PHYSICAL REVIEW E **83**, 031123 (2011)

Weibull-type limiting distribution for replicative systems

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(Received 17 December 2010; revised manuscript received 5 February 2011; published 21 March 2011)

The Weibull function is widely used to describe skew distributions observed in nature. However, the origin of this ubiquity is not always obvious to explain. In the present paper, we consider the well-known Galton-Watson branching process describing simple replicative systems. The shape of the resulting distribution, about which little has been known, is found essentially indistinguishable from the Weibull form in a wide range of the branching parameter; this can be seen from the exact series expansion for the cumulative distribution, which takes a universal form. We also find that the branching process can be mapped into a process of aggregation of clusters. In the branching and aggregation process, the number of events considered for branching and aggregation grows cumulatively in time, whereas, for the binomial distribution, an independent event occurs at each time with a given success probability.

DOI: 10.1103/PhysRevE.83.031123 PACS number(s): 05.40.−a, 89.75.Fb, 05.65.+b

I. INTRODUCTION

Various systems in nature exhibit skew distributions, which are properly fit to the Weibull distribution [1] as well as lognormal and power-law distributions; relations between those skew distributions have been discussed recently [2]. In particular, the Weibull distribution, despite the simple mathematical form, particularly for the cumulative distribution $F(x) = 1 - \exp[-(x/\eta)^{\beta}]$, has flexible shapes depending on the value of β and is widely used to describe size distributions of, e.g., material strengths [1,3], cloud droplets [4], biological tissues [5], ocean wave heights [6], and wind speeds [7]. However, there still lacks an appropriate explanation of its ubiquitous emergence, in sharp contrast with the Gaussian distribution, let aside the case-by-case derivation, such as material breaking with the weakest element [1], entropy maximization [4], material fragmentation [8], and extreme value statistics [9,10].

It is well known that the binomial distribution results from success events for given independent trials with the success probability p given. When the success is a rare event (i.e., p is small), it reduces to the Poisson distribution. According to the central limit theorem [11], (discrete) binomial and Poisson distributions approach the (continuous) Gaussian distribution in the limit of large trial numbers. In a similar spirit, here, we derive a continuous Weibull-like distribution from the discrete Galton-Watson branching process, motivated by cell replication in a tissue [5]. The branching process can serve as a basic model to describe discrete events having two possibilities, e.g., replication and nonreplication or nucleation and non-nucleation. The generating function for this distribution was first obtained in the seminal work of general branching processes [12,13]. Specifically, asymptotics were derived in the more general case of multiple replicates and extinction processes at each stage of the process added to possible immigration events (see, for example, Ref. [14]), but little is known about the shape of the distribution itself relative to other standard distributions, except for a few very specific cases where the limiting distribution can be computed exactly through the use of a rational form for the generating function at the first stage of the process and which usually leads to a simple exponential function. Here, we find that it is approached by the Weibull distribution in rather a wide and realistic range of the replication parameter p, making the two distributions surprisingly indistinguishable in practice.

This paper consists of four sections and an Appendix. In Sec. II, cell replication is described in terms of a branching process. The stationary distribution of the branching process is obtained, and its general properties are discussed. Results of Monte Carlo simulations are also presented. Section III examines the relation between the distributions for different replication probabilities and probes the scaling with the help of an ansatz, which is justified from the exact series expansion. Finally, Sec. IV discusses and summarizes the results. In the Appendix, all the moments of the distribution are obtained analytically from the recurrence relation of the generating function.

II. CELL REPLICATION AND BRANCHING PROCESS

For the binomial distribution, an independent event occurs at each time with given success probability. In cell replication, on the other hand, the number of replication events in consideration depends on the current cell number of a tissue. For example, even if there exists just a single mother cell initially, it may replicate from time to time, and there may occur many replications of the mother and daughter cells. Accordingly, we consider the probability distribution $f_n(l)$ of tissues with size (i.e., the number of cells) l at given time step n, which satisfies the normalization condition $\sum_{l=1}^{2^n} f_n(l) = 1$ with the maximum possible cell number in the tissue after the nth replication given by 2^n. Note that this process can be described in terms of a branching process with the branching probability p, as illustrated in Fig. 1. Each graph in the figure, where sites in the nth row represent cells at the time step n, corresponds to one possible configuration of cell growth for the given duration. Thus, each graph starts from a single site

