A_i \oplus A_j \to A_{i+j}$.)

Diffusion-controlled point-cluster processes with mass-independent hopping rates are still formidable strongly interacting systems, yet the asymptotic behaviors of such processes can often be understood. For instance, in the case of aggregation the critical dimension is known to be $d_c = 2$; the computations of the critical dimension in various diffusion-controlled processes are described, e.g., in Refs. [38] and [28]. The mean-field framework reproduces the asymptotic behavior above the critical dimension, $d > d_c = 2$, e.g., it correctly predicts the $t^{-1}$ decay of the cluster density. In two dimensions, the mean-field framework misses only logarithmic factors, e.g., $N \sim t^{-1} \ln t$. In one dimension, the deviations from the mean-field behavior are most pronounced, e.g., $N \sim t^{-1/2}$. The one-dimensional diffusion-controlled point-cluster aggregation process is actually solvable; see Refs. [39–41].

Let us now consider the maximal assortative exchange in which a monomer can be transferred only between clusters with equal masses: $A_m \oplus A_m \to (A_{m-1}, A_{m+1})$. In principle, an avalanche of exchanges can occur. As an example, consider what happens when $A_2$ hops to a site containing clusters $(A_1, A_2, A_3)$. After the hop there are four clusters $(A_1, A_2, A_2, A_3)$ at a site, and an avalanche of exchanges (participating pairs are shown) leads to

$$A_1 \underbrace{A_2 A_2} A_3 \to \underbrace{A_1 A_1}\,\underbrace{A_3 A_3} \to \underbrace{A_2 A_2}\, A_4 \to A_1 A_3 A_4.$$

Thus effectively $A_2 \oplus (A_1, A_2, A_3) \to (A_1, A_3, A_4)$.

In the long time limit the density of clusters approaches zero and avalanches become exceedingly rare. Indeed, the exchange $A_m \oplus A_m \to (A_{m-1}, A_{m+1})$ results in two clusters at a site, but these clusters quickly separate so that when $t \gg 1$ an occupied lattice site is almost surely occupied by a single cluster.

This problem appears analytically intractable even in one dimension, so we focus on the simplest characteristics, the decay exponents, and rely on heuristic arguments. As a check of such arguments let us first recover the exponents describing the decay of the monomer and cluster densities, which we know from the asymptotically exact analysis; see (19a) and (19b).

When $t \gg 1$, the left-hand side in (10) decays faster than the terms in the right-hand side, so the right-hand side must vanish: $c_{m+1}^2 - 2c_m^2 + c_{m-1}^2 = 0$. The general solution which agrees with convention $c_0 = 0$ is given by $c_m^2 = Am$. Using $c_m \propto \sqrt{m}$ in conjunction with the scaling form (12) we obtain $F(x) \sim \sqrt{x}$ and then $c_m \sim \sqrt{m/t^{5\beta}}$ when $m \ll t^\beta$. Combining $c_1 \sim t^{-5\beta/2}$ and $N \sim t^{-\beta}$ with the exact rate equation

$$\frac{dN}{dt} = -c_1^2, \tag{39}$$

we find $\beta = 1/4$ and therefore

$$c_1 \sim t^{-5/8}, \quad N \sim t^{-1/4}, \tag{40}$$

recovering the exponents in (19a) and (19b).

Consider now the maximal assortative exchange on the one-dimensional lattice. (In one dimension the lattice version is not necessary; we can treat clusters as point particles performing independent Brownian motions with the same diffusion coefficient $D$.) To estimate the decay of the total density, consider two adjacent monomers. They are separated by distance $\ell \sim c_1^{-1}$, and it takes time $T \sim \ell^2/D \sim D^{-1}c_1^{-2}$ for these monomers to meet. Thus the cluster density decays according to

$$\frac{dN}{dt} \sim -\frac{c_1}{T} \sim -Dc_1^3. \tag{41}$$

We now use rate equations similar to (10), but with $c_m^3$ instead of $c_m^2$ in the right-hand side. (This step involves an uncontrolled approximation, but such approximations have been used in various diffusion-controlled processes, and they always lead to correct asymptotic behaviors; see, e.g., Refs. [28,42,43].) In the long time limit we thus obtain $c_{m+1}^3 - 2c_m^3 + c_{m-1}^3 = 0$, from which $c_m \propto \sqrt[3]{m}$. Combining this with (12) we obtain $c_m \sim \sqrt[3]{m/t^{7\beta}}$ when $m \ll t^\beta$. Plugging $c_1 \sim t^{-7\beta/3}$ and $N \sim t^{-\beta}$ into (41) we deduce $\beta = 1/6$. Thus

$$c_1 \sim t^{-7/18}, \quad N \sim t^{-1/6}. \tag{42}$$

In the dimensionally correct form the decay laws read

$$c_1 \sim n_0^{2/9}(Dt)^{-7/18}, \quad N \sim n_0^{2/3}(Dt)^{-1/6}. \tag{43}$$

where $n_0$ is the initial density of monomers.

In two spatial dimensions, we similarly get

$$\frac{dN}{dt} \sim \frac{Dc_1^2}{\ln[c_1 a^2]}, \tag{44}$$

where $a$ is the lattice spacing. The same argument as before leads to $c_{m+1}^2 - 2c_m^2 + c_{m-1}^2 = 0$; more precisely one should write $c_m^2/\ln[c_m a^2]$, but since $c_m$ decays in time according to the same law, the logarithmic factor is independent on $m$ in the leading order. Thus $c_m \propto \sqrt{m}$ and more precisely $c_m \sim \sqrt{m/\mu^5}$, where we use

$$c(m,t) = \mu^{-2} F(x), \quad x = \frac{m}{\mu}. \tag{45}$$

We denote the typical size by $\mu$ rather than $t^\beta$ since in addition to the algebraic factor $\mu$ has a logarithmic factor. Plugging $c_1 \sim \mu^{-5/2}$ and $N \sim \mu^{-1}$ into (44) we find $\mu \sim (t/\ln t)^{1/4}$ leading to

$$c_1 \sim \left(\frac{\ln t}{t}\right)^{5/8}, \quad N \sim \left(\frac{\ln t}{t}\right)^{1/4}. \tag{46}$$

In the dimensionally correct form the decay laws read

$$c_1 \sim n_0^{3/8}\left(\frac{\ell}{Dt}\right)^{5/8}, \quad N \sim n_0^{3/4}\left(\frac{\ell}{Dt}\right)^{1/4} \tag{47}$$

with logarithmic factor

$$\ell = \ln\left(\frac{Dta^8}{n_0^3}\right). \tag{48}$$

Generally for $d < 2$ the proper generalization of (41) reads (see Ref. [28] for such arguments)

$$\frac{dN}{dt} \sim -\frac{c_1}{T} \sim -Dc_1^{1+2/d}. \tag{49}$$

The same arguments as before give $c_m \propto m^{d/(d+2)}$, and after the same steps as above one gets the announced asymptotic behaviors (4) and (7).

TABLE I. The number $J_{\mathcal{M}}$ of jammed states for $1 \leqslant \mathcal{M} \leqslant 20$.

| $\mathcal{M}$ | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| $J_{\mathcal{M}}$ | 1 | 1 | 2 | 2 | 3 | 4 | 5 | 6 | 8 | 10 | 12 | 15 | 18 | 22 | 27 | 32 | 38 | 46 | 54 | 64 |

## IV. FINAL STATES AND EVOLUTION IN FINITE SYSTEMS

In this section we explore the ultimate fate of *finite* systems undergoing a maximally assortative exchange process. In this situation, the difference between maximally assortative and ordinary exchange processes is more pronounced than for infinite systems. Indeed, in ordinary exchange processes all mass eventually accumulates in a single cluster. In a maximally assortative exchange process in a finite system, the final outcome is a jammed state containing clusters of different masses, so the exchange is no longer possible.

