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Markovian growth-fragmentation processes

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Consider a Markov process X on $[0,\infty)$ which has only negative jumps and converges as time tends to infinity a.s. We interpret $X(t)$ as the size of a typical cell at time t, and each jump as a birth event. More precisely, if $\Delta X(s) = -y < 0$, then s is the birthtime of a daughter cell with size y which then evolves independently and according to the same dynamics, that is, giving birth in turn to great-daughters, and so on. After having constructed rigorously such cell systems as a general branching process, we define growth-fragmentation processes by considering the family of sizes of cells alive a some fixed time. We introduce the notion of excessive functions for the latter, whose existence provides a natural sufficient condition for the non-explosion of the system. We establish a simple criterion for excessiveness in terms of X. The case when X is self-similar is treated in details, and connexions with self-similar fragmentations and compensated fragmentations are emphasized.

Keywords: branching process; growth-fragmentation; self-similarity

1. Introduction

The purpose of this work is to construct and study a fairly general family of stochastic processes describing the random evolution of particles which grow and split in two as time passes, independently of the other particles in the system. Our initial motivation stems from the study large random planar maps with a boundary, and more precisely from a weak limit theorem describing the structure of cycles at heights; see [4]. Another motivation comes from biology where such systems may be used to model a population of cells; see, for example, Doumic *et al.* [9] and references therein. Roughly speaking, growth-fragmentation processes can further be viewed as the stochastic counterparts of growth-fragmentation equations, which have received some attention in the recent years; see [6–8], and references therein.

In the pure (i.e., without growth) random fragmentation framework, the point of view which has often been taken in the literature (see [2] and references therein) consists in constructing first homogeneous versions where the rate at which particles dislocate does not depend on their sizes. Upon a logarithmic transform, the discrete time skeletons of homogeneous fragmentations can be viewed as branching random walks; the latter have been studied in depth for more than fours decades and yield many useful information and techniques relevant to homogeneous fragmentations; see, in particular, [5]. As a second step, one can then derive more general self-similar fragmentations from the homogeneous ones, by performing a time-substitution on each particle in a consistent way.

In order to define rigorously such time-substitutions on every particle, one needs to handle the genealogical structure of the system, and in this direction, the approach for self-similar fragmentations with binary dislocations which has been developed recently by Pitman and Winkel [14]

is very convenient. More precisely, Pitman and Winkel [14] start from a so-called fragmenter $(M(t), t \geq 0)$, that is the exponential of the negative of a subordinator, and consider a particle system which is defined as follows. Imagine that we start at time $t = 0$ from a single particle, whose size evolves according to M. Then interpret each (negative) jump of M as a branching event, in the sense that whenever $\Delta M(t) := M(t) - M(t-) = -y < 0$, a new particle with size y is born at time t. Assume that the evolution of the daughter particle is governed by the law of the same fragmenter (starting of course from y), and is independent of the processes of all the other daughter particles. And so on for the granddaughters, then great-granddaughters ... Then the sizes of the particles alive at time t can be ranked in the decreasing order and one can check that this yields a general homogeneous fragmentation process with binary dislocation measure. This construction is well-suited to perform time-changes, as the genealogical structure of the particle system is explicitly given. However, an obvious drawback is that it makes the handling of quantities involving all the particles at the same time more involved, as it is given from a genealogical perspective, and not in the universal time simultaneously for all the particles.

In this paper, we consider a natural generalization of the approach of Pitman and Winkel, in which the fragmenter M is replaced by a Markov process $(X(t), t \geq 0)$ with values in $[0, \infty)$, which has càdlàg sample paths and no positive jumps, and converges almost surely as time goes to infinity. We view X as the process of the size of a typical cell, the jumps of X as division events during which a daughter cell is born and splits from her mother, and then, putting jumps aside, the continuous evolution of X as a regular growth or decay. Such cell systems shall thus be thought of as fairly general Markovian growth-fragmentation processes, in which all dislocations are binary.