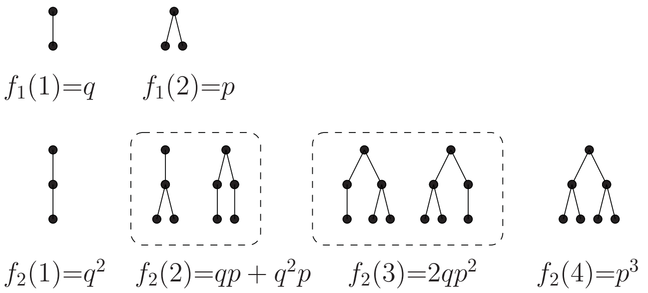

FIG. 1. Cell replication graphs for a branching process. Cell number configurations at time steps $n = 1$ and 2 are plotted with the replication probability at each step given by p; $q \equiv 1 - p$ corresponds to the probability that the cell does not replicate.

in the first row (i.e., a single mother cell initially); sites may replicate or not, giving birth to new sites at successive time steps (here, the time step is fixed to be a constant).

It is useful to consider the generating function for the distribution f_n at time n in the branching process [12,15],

$$g_n(z) = \sum_{l=1}^{2^n} f_n(l) z^l. \tag{1}$$

For example, the kth moment at time n, defined to be $\sum_{l=1}^{2^n} f_n(l) l^k$, can be computed by successively differentiating the generating function: $(z\frac{d}{dz})^k g_n(z)|_{z=1}$ with $g_n(1) = 1$ for all n (see the Appendix for the derivation of all the moments). In the following, for simplicity, we will impose $f_n(l) = 0$ for $l > 2^n$. At the initial time ($n = 0$), the system contains only one element, leading to $g_0(z) = z$. Since the distribution f_{n+1} is related to the preceding one f_n via combinatorial relations, it is easy to show that the generating function satisfies the nonlinear recursion equation $g_n(z) = g_1[g_{n-1}(z)]$ for $n \geqslant 1$, where $g_1(z) = qz + pz^2$. This equation provides a recursive function for the newly generated sites, which are all independent, with the generating function $g_1(z)$.

From this relation, we can deduce that the total number $N(n)$ of configurations or graphs at (discrete) time n satisfies the recurrence relation $N(n + 1) = N(n)[1 + N(n)]$, with the initial condition $N(0) = 1$, and grows rapidly in time. Indeed, this relation can be obtained easily from the observation that $N(n)$ is equal to $g_n(1)$ with p and q replaced formally by unity. Therefore, $N(n)$ satisfies the same relation as $g_n(1)$ above. It is also manifested from the physical point of view: Given $N(n)$ graphs at time n, there are two possible ways to generate graphs at time $(n + 1)$. (i) In the case of nonreplication of the original site, we simply have $N(n)$ graphs; (ii) in the case of replication of the same site, we can attach a total of $N(n)^2$ graphs to the two offspring. As a result, we obtain $N(n) + N(n)^2$ possible configurations at time $(n + 1)$. This can be checked in Fig. 1 for the first few graphs: $N(0) = 1$, $N(1) = 2$, $N(2) = 6$, and so on.

Because a tissue of size l results from $(l - 1)$-times proliferation starting from a single cell (see Fig. 1), the recurrence relation