### A. Final states

A state $(m_1, \ldots, m_p)$ with cluster masses satisfying

$$1 \leqslant m_1 < \cdots < m_p, \quad m_1 + \cdots + m_p = \mathcal{M} \tag{50}$$

is a jammed state of the system with total mass $\mathcal{M}$. The number of jammed states $J_{\mathcal{M}}$ increases with $\mathcal{M}$. For small $\mathcal{M}$ one easily computes these numbers by hand; Table I shows these numbers in the range $\mathcal{M} \leqslant 20$.

Contemplating about $J_{\mathcal{M}}$, i.e., the number of solutions of (50), one realizes that $J_{\mathcal{M}}$ is the number of partitions of $\mathcal{M}$ into distinct parts. Such partitions appear in combinatorics [44], they are known as strict partitions, and they have been also called Fermi partitions [45]. Strict partitions were first studied by Euler (see Ref. [46]), who expressed the generating function for such partitions through an infinite product

$$\sum_{\mathcal{M}\geqslant 0} J_{\mathcal{M}}\, Q^{\mathcal{M}} = \prod_{k\geqslant 1}(1 + Q^k). \tag{51}$$

(Here we have used the convention $J_0 = 1$.) Using (51) and analyzing the $Q \to 1$ behavior one can extract the asymptotic behavior: $\ln J_{\mathcal{M}} \simeq \pi\sqrt{\mathcal{M}/3}$ as $\mathcal{M} \to \infty$. A more comprehensive analysis [44] gives the Ramanujan asymptotic formula

$$J_{\mathcal{M}} \simeq \frac{1}{4 \times 3^{1/4}\, \mathcal{M}^{3/4}}\, \exp\left[\pi\sqrt{\frac{\mathcal{M}}{3}}\right]. \tag{52}$$

Despite this growth of the total number of jammed states, the fate of the system is surprisingly deterministic, e.g., for the most natural monomers-only initial condition the final state is unique. This outcome is universal, and the details of the exchange process are irrelevant; only the requirement that it is maximally assortative matters. The final state remains the same for many other initial conditions, e.g., if the initial number $N_m(0)$ of clusters of mass $m$ satisfies $N_m(0) > 0$ for all $m = 1, \ldots, m_{\max}$ and $N_m(0) = 0$ for $m > m_{\max}$; only if the initial mass distribution has big "holes" more complicated jammed states become possible.

The final state is particularly simple when the initial mass is a triangular number, $\mathcal{M} = T_n = n(n+1)/2$: In this case, the final state is a collection of clusters of mass $1, \ldots, n$. Let us represent the final states graphically by putting "•" at site $m$ if a cluster of mass $m$ is present and "○" if such a cluster is absent. For instance, if $\mathcal{M} = T_7 = 28$ the final state is

$$\bullet\bullet\bullet\bullet\bullet\bullet\bullet. \tag{53}$$

(We do not show absent clusters with masses exceeding the mass of the largest cluster.) Generally when $\mathcal{M}$ is a triangular number, the final state has no holes. If the initial mass is not a triangular number, the final state has a single hole. If we parametrize $\mathcal{M} = T_n - \ell$ with some $1 \leqslant \ell < n$, the final state

$$\underbrace{\bullet\cdots\bullet}_{\ell-1}\circ\underbrace{\bullet\cdots\bullet}_{n-\ell} \tag{54}$$

has a single hole, namely, the mass $m = \ell$ is absent. For instance, take $\mathcal{M} = 24 = T_7 - 4$; the hole is at mass $m = 4$, and hence the final state is

$$\bullet\bullet\bullet\circ\bullet\bullet\bullet. \tag{55}$$

For small $\mathcal{M}$ one can verify by hand that, independently on the details of the dynamics, the final state is unique and given by (54). The uniqueness is easy to appreciate for two dissimilar extremal dynamics arising in the $a \to -\infty$ or $a \to \infty$ limits; in the general case, the uniqueness can be established via the connection to the one-dimensional Oslo sand-pile model; see Appendix B.

### B. Completion time

The evolution towards the final state depends on the details of the dynamics, and even for the fixed dynamics the duration varies from realization to realization, that is, the time $t_{\text{final}}$ to reach the final state is a random variable. First, we estimate the completion time for the simplest maximally assortative exchange process with mass-independent migration rates. When $\mathcal{M} \gg 1$, the behavior is initially the same as the behavior of the infinite system (Sec. II A). Therefore the total number $N_m$ of clusters of mass $m$ is

$$N_m(t) = \frac{\mathcal{M}}{\sqrt{t}}\, G(y) \tag{56}$$

with $y = m/(80t)^{1/4}$ and $G(y)$ given by (18). These formulas apply when $N_m \gg 1$, but we can employ them up to $N_m = O(1)$ in estimates. Thus we use the criterion $\mathcal{M} \sim \sqrt{t_{\text{final}}}$ to estimate $t_{\text{final}} \sim \mathcal{M}^2$. A similar argument for maximally assortative exchange processes with algebraic migration rates $K(m) = m^a$ gives $\mathcal{M} \sim t_{\text{final}}^{2/(4-a)}$. Therefore the completion time scales as $t_{\text{final}} \sim \mathcal{M}^{2-a/2}$. This is valid when $-\infty < a \leqslant 1$. The population of monomers exceeds the population of clusters of any other mass when $a > 1$. It is still reasonable to estimate $t_{\text{final}}$ from the criterion $N_1(t_{\text{final}}) \sim 1$. Using (31a) we obtain $t_{\text{final}} \sim \mathcal{M}^{\frac{8-2a}{5-a}}$. This matches previous estimate at $a = 1$ and applies in the range $1 \leqslant a < 3$. Overall

$$t_{\text{final}} \sim \begin{cases} \mathcal{M} & a = -\infty \\ \mathcal{M}^{2-a/2} & -\infty < a \leqslant 1 \\ \mathcal{M}^{\frac{8-2a}{5-a}} & 1 \leqslant a < 3 \\ \mathcal{M}\ln\mathcal{M} & a = 3 \\ \mathcal{M} & a > 3 \end{cases}. \tag{57}$$

In the special cases $a = -\infty$ and $a = 3$, estimates of the the completion time given in (57) have been extracted from the asymptotic behaviors (34a) and (37a), respectively. In the

third special case, $a = \infty$, the asymptotic $t_{\rm final} \sim \mathcal{M}$ for the completion time is established below, Eq. (67). In the range $a > 3$, the completion time is bounded by $\mathcal{M} \ln \mathcal{M}$ from above and by $\mathcal{M}$ from below, so the estimate presented in (57) is conjectural (the true asymptotic is perhaps $\ln \mathcal{M}$ times larger).

We now compute the average completion time and its variance in two tractable limits: $a = -\infty$ and $a = \infty$.