The verbal description above can be made rigorous, and we shall first show how cell systems can be constructed as a general branching process, see, for example, Jagers [12]. An important point is that this construction is genealogical (first, the mother, then her daughters, ...), whereas we are rather interested in the system evolving in time. The possibility of growth for cells then yields difficulties. In particular, the jumps of X may not be summable (this typically occurs when the sample path of X has infinite variation), and the set of the sizes of all cells alive at time t may fail to be locally finite, and may even be everywhere dense!

The main purpose of this work is to provide simple conditions in terms of the process $(X(t), t \geq 0)$ that ensure that the particle system does not explode locally. In this direction, we study the existence of excessive functions for the cell system, that is of functions $f : (0, \infty) \to \mathbb{R}_+$ which remain bounded away from 0 on the interval (ε, ∞) for every $\varepsilon > 0$, and such that for every $x > 0$ and $t \geq 0$,

$$\mathcal{E}_x\left(\sum_{z \in \mathbf{X}(t)} f(z)\right) \leq f(x),$$

where $\mathbf{X}(t)$ denotes the family of cells alive at time t, and $\mathcal{E}_x$ refers to the mathematical expectation when the system starts at the initial time from a single cell with size x. Note that if f is an excessive function, then almost surely, the elements of $\mathbf{X}(t)$ can be ranked in the non-increasing order and form a null-sequence. In that case, the temporal branching property of the growth-fragmentation process holds: given the state of the system at time t, each cell alive at time t grows and divides according to the Markovian evolution prescribed by X, independently

of the other cells and of the past of the process. We call $(\mathbf{X}(t), t \geq 0)$ a (Markovian) growth-fragmentation process.

Our first general result provides a simple condition in terms of the cell process X which ensures that a given function is excessive for the cell-system. We shall then investigate in more details the case when the Markov process X is self-similar, relying on the fundamental connection between positive self-similar Markov processes and real-valued Lévy processes due to Lamperti [13]. In particular, we derive an explicit criterion in terms of the characteristics of the underlying Lévy process for a power function to be excessive for a self-similar growth-fragmentation process. We shall then relate homogeneous (i.e., self-similar with index 0) growth-fragmentations to the so-called compensated fragmentations introduced recently in [3]; more precisely, we shall show that compensated fragmentations having a binary dislocation measure are special cases of growth-fragmentation processes such that the driving cell process X is given by the exponential of a Lévy process without negative jumps. We shall connect self-similar growth-fragmentations with different indices of self-similarity by time-substitution, and further obtain a simple criterion for the almost-sure extinction. Finally, we observe that the families of the logarithms of the initial sizes of cells at each generation form a branching random walk, whose mean intensity can be computed explicitly. In particular, this entails that self-similar growth-fragmentation processes for which certain power functions are excessive, have càdlàg paths.

2. Cell systems and growth-fragmentation processes

2.1. Construction of a cell system as a general branching process

For every $x > 0$, we write P_x for the law of a Feller process $X = (X(t), t \geq 0)$ started from $X(0) = x$ and taking values in $(0, \infty) \cup \{\partial\}$, where as usual ∂ denotes a cemetery point. We also write $\zeta = \inf\{t \geq 0 : X(t) = \partial\}$ for its lifetime, which may of course be infinite. We call X a *cell process* provided that X has no positive jumps, that is, $\Delta X(t) := X(t) - X(t-) \leq 0$ for all $t \in (0, \zeta)$, and converges at infinity, that is, $\lim_{t\to\infty} X(t)$ exists P_x-a.s., where the limit equals ∂ when $\zeta < \infty$ and belongs to $[0, \infty)$ otherwise.

We now explain the rigorous construction of a *cell system* driven by X as a general branching process. We stress that when the set of jump times of X is discrete, there is a simpler and more direct construction as a branching Markov process, which presents no difficulty and is also easier to analyze. So our approach in terms of general branching processes is mainly relevant when the cell process jumps on a dense set of times.