$$g_{n+1}(z) = q g_n(z) + p g_n^2(z) \tag{2}$$

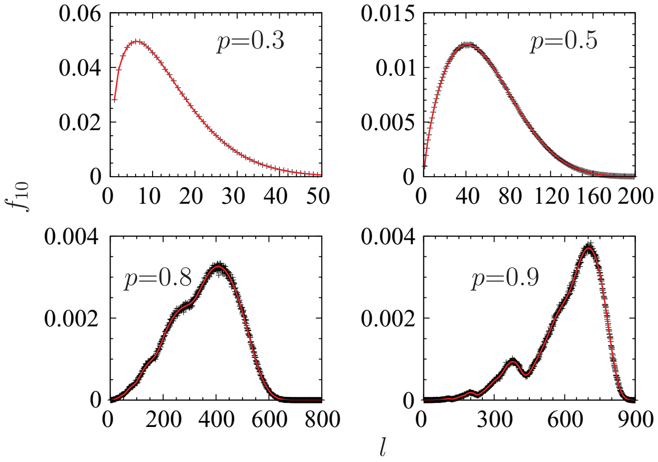

FIG. 2. (Color online) Comparison of the tissue size distribution $f_n(l)$ at time $n = 10$, for the replication probability $p = 0.3$, 0.5, 0.8, and 0.9. Solid lines, analytical and, + signs, simulation results agree perfectly, displaying multimodal shapes for large values of p. In the Monte Carlo simulations of the branching process, starting from a single cell, we let every cell replicate with a given replication probability at each Monte Carlo step. Data have been obtained from 10^6 trial moves.

leads to the recursive relation for the distribution $f_n(l)$ by simply identifying the coefficients of z^l on the left and right sides of the last expression,

$$f_{n+1}(l) = q f_n(l) + p \sum_{k=1}^{l-1} f_n(k) f_n(l-k). \tag{3}$$

Namely, a tissue of size l at time $n + 1$ can be generated in two ways: (i) no replication at the first time step followed by producing l descendants at the following n time steps and (ii) replication at the first time step followed by producing k descendants from one offspring and $l - k$ descendants from the other offspring at the following n time steps.

The size distribution, computed from Eq. (3), is exhibited in Fig. 2, together with that from Monte Carlo simulations, manifesting perfect agreement. It is of interest that Eq. (3) can be mapped into a process of random aggregation of clusters with the aggregation probability p. Thus, using $q = 1 - p$ and $\sum_{k=1}^{2^n} f_n(k) = 1$, we obtain

$$\Delta f_n(l) = -p \sum_{k=1}^{2^n} f_n(l) f_n(k) + p \sum_{k=1}^{l-1} f_n(k) f_n(l-k), \tag{4}$$

with $\Delta f_n(l) \equiv f_{n+1}(l) - f_n(l)$. Therefore, a cluster of size l can be formed from aggregation of a cluster of size k and a cluster of size $(l - k)$ with the aggregation probability p.

Figure 3 shows the normalized size distribution for $p = 0.3$ at several time steps $n = 10$, 12, and 14. Remarkably, when size l is rescaled by the factor $(1 + p)^n$, the distributions collapse into a single curve independent of n, suggesting the presence of a stationary distribution for the branching process [12]. Indeed, the average cell number in a tissue after the nth replication with the replication probability p is given by $(1 + p)^n = \sum_{l=1}^{2^n} l f_n(l)$. Note that $f_n(l)$ may be regarded as a continuous function $f_n(x)$ when n is large (see Fig. 3). Since

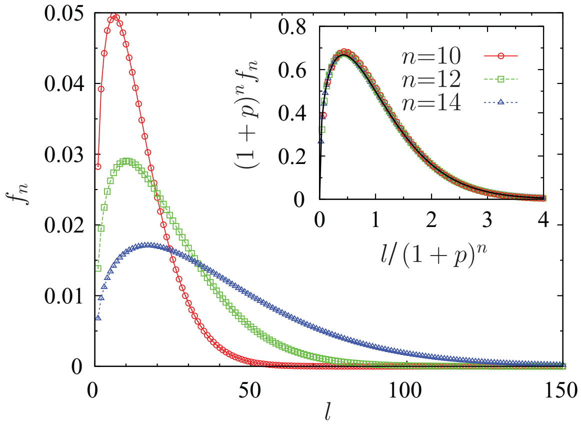

FIG. 3. (Color online) Weibull distribution of tissue sizes in the cell replication process. Cell-number distribution for $p = 0.3$ at three different time steps. Distributions versus the rescaled size are plotted in the inset; the collapse is fitted with a Weibull function with the shape parameter $\beta = 1.37$, represented by the black line.

the average cell number after the $(n-1)$th replication is $(1+p)^{n-1}$, we have the scaling relation

$$\int dx\, x f_n(x) = (1+p)\int dx' x' f_{n-1}(x') = \int dx (1+p)^{-1} x f_{n-1}[(1+p)^{-1}x], \quad (5)$$

which is consistent with the fact that the distribution in the long-time limit can be described by a time-independent stationary function $f(\tilde{x})$ with the rescaled size $\tilde{x} = x/\eta$ and the scale parameter $\eta = a(1+p)^n$. The scale factor a introduced here depends, in particular, on the replication probability p via boundary conditions, as discussed later.