### C. The monomer-dimer model ($a = -\infty$)

In each reaction step, the total number of monomers $N_1$ decreases by two: $N_1 \to N_1 - 2$. The rate of this process is $N_1(N_1 - 1)/\mathcal{M}$. The time for each transition step is exponentially distributed, and these transition times are independent random variables. In this simple situation the average, the variance, and all higher cumulants have simple expressions through the rates. For instance,

$$\langle t_{\rm final} \rangle = \sum_{n=1}^{\mathcal{M}/2} \frac{\mathcal{M}}{2n(2n-1)} \tag{58a}$$

if $\mathcal{M}$ is even and

$$\langle t_{\rm final} \rangle = \sum_{n=1}^{(\mathcal{M}-1)/2} \frac{\mathcal{M}}{2n(2n+1)} \tag{58b}$$

if $\mathcal{M}$ is odd. The variance is given by

$$\langle t_{\rm final}^2 \rangle - \langle t_{\rm final} \rangle^2 = \sum_{n=1}^{\mathcal{M}/2} \left[ \frac{\mathcal{M}}{2n(2n-1)} \right]^2 \tag{59a}$$

if $\mathcal{M}$ is even and by

$$\langle t_{\rm final}^2 \rangle - \langle t_{\rm final} \rangle^2 = \sum_{n=1}^{(\mathcal{M}-1)/2} \left[ \frac{\mathcal{M}}{2n(2n+1)} \right]^2 \tag{59b}$$

if $\mathcal{M}$ is odd. The sums in above equations converge, so we can replace the upper limits by infinity since we are interested in asymptotic behaviors. Computing those infinite sums we obtain

$$\frac{\langle t_{\rm final} \rangle}{\mathcal{M}} = \begin{cases} \ln 2 & \mathcal{M} \text{ even} \\ 1 - \ln 2 & \mathcal{M} \text{ odd} \end{cases} \tag{60}$$

and

$$\frac{\langle t_{\rm final}^2 \rangle - \langle t_{\rm final} \rangle^2}{\mathcal{M}^2} = \begin{cases} \frac{\pi^2}{6} - 2\ln 2 & \mathcal{M} \text{ even} \\ \frac{\pi^2}{6} - 3 + 2\ln 2 & \mathcal{M} \text{ odd} \end{cases}. \tag{61}$$

Thus even the asymptotic behaviors depend on whether we take the $\mathcal{M} \to \infty$ limit over even or odd $\mathcal{M}$.

### D. The extremal model ($a = \infty$)

Let us look at the maximally assortative exchange process with $a = \infty$, equivalently a process with infinitely fast migration rates $K(m) = \infty$ for all $m \geqslant 2$. In this extremal model the composition of the system is remarkably simple: When $t < t_{\rm final}$, we still have a lot of monomers, $N_1 \gg 1$, while the rest of the population is composed like (54), namely, $N_m = 1$ for $2 \leqslant m \leqslant m_0(t)$ with at most a single hole inside.

To describe the evolution we notice that the merging of two monomers takes a positive time, and it may trigger an avalanche of other exchanges which proceed instantaneously. Symbolically $1 \oplus 1 \to 2$ and there will be no other instantaneous exchanges if in the preceding configuration the dimer was absent; otherwise $2 \oplus 2 \to (1, 3)$ will occur, perhaps followed by a longer avalanche of instantaneous exchanges. Focusing on the population of monomers we have $N_1 \to N_1 - 2$ in the first case and $N_1 \to N_1 - 1$ in the second. In the long time limit a hole (if it exists) is usually far away, so that $N_1 \to N_1 - 1$ dominates. As long as $N_1 \gg 1$, we can use the rate equation

$$\frac{dc_1}{dt} = -c_1^2 \tag{62}$$

for the monomer density $c_1 = N_1/\mathcal{M}$. This is very simple, but conceptually remarkable, result. Recall that (21) predicts that the density of monomers satisfies

$$\frac{dc_1}{dt} = 2^a c_2^2 - 2c_1^2. \tag{63}$$

It is not immediately obvious how to interpret the first term on the right-hand side of (63) when $a = \infty$. The above analysis shows that we must drop this term and divide by two the prefactor of the second term. This is reminiscent of taking the zero-viscosity limit in turbulence, e.g., in Burgers turbulence one keeps the dissipation rate finite and justifies it by the appearance of shocks (see, e.g., Refs. [47–50]).

Solving (62) we get $c_1 = (1 + t)^{-1}$ and hence

$$N_1 = \frac{\mathcal{M}}{1+t}. \tag{64a}$$

The rest of the mass distribution is

$$N_m = 1, \quad 2 \leqslant m \leqslant m_0(t) \simeq \sqrt{2\mathcal{M}\,\frac{t}{1+t}}. \tag{64b}$$

The largest mass $m_0(t)$ is established from the requirement of mass conservation. In the interesting $1 \ll t \ll \mathcal{M}$ time range where we can employ deterministic rate equations the fraction of mass carried by monomers decreases as $t^{-1}$. We also notice that the total number of clusters

$$\mathcal{N} = N_1 + m_0(t) = \frac{\mathcal{M}}{1+t} + \sqrt{2\mathcal{M}\,\frac{t}{1+t}} \tag{65}$$

has an interesting behavior: The monomers provide the dominant contribution when $t \ll \sqrt{\mathcal{M}}$, while for $t \gg \sqrt{\mathcal{M}}$ the total number of clusters saturates to

$$\mathcal{N}_{\rm final} = \sqrt{2\mathcal{M}}. \tag{66}$$

Combining (64a) and the criterion $N_1 = O(1)$ we estimate the completion time

$$t_{\rm final} \sim \mathcal{M}. \tag{67}$$

It is easy to derive more precise results about the completion time. Indeed, in the most interesting case when $\mathcal{M} \gg 1$, we established that the dominant channel describing the decrease of monomers is $N_1 \to N_1 - 1$, i.e., monomers effectively undergo the coalescence process: $A_1 + A_1 \to A_1$. This stochastic process is well understood and the probability distribution for the completion time is known (see Ref. [28]).

For instance, the leading behaviors of the two basic moments of $t_{\rm final}$ are

$$\langle t_{\rm final}\rangle = \mathcal{M}, \quad \frac{\langle t_{\rm final}^2\rangle}{\langle t_{\rm final}\rangle^2} = \frac{\pi^2}{3} - 2. \tag{68}$$

One can also establish these results directly using the same approach as in deriving (60) and (61).

Fluctuations persist in the thermodynamic limit. To appreciate this assertion it suffices to note that the process $N_1 \to N_1 - 1$ occurs with rate $N_1(N_1-1)/\mathcal{M}$, so its average duration is $\frac{\mathcal{M}}{N_1(N_1-1)}$. Hence last steps when $N_1 = O(1)$ take time $O(\mathcal{M})$; this explains the non-self-averaging nature. Up until the very end, however, the evolution is essentially deterministic.

Overall, the extremal maximally assortative exchange process exhibits a very peculiar behavior. There is no gel (which by definition is a giant cluster containing a finite fraction of mass of the entire system). On the other side, in nongelling systems or nongelling phases, the largest cluster usually has a mass of the order of $\ln \mathcal{M}$, while in the extremal maximally assortative exchange process there are numerous clusters with masses of the order of $\sqrt{\mathcal{M}}$ and these clusters contain most of the mass.

## V. EXCHANGE PROCESSES DRIVEN BY A LOCALIZED INPUT OF MONOMERS

Reaction-diffusion processes driven by localized input often occur in nature, and they are also used in industrial applications. Some of these processes involve a few species of atoms; as examples we mention electropolishing [51], dissolution [52], corrosion [53], and erosion [54]. These processes are rather tractable [55–58] and well understood. Other processes involve numerous interacting subspecies, e.g., clusters in aggregation [42,43,59–62] and ordinary mass exchange [29]; the analysis of these systems is much more challenging and usually relies on nonrigorous tools.