We first introduce the Ulam–Harris tree $\mathbb{U} = \bigcup_{i=0}^{\infty} \mathbb{N}^i$ with $\mathbb{N} = \{1, 2, \ldots\}$ and the convention $\mathbb{N}^0 = \{\varnothing\}$. The ancestor $\varnothing$ is called Eve, and $\mathbb{N}^i$ is the set of her great-granddaughters at generation i. A node $u \in \mathbb{U}$ is thus a finite sequence $u = (u_1, \ldots, u_i)$ of positive integers where $i = |u|$ is the generation of u, and the children of u are given by the nodes $uk = (u_1, \ldots, u_i, k)$ for $k \in \mathbb{N}$.

We represent the cell system described informally in the Introduction as a family of processes indexed by $\mathbb{U}$,

$$\mathcal{X} := (\mathcal{X}_u, u \in \mathbb{U}),$$

where $\mathcal{X}_u = (\mathcal{X}_u(s), s \geq 0)$ is the process of the size of the cell labelled by u, measuring time from its birth, so that $\mathcal{X}_u(s)$ is the size of the cell u at age s. That is $\mathcal{X}_\varnothing$ is the process of the size

of the Eve cell, which is born at time $b_\varnothing = 0$. For every $u \in \mathbb{U}$ and $j \in \mathbb{N}$, the cell labelled uj is born at the instant $b_{uj} := b_u + \beta_{uj}$, where β_{uj} denotes the instant of jth largest jump of the process $\mathcal{X}_u$, and $\mathcal{X}_{uj}(s)$ represents the size of the cell uj at age s, that is, at time $b_{uj} + s$ for every $s \geq 0$. We implicitly agree that $b_{uj} = \infty$ and then $\mathcal{X}_{uj}(s) \equiv \partial$ when $\mathcal{X}_u$ has less than j jumps.

Given the size $x > 0$ at the initial time of Eve, the law $\mathcal{P}_x$ of the cell system $\mathcal{X}$ is described recursively as follows. Let $(\mathcal{X}_\varnothing(t), t \geq 0)$ have the law P_x and set $b_\varnothing = 0$. Given $\mathcal{X}_\varnothing$, we write $(x_1, \beta_1), (x_2, \beta_2), \ldots$ for the sequence of the jump sizes and times of $-\mathcal{X}_\varnothing$, that is, $x_i = \mathcal{X}_\varnothing(\beta_i -) - \mathcal{X}_\varnothing(\beta_i)$, ranked in the decreasing lexicographic order (i.e., either $x_i = x_{i+1}$ and then $\beta_i > \beta_{i+1}$, or $x_i > x_{i+1}$). In the case when $\mathcal{X}_\varnothing$ has only a finite number of jumps, say n, then we agree that $x_i = 0$ and $\beta_i = \infty$ for all $i > n$. We stress that the assumption that $\lim_{t\to\infty} X(t)$ exists P_x-a.s. ensures that the ranking is well-defined. We then assign to the processes of the sizes at the first generation, $\mathcal{X}_i = (\mathcal{X}_i(s), s \geq 0)$ for $i \in \mathbb{N}$, the distribution of a sequence of independent processes with respective laws P_{x_i}. We continue in an obvious way for the second generation, conditionally given generations 0 and 1. That is, typically, the cell $u = (u_1, u_2)$ is born at time $b_u = b_{u_1} + \beta_{u_2}$, where β_{u_2} denotes the instant of the u_2th largest jump of the process $\mathcal{X}_{u_1}$, and given $\Delta\mathcal{X}_{u_1}(\beta_{u_2}) = -y$, $\mathcal{X}_u$ has the law P_y and is independent of the process of the sizes of the other granddaughters. And so on for the next generations; we refer to Jagers [12] for the rigorous argument showing that this indeed defines uniquely the law $\mathcal{P}_x$. It will be convenient to agree that $\mathcal{P}_\partial$ denotes the law of the degenerate process on $\mathbb{U}$ such that $\mathcal{X}_u \equiv \partial$ for every $u \in \mathbb{U}$, $b_\varnothing = 0$ and $b_u = \infty$ for $u \neq \varnothing$. We shall also write $\mathcal{E}_x$ for the mathematical expectation under the law $\mathcal{P}_x$.