Finally, a quantity of interest is given by the Laplace transform $\hat{f}(\lambda) \equiv \int_0^\infty d\tilde{x} e^{-\lambda\tilde{x}} f(\tilde{x})$, for which the recursive relation in Eq. (3) reads [12]

$$\hat{f}[(1+p)\lambda] = q\hat{f}(\lambda) + p\hat{f}(\lambda)^2. \quad (6)$$

Equation (6) takes the form of a Poincaré-type equation [16], which is directly related in property to Mahler functional equations [17] via an appropriate change of variables [18].

In the limit of small p where cells replicate very rarely, one may expand Eq. (6) as $\hat{f}[(1+p)\lambda] \approx \hat{f}(\lambda) + p\lambda\hat{f}'(\lambda)$ to obtain the differential equation,

$$\lambda\hat{f}'(\lambda) = \hat{f}(\lambda)^2 - \hat{f}(\lambda), \quad (7)$$

with the initial conditions $\hat{f}(0) = 1$ and $\hat{f}'(0) = -a^{-1}$. The solution reads $\hat{f}(\lambda) = a(\lambda + a)^{-1}$, the inverse Laplace transform of which is given by the simple exponential function $f(\tilde{x}) = a\exp(-a\tilde{x})$. With the constraint $F(1) = 1 - e^{-1}$ on the cumulative distribution $F(\tilde{x}) \equiv \int_0^{\tilde{x}} d\tilde{x}' f(\tilde{x}')$, we obtain the scaling factor $a = 1$, and, therefore, $f(\tilde{x}) = \exp(-\tilde{x})$. In the opposite case of $p = 1$ where every cell replicates, we have $\hat{f}(2\lambda) = \hat{f}(\lambda)^2$, with the simple solution satisfying the initial conditions given by $\hat{f}(\lambda) = \exp(-\lambda/a)$. This leads to the Dirac δ distribution $f(\tilde{x}) = \delta(\tilde{x} - a^{-1})$ and the Heaviside cumulative distribution $F(\tilde{x}) = \theta(\tilde{x} - a^{-1})$. The constraint on $F(1)$ again imposes $a = 1$.

III. SCALING OF THE SIZE DISTRIBUTION

In this section, we consider the general case of $0 < p < 1$. As for the unique stationary distribution $f(\tilde{x})$ for given p, one may question whether there exists any relation between the distribution $f(\tilde{x})$ corresponding to two different replication probabilities p and p_0, respectively. Since the final stationary distributions result from the same branching process, albeit with different branching probabilities, they are expected to qualitatively share the same properties.

To probe the scaling of the tissue size in the replication process, in Fig. 4, we display the cumulative distribution for the replication probability $p = 0.1$, 0.3, and 0.5. Note that the scale factor a in the rescaling of the size has been adjusted to satisfy the condition $F(\tilde{x}{=}1) = 1 - e^{-1}$. To probe the functional relations between the cumulative distributions for different values of p under the constraints for F, we consider the change of variable $\tilde{x} \to \tilde{x}^\beta$, as the simplest possibility, where the exponent $\beta = \beta(p)$ is then adjusted to make all curves for considered values of p collapse onto a single curve. This ansatz indeed leads to the collapse of different cumulative distributions into a unique distribution $F_0(\tilde{x}) = 1 - e^{-\tilde{x}}$, as shown in the inset. Therefore, the new variable $\tilde{x}^\beta$ determines the functional form of $F(\tilde{x})$, at least for the numerical cases considered. Indeed, using the known result $F(\tilde{x}) = 1 - e^{-\tilde{x}}$ in the limit $p \to 0$, we obtain $F(\tilde{x}) = 1 - e^{-\tilde{x}^\beta}$ with good precision for $p > 0$, which leads to the Weibull distribution.