Here we study maximally assortative exchange processes driven by a localized input. The densities $c_m(\mathbf{r}, t)$ obey an infinite system of nonlinear coupled PDEs:

$$\frac{\partial c_m}{\partial t} = K(m+1)c_{m+1}^2 - 2K(m)c_m^2 + K(m-1)c_{m-1}^2 + D_m\nabla^2 c_m + J\delta_{m,1}\delta(\mathbf{r})\theta(t). \tag{69}$$

The first three terms on the right-hand side of (69) account for exchange. The fourth term describes mixing due to diffusion, and the last term represents the input of monomers at the origin ($J$ is the strength of the flux). We are interested in the behavior on distances greatly exceeding the size of the region where monomers are injected, and hence we model the flux using the delta function $\delta(\mathbf{r})$. The Heaviside step function $\theta(t)$ on the right-hand side of (69) asserts that the source is turned at $t = 0$. We assume that the system was initially empty, and we study the evolution at $t > 0$, so below we do not explicitly write $\theta(t) = 1$.

### A. Mass-independent hopping rates

Here we study the model with mass-independent migration rates and diffusion coefficients. For the diffusion-controlled point cluster exchange process on the lattice, the migration rates are proportional to the corresponding hopping rates, $K(m) \sim D_m$, so if diffusion coefficients are mass-independent, the migration rates are also mass-independent. Equations (69) for this model become

$$\frac{\partial c_m}{\partial t} = \nabla^2 c_m + c_{m+1}^2 - 2c_m^2 + c_{m-1}^2 + J\delta_{m,1}\delta(\mathbf{r}), \tag{70}$$

where we have set $K(m) = 1$ and $D_m = 1$.

The mass density $M(\mathbf{r}, t) = \sum_{m\geqslant 1} m c_m(\mathbf{r}, t)$ is now spatially dependent, and it also depends on time. The mass is not affected by the exchange, so it satisfies the diffusion equation with a localized source

$$\frac{\partial M}{\partial t} = \nabla^2 M + J\delta(\mathbf{r}), \tag{71}$$

which can be solved in an arbitrary dimension.

#### 1. Three dimensions

In the most physically relevant three-dimensional case the rate equation approach is applicable. An extra simplification is that in three dimensions (and generally when $d > 2$), the mass density is stationary; more precisely, the mass density coincides with Coulomb potential generated by "charge" $J$, *viz.*,

$$M = \frac{J}{4\pi r}. \tag{72}$$

Since the source is turned on at $t = 0$ and clusters propagate diffusively, the stationarity ceases to hold when $r \sim \sqrt{t}$; the mass density $M(r, t)$ quickly approaches zero as $rt^{-1/2}$ increases.

Some basic quantities do not satisfy closed equations. For instance, the cluster density $N(\mathbf{r}, t) = \sum_{m\geqslant 1} c_m(\mathbf{r}, t)$ evolves according to

$$\frac{\partial N}{\partial t} = \nabla^2 N - c_1^2 + J\delta(\mathbf{r}). \tag{73}$$

It is reasonable to assume that in the long time limit the densities become stationary. More precisely, they are stationary as long as the distance is not too far from the source, namely, $r \ll \sqrt{t}$. In the stationary regime in three dimensions, Eq. (73) becomes

$$\frac{1}{r^2}\frac{d}{dr}\left(r^2\frac{dN}{dr}\right) - c_1^2 + J\delta(\mathbf{r}) = 0. \tag{74}$$

Further, in the stationary regime in three dimensions Eqs. (70) read

$$\frac{1}{r^2}\frac{\partial}{\partial r}\left(r^2\frac{\partial c}{\partial r}\right) + \frac{\partial^2}{\partial m^2}c^2 = 0, \tag{75}$$

where we have replaced $c_{m+1}^2 - 2c_m^2 + c_{m-1}^2$ by the second derivative, which should be asymptotically exact when $m \gg 1$. We seek a solution to (75) in a scaling form

$$c(m, r) = c_m(r) = r^{-2\beta-1}\Phi(x), \quad x = \frac{m}{r^\beta}. \tag{76}$$

The prefactor $r^{-2\beta-1}$ is chosen to be consistent with (72). Indeed,

$$M(r) = \sum_{m\geqslant 1} m c_m(r) \simeq r^{-1} \int_0^\infty dx\, x\Phi(x) \tag{77}$$

has correct spatial dependence; the complete match is obtained if

$$\int_0^\infty dx\, x\Phi(x) = \frac{J}{4\pi}. \tag{78}$$

By inserting (76) into (75) we deduce $\beta = 1/4$ and

$$16(\Phi^2)'' + x^2\Phi'' + 9x\Phi' + 12\Phi = 0. \tag{79}$$

This nonlinear second-order ODE with nonconstant coefficients is soluble. First we notice that (79) admits an integrating factor: Multiplying (79) by $x$ we obtain

$$[16x(\Phi^2)' - 16\Phi^2 + x^3\Phi' + 6x^2\Phi]' = 0,$$

which we integrate and write the outcome as

$$16\,\frac{d}{dx}\left(\frac{\Phi^2}{x}\right) + x\,\frac{d\Phi}{dx} + 6\Phi = 0. \tag{80}$$

[The integration constant equals zero ensuring that $\Phi(x)$ vanishes as $x \to \infty$.] We simplify this first-order ODE by making the transformation

$$\Phi(x) = \sqrt{x}\,\Psi(x). \tag{81}$$

Using $Y = x^{3/2}$ instead of $x$ we find that $\psi(Y) = \Psi(x)$ satisfies

$$3\frac{d\psi}{dY} + \frac{13\psi}{32\Psi + Y} = 0. \tag{82}$$

Instead of $\psi(Y)$ it is convenient to work with inverse function $Y(\psi)$:

$$\frac{13}{3}\,\frac{dY}{d\psi} = -32 - \frac{Y}{\psi}.$$

Solving this equation gives

$$Y = 6(C\,\psi^{-3/13} - \psi), \tag{83}$$

where $C$ is an integration constant. Returning to the original variables we obtain an implicit solution

$$\frac{x^2}{6} = C\left[\frac{x^8}{\Phi^3}\right]^{\frac{1}{13}} - \Phi. \tag{84}$$

The limiting behaviors of the scaled mass distribution are (see also Fig. 1)

$$\Phi \simeq \begin{cases} C^{\frac{13}{16}}\sqrt{x} & x \to 0 \\ (6C)^{\frac{13}{3}}\,x^{-6} & x \to \infty \end{cases}. \tag{85}$$

The constant $C$ is fixed by (78). To compute the integral in (78) we first rewrite it as

$$\int_0^\infty dx\, x\Phi(x) = \frac{2}{3}\int_0^\infty dY\, Y^{\frac{2}{3}}\psi(Y). \tag{86}$$

Equation (83) shows that $0 \leqslant \psi \leqslant \psi_0 = C^{13/16}$. We can now compute the integral in (86) using integration by parts,

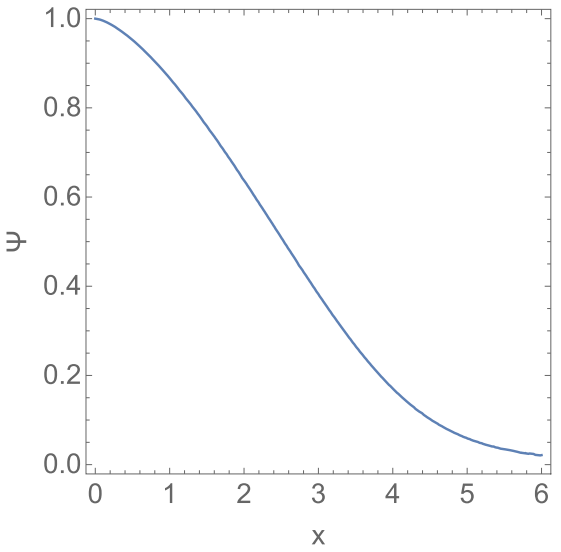


FIG. 1. The renormalized scaled mass distribution $\Psi(x)$ defined via (81). The parameter $C$ in (84) is chosen to be $C = 1$; this corresponds to the flux strength $J = A^{-1}$ with $A$ appearing in (88).