This construction is only a slight modification of that of a general branching process, as in the latter, daughters are usually enumerated according to their birth-time rather than their sizes. The reason for ordering daughter-cells according to their size at birth in our setting, is that when the set of jump times of X is dense, jump-times cannot be enumerated in the increasing order; however jump sizes can always be listed in decreasing order. Our construction of the cell system is elementary; however we stress that there is a technical difficulty when we wish to study the evolution of cell systems as time passes. Specifically, note that in general, the sigma-field

$$\sigma\left(\mathbf{1}_{b_u \leq s}\mathcal{X}_u(s - b_u) : 0 \leq s \leq t, u \in \mathbb{U}\right)$$

generated by the observation of the cells alive up to time t contains information about the future of the cells after time t. For instance, if $b_1 \leq t$ and $\mathcal{X}_1(0) = x$, then we know that $\mathcal{X}_\varnothing$ can have no jump of size less than $-x$ after time t.

In this setting, the branching property of general branching processes can be stated as follows.

Proposition 1 (Genealogical branching property). *For every $u \in \mathbb{U}$, write $\mathcal{X}^u = (\mathcal{X}^u_v, v \in \mathbb{U})$ for the process such that $\mathcal{X}^u_v = \mathcal{X}_{uv}$ for every $v \in \mathbb{U}$. For every fixed generation $i \in \mathbb{N}$, conditionally on $(\mathcal{X}_v, v \in \mathbb{U}$ and $|v| \leq i)$, the processes $\mathcal{X}^{uj}$ for $u \in \mathbb{N}^i$ and $j \in \mathbb{N}$ are independent. Further, each $\mathcal{X}^{uj}$ has the law $\mathcal{P}_y$, with y the size of the jth largest jump (in absolute value) of the process $\mathcal{X}_u$.*

We recall that Jagers [12] showed that this genealogical branching property holds more generally at optional stopping lines, which can be viewed as a strong branching property. Recall however that deterministic times cannot be expressed as stopping lines for the system.

2.2. Growth-fragmentation processes and excessive functions

The cell system being constructed, we now define for every $t \geq 0$ the cell population at time t as the family of the sizes of the cells alive at time t, viz.

$$\mathbf{X}(t) = \big\{\!\big\{ \mathcal{X}_u(t - b_u) : u \in \mathbb{U}, b_u \leq t < b_u + \zeta_u \big\}\!\big\},$$

where ζ_u denotes the lifetime of $\mathcal{X}_u$ and the notation $\{\{\cdots\}\}$ refers to multiset (i.e., elements are repeated according to their multiplicities). Letting the time parameter t vary, we call the process of cell populations $(\mathbf{X}(t), t \geq 0)$ a *growth-fragmentation process* associated to the cell process X.

We denote by $\mathbf{P}_x$ the law of the process $\mathbf{X} = (\mathbf{X}(t), t \geq 0)$ under $\mathcal{P}_x$. We stress that the family of laws $(P_y)_{y>0}$ of the cell process X determines the law $\mathcal{P}_x$ of the cell system $\mathcal{X}$, and conversely one recovers P_x from $\mathcal{P}_x$ simply by focusing on the distribution of the process of the size of Eve. However, one cannot recover the whole cell system $\mathcal{X}$ from the growth-fragmentation process $(\mathbf{X}(t), t \geq 0)$ in full generality, because it is not always possible to retrieve the genealogical structure of $\mathcal{X}$ solely from the latter, and in general the law $\mathbf{P}_x$ of the growth-fragmentation process does not determine that of the cell process X. See Pitman and Winkel [14] and Shi [15] for a discussion.