The ansatz of the scaling $\tilde{x}^\beta$ can be justified from the exact series expansion of the distribution $f(\tilde{x})$. Multiplying both sides of Eq. (6) by $\exp(-i\lambda\tilde{x})$, performing the rotation $\lambda \to i\lambda$, and integrating over λ along the real axis, we obtain

$$\frac{1}{1+p} f[(1+p)^{-1}\tilde{x}] = qf(\tilde{x}) + p\int_0^{\tilde{x}} d\tilde{x}' f(\tilde{x}') f(\tilde{x} - \tilde{x}'). \quad (8)$$

It can be shown that $f(\tilde{x})$ admits a series expansion in powers of $\tilde{x}$ consistent with the previous relation. In particular, $f(\tilde{x})$ vanishes at the origin as $f(\tilde{x}) \approx a_0\tilde{x}^{\beta-1}$, with some constant a_0 and exponent $\beta = -[\ln(1+p)]^{-1}\ln(1-p) \geqslant 1$ [12]. Here,

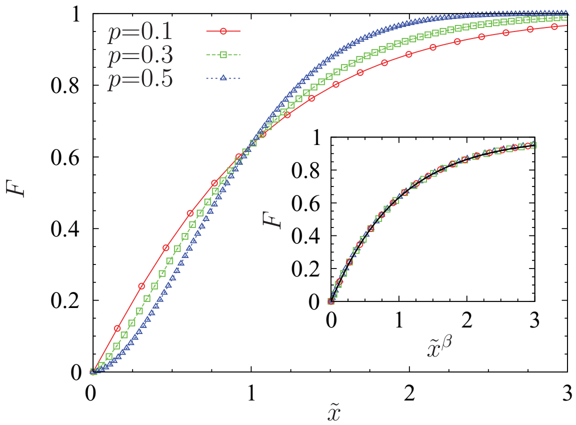

FIG. 4. (Color online) Cumulative distribution for $p = 0.1$, 0.3, and 0.5. The rescaled size is given by $\tilde{x} = a^{-1}(1+p)^{-n} l$ with $n = 20$, where a is the scale factor to adjust $F(1) = 1 - e^{-1}$. The black line in the inset describes rescaled cumulative distribution functions, disclosing the collapse into the function $F(\tilde{x}) = 1 - e^{-\tilde{x}^\beta}$.

this analysis can be extended to consecutive terms to yield the following expansion:

$$f(\tilde{x}) = \tilde{x}^{\beta-1} \sum_{k \geqslant 0} a_k \tilde{x}^{k\beta}, \tag{9}$$

where identifying the powers in Eq. (8) gives the recursion relation for the coefficients,

$$(q^{k+1} - q)a_k = p \sum_{l=0}^{k-1} B[\beta(1+l), \beta(k-l)] a_l a_{k-1-l}, \tag{10}$$

with the β function $B(x,y) = \int_0^1 dt t^{x-1}(1-t)^{y-1}$. Here, a_0 is the only unknown parameter depending on boundary conditions, since Eq. (10) implies the proportionality relation $a_k \propto a_0^{1+k}$.

From these results, it is easy to see that $f(\tilde{x})$ can be cast into the form

$$f(\tilde{x}) = a_0 \tilde{x}^{\beta-1} \mathcal{F}(a_0 \tilde{x}^{\beta}), \tag{11}$$

with the unique regular expansion of the scaling function $\mathcal{F}(\tilde{x}) = \sum_{k \geqslant 0} \tilde{a}_k \tilde{x}^k$, where $\tilde{a}_k$ satisfies the relation in Eq. (10) but with the initial term $\tilde{a}_0 = 1$; this uniquely determines all the other coefficients $\tilde{a}_k$ for $k \geqslant 1$. The cumulative distribution $F(\tilde{x})$ is equal to a scaling function of the variable $a_0 \tilde{x}^{\beta}$ alone since

$$F(\tilde{x}) = \frac{1}{\beta} \sum_{k \geqslant 0} \frac{\tilde{a}_k}{k+1} (a_0 \tilde{x}^{\beta})^{k+1} = \mathcal{G}(a_0 \tilde{x}^{\beta}), \tag{12}$$