Eq. (83), and straightforward transformations:

$$\begin{aligned}\frac{2}{3}\int_0^\infty dY\, Y^{\frac{2}{3}}\psi(Y) &= \frac{2}{5}\int_0^{\psi_0} d\psi\, Y^{\frac{5}{3}} \\ &= \frac{2}{5}\,6^{\frac{5}{3}}\int_0^{\psi_0} d\psi\,(C\,\psi^{-3/13} - \psi)^{\frac{5}{3}} \\ &= \frac{2}{5}\,6^{\frac{5}{3}}\,\psi_0^{\frac{8}{3}}\int_0^1 du\,(u^{-3/13} - u)^{\frac{5}{3}} \\ &= 6^{\frac{5}{3}}\,C^{\frac{13}{6}}\,\frac{13\sqrt{\pi}\,\Gamma\left(\frac{8}{3}\right)}{40\,\Gamma\left(\frac{19}{6}\right)}.\end{aligned} \tag{87}$$

Combining this with (78) we express the amplitude $C$ through the flux:

$$C = (AJ)^{6/13}, \quad A = \frac{10\,\Gamma\left(\frac{19}{6}\right)}{13\pi^{3/2}\,6^{5/3}\,\Gamma\left(\frac{8}{3}\right)}. \tag{88}$$

Let us also compute the cluster density. We have

$$N(r) = \sum_{m\geqslant 1} c_m(r) \simeq r^{-5/4}\int_0^\infty dx\,\Phi(x). \tag{89}$$

The last integral is computed using the same tricks as in the computation in Eq. (87). We get

$$\begin{aligned}\int_0^\infty dx\,\Phi(x) &= \frac{2}{3}\int_0^\infty dY\,\psi(Y) \\ &= \frac{2}{3}\int_0^{\psi_0} d\psi\, Y \\ &= 4\int_0^{\psi_0} d\psi\,(C\,\psi^{-3/13} - \psi) \\ &= \frac{16}{5}\,\psi_0^2 = \frac{16}{5}\,C^{\frac{13}{8}},\end{aligned}$$

leading to

$$N(r) = \tfrac{16}{5}\,(AJ)^{3/4}\,r^{-5/4}. \tag{90a}$$

The monomer density is found from (76) and the $x \to 0$ asymptotic of $\Phi(x)$ [see (85)] to give

$$c_1(r) = (AJ)^{3/8}\,r^{-13/8}. \tag{90b}$$

As a useful consistency check we note that (90a) and (90b) agree with (74).

### 2. High dimensions

The three-dimensional case is most relevant, but it is amusing to explore the behavior in dimension $d = 4$ and higher. It turns out that the exchange is barely relevant at the "upper" critical dimension $d = d^c = 4$ and asymptotically irrelevant in higher dimensions. To see this let us treat $d$ as a continuous parameter. The rate equation approach is generally applicable when $d > 2$. The mass density is stationary and given by

$$M = \frac{J}{(d-2)\Omega_d\,r^{d-2}}, \tag{91}$$

where $\Omega_d = \frac{2\pi^{d/2}}{\Gamma(d/2)}$ is the "area" of unit sphere $\mathbb{S}^{d-1}$. Equation (91) suggests that the relevant generalization of the three-dimensional scaling form (76) is

$$c(m,r) = c_m(r) = r^{-2\beta-d+2}\Phi(x), \quad x = \frac{m}{r^\beta}. \tag{92}$$

Plugging (92) into

$$\frac{1}{r^{d-1}}\,\frac{\partial}{\partial r}\left(r^{d-1}\,\frac{\partial c}{\partial r}\right) + \frac{\partial^2}{\partial m^2}\,c^2 = 0, \tag{93}$$

we deduce $\beta = 1 - d/4$ and determine the scaled mass density (see Appendix C).

The small mass behavior is again $\Phi \sim \sqrt{x}$, and the monomer density decays according to

$$c_1(r) = (A_d J)^{3/8}\,r^{-(3d+4)/8}. \tag{94}$$

The cluster density is given by

$$N(r) = \tfrac{16}{(3d-4)(4-d)}\,(A_d J)^{3/4}\,r^{-(3d-4)/4}. \tag{95}$$

The decay law (95) can be extracted from (94) and

$$\frac{1}{r^{d-1}}\,\frac{d}{dr}\left(r^{d-1}\,\frac{dN}{dr}\right) - c_1^2 = 0.$$

The scaling form (92) is applicable when $2 < d < 4$. Below two dimensions, $d \leqslant d_c = 2$, we cannot use mean-field rate equations. The upper bound $d < d^c = 4$ is obvious from the above formulas, e.g., the exponent $\beta = 1 - d/4$ must be positive, yet it vanishes at $d = 4$ and becomes negative when $d > 4$. In sufficiently high dimensions, $d > 4$, clusters essentially do not "see" each other. More precisely, some exchange processes occur near the source, but then clusters hardly meet. Therefore both the monomer density and the total cluster density decay similarly to the mass density:

$$c_1 \sim r^{-(d-2)}, \quad N \sim r^{-(d-2)}. \tag{96}$$

The exponent $d-2$ approaches to two as $d \to 4$. Since $\beta = 0$ at the upper critical dimension $d = d^c = 4$, we anticipate that $m$ scales logarithmically. Thus we seek the mass distribution in the form

$$c_m(r) = r^{-2}C_m(\rho), \quad \rho = \ln r. \tag{97}$$

Plugging this ansatz into the governing equations

$$\frac{1}{r^3}\,\frac{d}{dr}\left(r^3\,\frac{dc_m}{dr}\right) + c_{m-1}^2 - 2c_m^2 + c_{m+1}^2 = 0, \tag{98}$$

we obtain

$$2\frac{dC_m}{d\rho} + \frac{d^2C_m}{d\rho^2} = C_{m-1}^2 - 2C_m^2 + C_{m+1}^2. \tag{99}$$

The interesting behavior occurs far from the source where the second term on the right-hand size of (99) is negligible in comparison with the first term. (This is asymptotically true; however, the ratio of these two terms vanishes as $\rho^{-1}$, and since $\rho = \ln r$ the ratio decays very slowly.) Dropping the second term on the right-hand size of (99) we arrive at

$$2\frac{dC_m}{d\rho} = C_{m-1}^2 - 2C_m^2 + C_{m+1}^2. \tag{100}$$

This set of equations can be identified with (10) after the transformation

$$C_m(\rho) = \frac{J}{4\pi^2}\,c_m\!\left(\frac{J\rho}{8\pi^2}\right), \tag{101}$$

which also matches (9) with $\sum_{m\geqslant 1} mC_m = \frac{J}{4\pi^2}$ following from (91) at $d = 4$. Using previous results we deduce that when $y < 1$ the mass density distribution is given by

$$c_m(r) = \sqrt{\frac{5J}{18\pi^2}}\,\frac{\sqrt{y}-y^2}{r^2\rho^{1/2}}, \quad y = m\left(\frac{10J\rho}{\pi^2}\right)^{-1/4}. \tag{102}$$

In particular

$$N(r) = B\,\frac{J^{3/4}}{r^2\rho^{1/4}}, \tag{103a}$$

$$c_1(r) = B_1\,\frac{J^{3/8}}{r^2\rho^{5/8}}, \tag{103b}$$

with

$$B_1 = \frac{5^{3/8}}{3\times 2^{5/8}\times\pi^{3/4}}, \quad B = \frac{5^{3/4}}{9\times 2^{1/4}\times\pi^{3/2}}.$$

### 3. Low dimensions

When $d \leqslant 2$ the rate equation approach becomes erroneous. There are no closed form exact equations for cluster densities, but modified rate equations provide qualitatively correct results and lead to exact scaling. We now outline the results for $d = 1$ and $d = 2$.