Recall that a function $f : (0, \infty) \to [0, \infty)$ is called excessive for the Markov process X if

$$E_x\big(f\big(X(t)\big)\big) \leq f(x) \qquad \text{for all } t \geq 0 \text{ and } x > 0,$$

with the convention that $f(\partial) = 0$. We shall now introduce a stronger notion for growth-fragmentations, that will have an important role in our study. Recall first that if $\mathcal{I}$ is a family of positive real numbers, that is, a multiset in $(0, \infty)$, then $\sum_{z\in\mathcal{I}} f(z)$ denotes the sum of the $f(z)$ where the elements z of $\mathcal{I}$ are repeated according to their multiplicity. In other words, a multiset $\mathcal{I}$ can be viewed as a point measure with atoms at the elements of $\mathcal{I}$, where the mass of an atom is given by the multiplicity of the element, and $\sum_{z\in\mathcal{I}} f(z)$ then denotes the integral of f against this point measure. In this setting, if $(\mathcal{I}_j : j \in \mathcal{J})$ is a collection of multisets, then the union $\mathcal{I} = \bigsqcup \mathcal{I}_j$ can be identified with the sum of the point measures associated to each $\mathcal{I}_j$.

Definition 1. *Let $f : (0, \infty) \to [0, \infty)$ be a measurable function which is bounded away from 0 on semi-infinite intervals, viz.*

$$\inf_{x>a} f(x) > 0 \qquad \textit{for every } a > 0. \tag{1}$$

We say that f is **excessive** *for the growth-fragmentation process $\mathbf{X}$ (or for the cell system $\mathcal{X}$) if for each $t \geq 0$ and $x > 0$, we have*

$$\mathbf{E}_x\bigg(\sum_{z\in\mathbf{X}(t)} f(z)\bigg) \leq f(x). \tag{2}$$

We henceforth assume the existence of an excessive function f, and write $\mathcal{M}_f$ for the space of multisets $\mathcal{I}$ on $(0, \infty)$ with $\sum_{z\in\mathcal{I}} f(z) < \infty$. We stress that (1) ensures that every multiset $\mathcal{I} \in \mathcal{M}_f$ has only finitely many elements (counted with their multiplicity) in semi-infinite intervals

(a, ∞), and hence $\mathcal{I}$ can be viewed as a locally finite point measure on $(0, \infty]$. We endow $\mathcal{M}_f$ with the topology of vague convergence for the corresponding point measures, that is a sequence $\mathcal{I}_n \in \mathcal{M}_f$ converges to $\mathcal{I} \in \mathcal{M}_f$ if and only if

$$\lim_{n\to\infty} \sum_{z\in\mathcal{I}_n} g(z) = \sum_{z\in\mathcal{I}} g(z)$$

for every continuous function $g : (0, \infty] \to \mathbb{R}$ such that $g(x) = 0$ for all sufficiently small $x > 0$. Alternatively, every multiset $\mathcal{I} \in \mathcal{M}_f$ can be expressed uniquely in the form of a non-increasing null sequence, that is $\mathcal{I} = \{\{z_1, z_2, \ldots\}\}$ with $z_1 \geq z_2 \geq \cdots > 0$. In this setting, convergence in $\mathcal{M}_f$ is equivalent to simple convergence for non-increasing null sequences. We can now view $\mathbf{X}(t)$ as a random variable with values in $\mathcal{M}_f$, and thus a growth-fragmentation as a stochastic process with values in $\mathcal{M}_f$.

We next introduce a family of probability kernels on $\mathcal{M}_f$ as follows. Given a multiset $\mathcal{I}$ in $\mathcal{M}_f$, consider a family $(\eta_x, x \in \mathcal{I})$ of independent variables in $\mathcal{M}_f$, where each η_x has the law of $\mathbf{X}(t)$ under $\mathcal{P}_x$. Observe that the union of multisets $\eta = \bigsqcup \eta_i$ fulfills

$$\mathbf{E}\left(\sum_{z\in\eta} f(z)\right) = \sum_{x\in\mathcal{I}} \mathbf{E}\left(\sum_{z\in\eta_x} f(z)\right) \leq \sum_{x\in\mathcal{I}} f(x) < \infty,$$

and as a consequence, η is a random multiset in $\mathcal{M}_f$. We denote its law by $\rho_t(\mathcal{I}, \cdot)$.