where $\mathcal{G}$ is, like $\mathcal{F}$, uniquely defined by the coefficients $\tilde{a}_k$. The parameter a_0 is defined according to the constraint $F(1) = 1 - e^{-1}$ and can be related to a via the equation for the first moment $\int_0^{\infty} d\tilde{x} \tilde{x} f(\tilde{x}) = a^{-1}$. This relation simply gives $a_0 = a^{\beta} [\int_0^{\infty} u^{1/\beta} \mathcal{F}(u) du]^{\beta}$. Note that the cumulative distribution F is a function of the variable $\tilde{x}^{\beta}$ up to a scaling factor, which is also true for the Weibull distribution $F(\tilde{x}^{\beta}) = 1 - \exp(-\tilde{x}^{\beta})$ with $\tilde{x} = x/\eta$. In the limit of small p, β is close to unity, and one can show that the expansion coefficients satisfying Eq. (10) are approximately given by $\tilde{a}_k = (-1)^k/k!$. Therefore, $\mathcal{G}(a_0 \tilde{x}^{\beta}) \approx 1 - \exp(-a_0 \tilde{x}^{\beta})$ is indeed close to the Weibull distribution.

The previous results show that the distribution can be expanded as a series and vanishes as a power law with the exponent $\beta - 1$ related to the replication probability p. In the opposite case of large $\tilde{x}$, the integral equation (8) can be analyzed. Since we expect $f(\tilde{x})$ to decrease with $\tilde{x}$ and assume the stretched exponential behavior $f(\tilde{x}) \approx \exp(-a_{\infty} \tilde{x}^{\beta'})$ with a_{∞} constant, we observe that, in Eq. (8), the left-hand-side term $f[(1+p)^{-1}\tilde{x}] \propto \exp[-a_{\infty}(1+p)^{-\beta'} \tilde{x}^{\beta'}]$ is dominant over the first term $f(\tilde{x})$ on the right-hand side. The last term can be analyzed by means of the saddle point analysis for the function $\tilde{x}'^{\beta'} + (\tilde{x} - \tilde{x}')^{\beta'}$ appearing in the exponential contribution. The saddle point, obtained by taking the extremum of this quantity with respect to $\tilde{x}'$, corresponds to the middle point of the integration $\tilde{x}' = \tilde{x}/2$. Therefore, the overall integral gives a dominant contribution proportional to $\exp[-2a_{\infty}(\tilde{x}/2)^{\beta'}]$. The ansatz is consistent if the two coefficients satisfy the relation $(1+p)^{-\beta'} = 2^{1-\beta'}$. This results in a new exponent $\beta' = \ln 2 [\ln 2 - \ln(1+p)]^{-1}$ valid in the asymptotic limit; this was also obtained in Ref. [12].

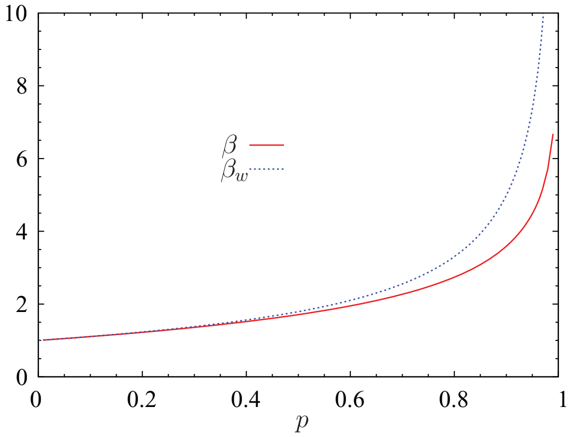

FIG. 5. (Color online) Relation between exponent β_w of the Weibull distribution and the replication probability p of the branching process. The exponent β is also plotted for comparison.

IV. DISCUSSION

It has been shown that the replication process of cells with not too large replication probability ($p \lesssim 0.5$) gives rise to a distribution extremely close to the Weibull function. The parameters of the Weibull distribution can then be related to the first two moments of the distribution function $f_n(x)$: $(1+p)^n = \eta \Gamma(1 + \beta_w^{-1})$ and $2(1+p)^{2n-1} = \eta^2 \Gamma(1 + 2\beta_w^{-1})$, where $\Gamma(x)$ is the gamma function. This leads to the following relation between the replication probability p and the shape parameter β_w of the Weibull distribution:

$$p = 2 \frac{\Gamma^2\left(1 + \beta_w^{-1}\right)}{\Gamma\left(1 + 2\beta_w^{-1}\right)} - 1, \tag{13}$$