In one dimension, we seek the scaling solution in the form $c(m,r) = m^{-\alpha}F(m/r^\beta)$. Plugging this ansatz into the analog of (93), namely, $\frac{\partial^2 c}{\partial r^2} + \frac{\partial^2 c^3}{\partial m^2} = 0$, we deduce the relation $\beta = (1+\alpha)^{-1}$ between the scaling exponents. Estimating $\sum_{m\geqslant 1} mc_m \sim r^{(2-\alpha)\beta}$ and noting that it should scale as $r$ we deduce the second relation $\beta(2-\alpha) = 1$. Using these relations we fix the scaling exponents: $\alpha = \frac{1}{2}$ and $\beta = \frac{2}{3}$. One can also establish proper powers of the source strength

(omitted above). The scaling form reads

$$c_m(r) = \sqrt{\frac{J}{m}}\,\Phi(x), \quad x = \frac{m}{J^{1/3}r^{2/3}}. \tag{104}$$

Using this expression we estimate the cluster density

$$N(r) \sim J^{2/3} r^{1/3}. \tag{105a}$$

Equations (104) and (105a) are consistent with $\frac{d^2N}{dr^2} \sim c_1^3$ if $\Phi(x) \sim x^{5/6}$ as $x \to 0$. Thus

$$c_1(r) \sim J^{2/9} r^{-5/9}. \tag{105b}$$

In two dimensions, we obtain

$$N(r) \sim J^{3/4}\rho^{1/4} r^{-1/2}, \tag{106a}$$

$$c_1(r) \sim J^{3/8}\rho^{5/8} r^{-5/4}, \tag{106b}$$

where we again shortly write $\rho = \ln r$.

#### *4. Total numbers of monomers and clusters*

The total number of monomers $\mathcal{C}_1(t)$ is estimated by integrating the stationary density till $r = \sqrt{t}$. Thus

$$\mathcal{C}_1(t) \sim \int_0^{\sqrt{t}} dr\, r^{d-1} c_1(r).$$

Using (105b), (106b), (90b), and (103b) we obtain

$$\mathcal{C}_1 \sim \begin{cases} J^{2/9} t^{2/9} & d = 1 \\ J^{3/8} t^{3/8} (\ln t)^{5/8} & d = 2 \\ J^{3/8} t^{11/16} & d = 3 \\ J^{3/8} t (\ln t)^{-5/8} & d = 4 \\ Jt & d > 4 \end{cases}. \tag{107}$$

Similarly the total number of clusters is estimated from

$$\mathcal{N}(t) \sim \int_0^{\sqrt{t}} dr\, r^{d-1} N(r).$$

Using (105a), (106a), (90a), and (103a) we obtain

$$\mathcal{N} \sim \begin{cases} J^{2/3} t^{2/3} & d = 1 \\ J^{3/4} t^{3/4} (\ln t)^{1/4} & d = 2 \\ J^{3/4} t^{7/8} & d = 3 \\ J^{3/4} t (\ln t)^{-1/4} & d = 4 \\ Jt & d > 4 \end{cases}. \tag{108}$$

### B. Mass-dependent rates

Diffusion coefficients generally decrease with mass. An algebraic decay, $D_m \sim m^{-\nu}$, often occurs, e.g., the mobility exponents $\nu = 1$ and $\nu = 3/2$ arise in problems involving two-dimensional clusters [63]. For the diffusion-controlled point cluster exchange processes on the lattice, the migration rates are proportional to the hopping rates, $K(m) \sim D_m$, suggesting the study of models with $D_m \sim K(m) \sim m^{-\nu}$. The behavior of such models driven by a local source can be treated using the same scheme as before, namely, assuming the emergence of a stationary mass distribution and the validity of scaling.

As a concrete example, let us consider the model with $D_m = K(m) = m^{-1}$. The rate equations read

$$\frac{\partial c_m}{\partial t} = (m+1)^{-1} c_{m+1}^2 - 2m^{-1} c_m^2 + (m-1)^{-1} c_{m-1}^2 + m^{-1}\nabla^2 c_m + J\delta_{m,1}\delta(\mathbf{r}). \tag{109}$$

The mass density now varies according to

$$\frac{\partial M}{\partial t} = \nabla^2 N + J\delta(\mathbf{r}). \tag{110}$$

In the most physically relevant three-dimensional case, Eq. (110) gives a simple expression

$$N = \frac{J}{4\pi r} \tag{111}$$

for the cluster density in the long time limit.

Let us explore the stationary regime in three dimensions in more detail. We simplify Eqs. (109) to

$$\frac{1}{r^2}\frac{\partial}{\partial r}\left(r^2 \frac{\partial c}{\partial r}\right) + m\,\frac{\partial^2}{\partial m^2}\frac{c^2}{m} = 0 \tag{112}$$

and seek a solution to (112) in a scaling form

$$c(m, r) = c_m(r) = r^{-\beta-1}\Phi(x), \quad x = \frac{m}{r^\beta}. \tag{113}$$

The prefactor $r^{-\beta-1}$ is consistent with (111). Indeed,

$$N(r) = \sum_{m \geqslant 1} c_m(r) \simeq r^{-1} \int_0^\infty dx\, \Phi(x) \tag{114}$$

ensures the correct spatial decay of the cluster density, and the constraint

$$\int_0^\infty dx\, \Phi(x) = \frac{J}{4\pi} \tag{115}$$

provides the complete match with (111). By inserting (113) into (112) we deduce $\beta = 1/3$ and

$$9x(x^{-1}\Phi^2)'' + x^2\Phi'' + 6x\Phi' + 4\Phi = 0, \tag{116}$$

which is integrated to yield $9(x^{-2}\Phi^2)' + \Phi' + 4x^{-1}\Phi = 0$. The implicit solution to this equation reads

$$\tfrac{1}{3}x^2 = C(x^6/\Phi)^{1/5} - \Phi \tag{117}$$

with $C$ being an integration constant. The limiting behaviors of the scaled mass distribution are (see also Fig. 2)

$$\Phi \simeq \begin{cases} C^{\frac{5}{6}} x & x \to 0 \\ (3C)^5\, x^{-4} & x \to \infty \end{cases}. \tag{118}$$

Using (117) we compute the integral in (115) and extract the amplitude $C = (\frac{J}{16\pi})^{2/5}$. In particular,

$$c_1(r) = \left(\frac{J}{16\pi}\right)^{2/5} r^{-5/3}. \tag{119}$$

To determine the spatial size $R$ of the region where the densities have become stationary, we first compute the mass density:

$$M(r) = \sum_{m \geqslant 1} m c_m(r) \simeq r^{-2/3} \int_0^\infty dx\, x\Phi(x).$$

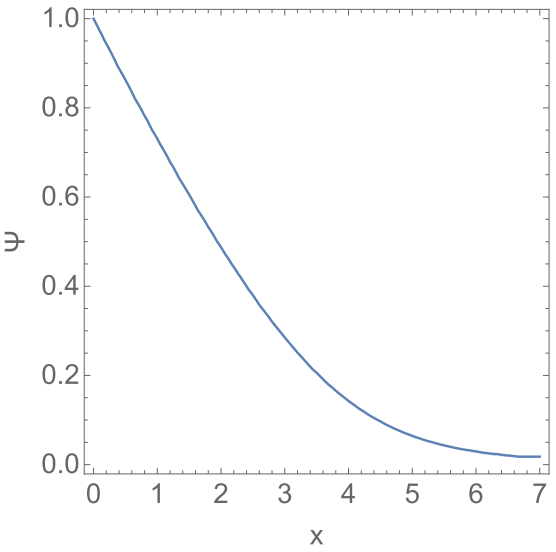


FIG. 2. The renormalized scaled mass distribution defined via $\Psi(x) = x^{-1}\Phi(x)$. The parameter $C$ in (117) is chosen to be $C = 1$; this corresponds to the flux strength $J = 16\pi$.