which is exhibited in Fig. 5. In addition, the scale factor a in the rescaling parameter $\eta = a(1+p)^n$ is given by $a = \Gamma^{-1}(1 + \beta_w^{-1})$. Note that the exponents β and β_w are hardly distinguishable for $p \lesssim 0.5$, where the scaling function $\mathcal{F}$ is asymptotically similar to an exponential. This suggests that the distribution in Eq. (11) belongs to the Weibull class for small p. This regime applies to many cases in nature that a certain event, such as replication or nucleation, occurs with probability less than 50% at a given time unit. On the other hand, the replication process with a large value of p results in a different type of distribution, e.g., a multimodal distribution (see Fig. 2).

In conclusion, the branching process provides a general mechanism of the Weibull distribution with $\beta \lesssim 2$, corresponding to the branching probability $p \lesssim 0.5$. We also have found that the branching process can be mapped into a process of aggregation of clusters. A recent example includes the protein aggregation process with fission, where the Weibull distribution with $\beta \sim 2$ emerges as a stationary solution [19].

ACKNOWLEDGMENTS

One of us (M.Y.C.) thanks the Département de Physique de la Matière et des Matériaux, Institut Jean Lamour, at Université Henri Poincaré, where part of this work was carried out, for hospitality during his stay. This work was supported by the intramural research program of the NIH, NIDDK (J.J.), and by the NRF through the Basic Science Research Program (Grant No. 2009-0080791) (M.Y.C.).

APPENDIX: MOMENT EXPRESSION

The functional equation, given by Eq. (6), for the Laplace transform of the size distribution can also be derived with the help of moments of the distribution. Here, we briefly mention how to recursively evaluate all these moments starting from the generating function. From the relation

$$\langle x\rangle_n = z\frac{d}{dz}g_n(z)|_{z=1} = zg_1'[g_{n-1}(z)]g_{n-1}'(z)|_{z=1}, \quad \text{(A1)}$$

with the initial condition $g_0'(1)=1$, the average number of elements is simply

$$\langle x\rangle_n = (1+p)\langle x\rangle_{n-1} = (1+p)^n,$$

whereas, the second moment is given by

$$\langle x^2\rangle_n = zg_n'(z) + z^2 g_n''(z)|_{z=1}. \quad \text{(A2)}$$

To evaluate $g_n''(1)$, we differentiate the recursion relation for the generating function and obtain

$$g_{n+1}''(z) = g_1''[g_n(z)]g_n'^2(z) + g_1'[g_n(z)]g_n''(z),$$

which leads to

$$g_{n+1}''(1) = 2p(1+p)^{2n} + (1+p)g_n''(1).$$

Noting that $g_1''(1)=2p$ and $g_0''(1)=0$, we obtain the general solution of the previous recursion,

$$g_n''(1) = 2[(1+p)^{2n-1} - (1+p)^{n-1}],$$

and the second moment,

$$\begin{aligned}\langle x^2\rangle_n &= 2(1+p)^{2n-1} - (1-p)(1+p)^{n-1}\\ &\approx 2(1+p)^{2n-1}.\end{aligned} \quad \text{(A3)}$$

In this large-n (i.e., long-time) limit, one may define the scaling relation $\langle x^k\rangle_n \simeq g_n^{(k)}(1) \simeq h_k(1+p)^{kn}$, where the first few coefficients read

$$h_0 = h_1 = 1, \qquad h_2 = \frac{2}{1+p}. \quad \text{(A4)}$$

For the kth moment $\langle x^k\rangle_n$, given by a sum of derivatives of g_n, it is indeed sufficient to compute the largest (i.e., kth) derivative of g_n, which gives the essential contribution to the coefficient h_k.