The integral is calculated using (117) to yield

$$M(r) = \frac{729}{56}\left(\frac{J}{16\pi}\right)^{4/3} r^{-2/3}. \tag{120}$$

Ignoring numerical factors we estimate the total mass

$$\mathcal{M} \sim \int_0^R dr\, r^2 M(r) \sim J^{\frac{4}{3}}\, R^{\frac{7}{3}}.$$

Since $\mathcal{M} = Jt$ we have $R \sim J^{-1/7} t^{3/7}$. Using this result and (111) we estimate the total number of clusters

$$\mathcal{N}(t) \sim \int_0^R dr\, r^2 N(r) \sim JR^2 \sim J^{\frac{5}{7}}\, t^{\frac{6}{7}}. \tag{121}$$

Note also the asymptotic growth law for the total number of monomers

$$\mathcal{C}_1(t) \sim J^{\frac{22}{105}}\, t^{\frac{4}{7}}. \tag{122}$$

## VI. DISCUSSION

Maximally assortative exchange processes are mathematically challenging, and not a single one has been solved so far. For a class of models with algebraic migration rates, $K(m) = m^a$, we relied on scaling to establish the asymptotic behaviors in the $a \leqslant 3$ range. On the physical grounds, reaction rates cannot grow faster than the mass of each reactant, so in an exchange between clusters of the same mass we anticipate that $K(m) \leqslant m^2$, that is, $a \leqslant 2$. Still, it would be interesting to understand the behavior when $a > 3$ where scaling is violate.

When scaling holds, a single typical mass characterizes the mass distribution. The mass distribution in the extremal model ($a = \infty$) has two scales: $m = 1$ corresponding to the monomers and the scale $m_0$ [see (64b)] characterizing the rest of the system. This suggests that when $3 < a < \infty$ there may be two scales, an inner region $m \sim t^{\beta_-}$ and an outer region $m \sim t^{\beta_+}$ with $\beta_+ > \beta_-$. Mass distributions with two, and even three, scales have appeared in a few models of aggregation with uniform input; see Refs. [64–66]. In the present situation, however, we haven't succeeded in establishing a consistent a boundary layer structure of the mass distribution.

A strange feature of the mass distribution in the extremal model is that the outer scale $m_0$ is asymptotically independent on time but depends on the total mass of the system: $m_0 \simeq \sqrt{2\mathcal{M}}$. Thus for infinite systems, $\mathcal{M} = \infty$, the extremal model provides little insight for guessing the behavior when $3 < a < \infty$, or perhaps the message is hidden. The extremal model resembles taking the zero-viscosity limit in turbulence—the terms containing $a = \infty$ formally disappear, yet they affect the evolution.

The behavior of maximally assortative exchange processes substantially differs from the behavior of ordinary exchange processes. To study the interpolation between these two extremes one can introduce parameter $r \in [0, 1]$ measuring the degree of assortatitivity by postulating that the reaction channel (1) operates only when $r \leqslant \frac{i}{j} \leqslant r^{-1}$. With this definition, $r = 1$ corresponds to maximally assortative exchange processes and $r = 0$ corresponds to ordinary exchange processes. The extreme behaviors are known for simple rates rates such as $K_{i,j} = (ij)^{a/2}$; ordinary exchange processes with these rates were studied in Ref. [26], while for maximally assortative exchange processes we recover the rates $K(m) = m^a$. We know that, e.g., the cluster density decays as

$$N \sim \begin{cases} t^{-1/(3-a)} & \text{when } r = 0 \\ t^{-1/(4-a)} & \text{when } r = 1 \end{cases}. \tag{123}$$

These asymptotic results are valid when $a < 3$. One would like to understand how $r$ affects the decay law for the cluster density and behaviors of other quantities.


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## APPENDIX A: MODELS WITH $K(m) = m^a$ WITH $a > 3$

First, we recall that for ordinary exchange processes with generalized product kernels $K_{i,j} = (ij)^\lambda$, it has been shown [26] that (i) scaling holds when $\lambda \leqslant \frac{3}{2}$; (ii) an infinite cluster containing the finite fraction of the entire mass is formed at a finite time if $\frac{3}{2} < \lambda \leqslant 2$; and (iii) an infinite cluster is formed at time $t = 0^+$ when $\lambda > 2$ and gelation is complete, i.e., $c_m(t) = 0$ for all $m \geqslant 1$ at $t > 0$.

For maximally assortative exchange processes with $K(m) = m^a$, scaling holds when $a < 3$. Analogously to ordinary exchange processes one may anticipate gelation when $a > 3$ and complete instantaneous gelation for sufficiently large $a$. We already analyzed (Sec. IV D) the maximally assortative exchange process with $a = \infty$. In this extremal model $K(m) = \infty$ for all $m \geqslant 2$, and the emerging mass distribution has certain features resembling instantaneous gelation, despite of the lack of an infinite cluster. More precisely, in the infinite-system limit the rate equations are mathematically ill-defined for the extremal model. We thus considered the extremal

model with finite total mass $\mathcal{M}$ and established [see (64a) and (64b)] the following mass distribution:

$$c_m = \begin{cases} (1+t)^{-1} & m = 1 \\ \mathcal{M}^{-1} & 2 \leqslant m \leqslant \sqrt{2\mathcal{M}\frac{t}{1+t}} \end{cases}. \tag{A1}$$

Thus in the $\mathcal{M} \to \infty$ limit all cluster densities apart from the monomer density vanish: $c_m(t) = 0$ for all $m \geqslant 2$ at $t > 0$. This is similar to instantaneous gelation but without an infinite cluster.

The knowledge of the behavior in the range $a \leqslant 3$ and at $a = \infty$ allows one to guess the behavior in the $a > 3$ range. For instance, the cluster density decays as

$$N \simeq \begin{cases} B(a)\, t^{-1/(4-a)} & a < 3 \\ (4t)^{-1}(\ln t)^2 & a = 3 \\ t^{-1} & a = \infty \end{cases}. \tag{A2}$$

with $B(a)$ appearing in (32). Equation (A2) suggests the upper and lower bounds for $N(t)$:

$$(4t)^{-1}(\ln t)^2 < N(t) < t^{-1} \tag{A3}$$

when $a > 3$. Logarithmic corrections usually appear in the marginal cases, like $a = 3$ in our situation, so for all $a > 3$ we anticipate a simple decay

$$N \simeq \frac{B^+(a)}{t}. \tag{A4}$$

The unknown amplitude $B^+(a)$ should decrease from $\lim_{a\to 3+0} B^+(a) = \infty$ to $\lim_{a\to\infty} B^+(a) = 1$.

Similarly for the density of monomers we have established the following decay laws:

$$c_1 \simeq \begin{cases} B_1(a)\, t^{-1/(4-a)} & a < 3 \\ (2t)^{-1} \ln t & a = 3 \\ t^{-1} & a = \infty \end{cases} \tag{A5}$$

with $B_1(a)$ appearing in (32). Thus the bounds are

$$(2t)^{-1} \ln t < c_1(t) < t^{-1} \tag{A6}$$

for $a > 3$, and we actually expect a simple decay

$$c_1 \simeq \frac{B_1^+(a)}{t}. \tag{A7}$$

Similarly to $B^+(a)$, the amplitude $B_1^+(a)$ should decrease from $\lim_{a\to 3+0} B_1^+(a) = \infty$ to $\lim_{a\to\infty} B_1^+(a) = 1$, and the inequality $B_1^+(a) \leqslant B^+(a)$ should be valid.

## APPENDIX B: FINAL STATES

In a finite system, the evolution depends on the exchange rules, and even for fixed rules the evolution varies from realization to realization due to the stochasticity of the exchange process. The final state, however, is independent on the order of the exchange events. To appreciate this Abelian property let us first consider two dissimilar extremal dynamics where this property is easy to understand. In the extremal dynamics arising in the $a \to \infty$ limit, the exchanges between clusters heavier than monomers proceed instantaneously. At any time, the mass distribution may have many monomers but otherwise looks like (53)–(55). If there are no holes,

$$\left[\mathcal{M} - \frac{n^2+3n}{2}\right] \underbrace{\bullet\cdots\bullet}_{n}, \tag{B1}$$

where the factor in the square brackets represents the number of monomers (indeed, the rest of the system has mass $\sum_{2\leqslant j\leqslant n+1} j = \frac{n^2+3n}{2}$). If there is a single hole, say, at mass $m = \ell + 1$, the mass distribution is

$$\left[\mathcal{M} - \frac{n^2+3n}{2} + \ell + 1\right] \underbrace{\bullet\cdots\bullet}_{\ell-1} \circ \underbrace{\bullet\cdots\bullet}_{n-\ell}. \tag{B2}$$

It suffices to know the total number of monomers $N_1$, and then there is a unique way of writing $N_1$ either in the form $N_1 = \mathcal{M} - \frac{n^2+3n}{2}$ leading to (B1) or in the form $N_1 = \mathcal{M} - \frac{n^2+3n}{2} + \ell + 1$ with $0 \leqslant \ell < n$ leading to (B2).

One can directly verify (B1) and (B2) for small $n$ and $\ell < n$. Indeed, the evolution is deterministic, and starting with $[\mathcal{M}]$ we obtain $[\mathcal{M}-2]\bullet$. The following mass distributions are

$$\begin{aligned} &[\mathcal{M}-3]\circ\bullet, \\ &[\mathcal{M}-5]\bullet\bullet, \\ &[\mathcal{M}-6]\bullet\circ\bullet, \\ &[\mathcal{M}-7]\circ\bullet\bullet, \\ &[\mathcal{M}-9]\bullet\bullet\bullet, \end{aligned} \tag{B3}$$

etc. Generally one can prove by induction that at any time the mass distribution is given by either (B1) or (B2). Indeed, the evolution of states (B1) and (B2) is obvious already from examples given in (B3). For instance, the daughter state of (B2) is

$$\left[\mathcal{M} - \frac{n^2+3n}{2} + \ell\right] \underbrace{\bullet\cdots\bullet}_{\ell-2} \circ \underbrace{\bullet\cdots\bullet}_{n-\ell+1}$$

when $1 < \ell < n$ and (B1) if $\ell = 1$, while the daughter state of (B1) is

$$\left[\mathcal{M} - \frac{n^2+3n}{2} - 1\right] \underbrace{\bullet\cdots\bullet}_{n-1} \circ \bullet.$$

It is easy to see that the jammed states are unique and given by (54) for the dynamics corresponding to $a \to \infty$.

For the extremal dynamics arising in the $a \to -\infty$ limit, at the first stage when there are monomers in the system we use the original time variable, $t_1 = t$, so only monomers are active. At the end of this stage the mass distribution is

$$\begin{cases} \circ[\mathcal{M}/2] & \mathcal{M} \text{ even} \\ \bullet[(\mathcal{M}-1)/2] & \mathcal{M} \text{ odd} \end{cases}. \tag{B4}$$

Then we use the time variable $t_2 = 2^a t$, so that dimers participate in exchanges, the merging of monomers which are formed after two exchange events involving dimers is instantaneous, while clusters of mass $m > 2$ are passive. At the end of this second stage the mass distribution is

$$\begin{cases} \bullet\circ[(\mathcal{M}-1)/3] & \mathcal{M} \equiv 1 \pmod 3 \\ \circ\bullet[(\mathcal{M}-2)/3] & \mathcal{M} \equiv 2 \pmod 3 \\ \bullet\bullet[(\mathcal{M}-3)/3] & \mathcal{M} \equiv 0 \pmod 3 \end{cases}. \tag{B5}$$

The interesting part of the mass distribution preceding the trimers has at most one hole.

During the third stage we take $t_3 = 3^a t$ as the new time variable and observe that trimers participate in exchanges, and the merging of monomers and exchanges of dimers are instantaneous (although the former are still infinitely faster than the latter), while clusters of mass $m > 3$ are passive. Proceeding along these lines one can verify that at the end of every stage the interesting part of the mass distribution has at most one hole.

Thus for these two dissimilar extremal dynamics the final jammed states are the same. This hints on the validity of the Abelian property of the maximally assortative exchange processes. It suffices to notice that our process is essentially identical to the one-dimensional Oslo rice-pile model [67], after one identifies the spatial coordinate of the Oslo model with the mass variable in the exchange process, and the height variable $H_m$ in the Oslo model with the total number of clusters with mass $\geqslant m$. The Abelian property for the one-dimensional Oslo model is established in Ref. [68].

## APPENDIX C: MASS DENSITY IN HIGH DIMENSIONS ($d > 2$)

To determine the scaled mass density in $d$ dimensions, we insert the scaling ansatz (92) into the governing equation (93) and deduce the scaling exponent $\beta = 1 - d/4$ together with the ODE for the scaled mass density

$$\left(1-\frac{d}{4}\right)^{-1}(\Phi^2)'' + \left(1-\frac{d}{4}\right)x^2\Phi'' + \left(3-\frac{d}{4}\right)x\Phi' + d\Phi = 0. \tag{C1}$$

Multiplying by $x$ and integrating we obtain

$$\left(1-\frac{d}{4}\right)^{-2}\frac{d}{dx}\left(\frac{\Phi^2}{x}\right) + x\,\frac{d\Phi}{dx} + \frac{2d}{4-d}\,\Phi = 0. \tag{C2}$$

Making the same transformation (81) and using again $Y = x^{3/2}$ we obtain

$$Y = \frac{6}{4-d}(C\,\psi^{-\delta} - \psi), \quad \delta = 3\,\frac{4-d}{4+3d}, \tag{C3}$$

indicating that the results are applicable when $d < 4$.

The same computation as in Eq. (87) allows one to fix the amplitude:

$$\begin{aligned}\frac{J}{(d-2)\Omega_d} &= \frac{2}{5}\int_0^{\psi_0} d\psi\, Y^{\frac{5}{3}} \\ &= \frac{2}{5}\left(\frac{6}{4-d}\right)^{\frac{5}{3}}\int_0^{\psi_0} d\psi\,(C\,\psi^{-\delta} - \psi)^{\frac{5}{3}} \\ &= \frac{2}{5}\left(\frac{6}{4-d}\right)^{\frac{5}{3}}\psi_0^{\frac{8}{3}}\int_0^1 du\,(u^{-\delta} - u)^{\frac{5}{3}} \\ &= \frac{2}{5}\left(\frac{6}{4-d}\right)^{\frac{5}{3}} C^{\frac{4+3d}{6}}\,\frac{\Gamma(\Delta)\,\Gamma\left(\frac{8}{3}\right)}{(1+\delta)\,\Gamma\left(\Delta+\frac{8}{3}\right)},\end{aligned}$$

where $\Delta = (1+\delta)^{-1} - 5\delta/3$. Thus

$$C = (A_d J)^{6/(4+3d)} \tag{C4}$$

with a cumbersome expression for the numerical factor $A_d$ following from the above formulas.


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