A general method can be developed to evaluate the successive moments by computing the dominant part of the derivatives of $g_n(z)$ in the large-n limit. The kth derivative $g_n^{(k)}(z)$ indeed satisfies the following relation:

$$g_{n+1}^{(k)}(z) = g_1''[g_n(z)]T_{n,k}(z) + g_1'[g_n(z)]g_n^{(k)}(z), \quad \text{(A5)}$$

with the initial conditions $T_{n,1}(z)=0$, $T_{n,2}(z)=g_n'^2(z)$, and $T_{n,3}(z)=3g_n'(z)g_n''(z)$. Taking the derivative of Eq. (A5) with respect to z, we obtain the relation for the coefficient $T_{n,k}(z)$,

$$T_{n,k+1}(z) = \frac{\partial}{\partial z}T_{n,k}(z) + g_n'(z)g_n^{(k)}(z). \quad \text{(A6)}$$

This can be solved by iterations,

$$\begin{aligned}T_{n,k+1}(z) &= \sum_{m=0}^{k-1}\frac{\partial^m}{\partial z^m}\left[g_n'(z)g_n^{(k-m)}(z)\right]\\ &= \sum_{m=0}^{k-1}\sum_{l=0}^{m}\binom{m}{l}g_n^{(l+1)}(z)g_n^{(k-l)}(z),\end{aligned} \quad \text{(A7)}$$

where it has been noticed that $T_{n,k}(z)$ contains, at most, the $(k-1)$th derivative of $g_n(z)$.

Since $g_1'(1)=1+p$ and $g_1''(1)=2p$, Eq. (A5), together with Eq. (A7), bears the solution for $z=1$,

$$\begin{aligned}g_{n+1}^{(k)}(1) &= 2p\sum_{j=0}^{n-1}(1+p)^j T_{n-j,k}(1)\\ &= 2p\sum_{m=0}^{k-2}\sum_{l=0}^{m}\sum_{j=0}^{n-1}(1+p)^j\binom{m}{l}g_{n-j}^{(l+1)}(1)g_{n-j}^{(k-1-l)}(1).\end{aligned} \quad \text{(A8)}$$

In the large-n limit, we may use the scaling relation $g_n^{(k)}(1) = h_k(1+p)^{kn}$ so that the dependency on n can be factorized, which leads to the nonlinear recursive relation for h_k,

$$\begin{aligned}h_k &= \frac{\langle x^k\rangle_n}{(1+p)^{kn}}\\ &= \frac{2p}{(1+p)^k - (1+p)}\sum_{m=0}^{k-2}\sum_{l=0}^{m}\binom{m}{l}h_{l+1}h_{k-1-l}.\end{aligned} \quad \text{(A9)}$$

This equation, together with the low-order coefficients in Eq. (A4), gives all the successive coefficients by simple iterations.

From the nonlinear relations in Eq. (A9), one can directly reconstruct the Laplace transform of the stationary distribution in Eq. (6),

$$\hat{f}(\lambda) \equiv \int_0^\infty d\tilde{x}\; e^{-\lambda\tilde{x}}f(\tilde{x}) = \sum_{k\geqslant 0}\frac{(-\lambda)^k}{a^k k!}h_k \quad \text{(A10)}$$

for which the functional equation can be obtained.

In addition, Eq. (9) directly gives the exact large-λ behavior of the Laplace transform $\hat{f}(\lambda)$ (see also Ref. [12]), which can be written as

$$\begin{aligned}\hat{f}(\lambda) &= \int_0^\infty d\tilde{x}e^{-\lambda\tilde{x}}f(\tilde{x}) = \sum_{k\geqslant 0}a_k\int_0^\infty e^{-\lambda\tilde{x}}\tilde{x}^{\beta(k+1)-1}d\tilde{x}\\ &= \sum_{k\geqslant 0}a_k\frac{\Gamma[\beta(k+1)]}{\lambda^{\beta(k+1)}} \overset{\lambda\gg 1}{\approx} \frac{a_0\Gamma(\beta)}{\lambda^\beta}.\end{aligned} \quad \text{(A11)}$$

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[18] Indeed, introducing the new variable $z = \lambda^{\ln 2/\ln(1+p)}$ and defining $\bar{\hat{f}}(z) \equiv p\hat{f}(z)/2 + q/4$, we obtain a *duplication* formula in the reduced form $\bar{\hat{f}}(2z) = 2\bar{\hat{f}}(z)^2 + (1-p^2)/8$. In general, there is no explicit solution available, making it necessary to resort to series expansion. Trivial solutions are found for particular values of $p = \pm 3$, outside the range $0 \leqslant p \leqslant 1$, where we recover usual duplication formulas for trigonometric and hyperbolic functions.

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