The main observation of this section is that growth-fragmentation processes fulfill the branching process (in time).

Proposition 2 (Temporal branching property). *Suppose that the growth-fragmentation process* $\mathbf{X}$ *possesses an excessive function* f*. Then for every* $s, t \geq 0$ *and* $x > 0$*, the conditional distribution under* $\mathbf{P}_x$ *of* $\mathbf{X}(t + s)$ *given* $(\mathbf{X}(r), 0 \leq r \leq s)$ *is* $\rho_t(\mathbf{X}(s), \cdot)$*.*

Proof. Although this temporal branching property should certainly not come as a surprise, providing all the technical details of the proof would be rather cumbersome, and we shall merely present the main steps.

For every $\varepsilon > 0$, we write $\mathcal{X}^{(\varepsilon)}$ for the system obtained from $\mathcal{X}$ by killing each cell together with its future descent when its size becomes less than ε. In the obvious notation, $\mathbf{X}^{(\varepsilon)}(t) \subseteq \mathbf{X}(t)$ for every $t \geq 0$, and as a consequence, f is also an excessive function for $\mathbf{X}^{(\varepsilon)}$, in the sense that (2) holds with $\mathbf{X}(t)$ replaced by $\mathbf{X}^{(\varepsilon)}(t)$. The point in introducing this killed system is that its temporal evolution can be described as a branching Markov process. Specifically, starting from a single cell with size $x > \varepsilon$, we let its size evolve until possibly a first jump of size smaller than $-\varepsilon$ occurs (recall also that the cell is killed when its size becomes less than ε, so death may occur when making this jump). If such a jump occurs, we then create a first daughter cell with size given by the (opposite of the) size of the jump. After this first division event, both the mother cell and her first daughter follow the same evolution independently one of the other, and so on for the next birth events.

We stress that no explosion occurs for $\mathbf{X}^{(\varepsilon)}$ viewed as a branching process in universal time, since, by construction, all the cells of $\mathbf{X}^{(\varepsilon)}(t)$ have size at least ε and can be found amongst

the cell population $\mathbf{X}(t)$. Further, we know that $\mathbf{X}(t)$ has only finitely many elements larger than ε, $\mathbf{P}_x$-a.s. The temporal branching structure of $\mathbf{X}^{(\varepsilon)}$ is discrete, in the sense that for each cell in $\mathbf{X}^{(\varepsilon)}$, the set of times at which this cell begets is discrete, and one can then check (albeit technical details are somewhat cumbersome) that $\mathbf{X}^{(\varepsilon)}(t)$ fulfills the temporal branching property analogous to that in the statement.

To complete the proof, we let ε decrease to 0 and observe that

$$\lim_{\varepsilon\to 0+} \mathbf{E}_x\left(\sum_{\mathbf{X}(t)\setminus\mathbf{X}^{(\varepsilon)}(t)} f(z)\right) = 0. \tag{3}$$

Indeed, because the cell process X lives in $(0,\infty)$, if a cell $u\in\mathbb{U}$ is alive at time t in the cell system $\mathcal{X}$ (i.e., $b_u \le t < b_u + \zeta_u$), then its ancestral lineage has a size which remains bounded away from 0 on the time-interval $[0,t]$. That is, if for $0\le s\le t$, we denote by $u(s)$ the youngest ancestor of u alive at time s, then $\inf_{0\le s\le t} \mathcal{X}_{u(s)}(s-b_{u(s)}) > 0$. Therefore, if a cell $u\in\mathbb{U}$ is alive at time t in the cell system $\mathcal{X}$, then it is also alive in the system $\mathcal{X}^{(\varepsilon)}$ for all ε sufficiently small. Our claim now follows from (2) by dominated convergence.

We know from (3) that $\mathbf{X}^{(\varepsilon)}(t)$ increases to $\mathbf{X}(t)$ for each $t\ge 0$ when $\varepsilon\downarrow 0$, and because for every fixed $a>0$, $\mathbf{X}(t)\cap(a,\infty)$ is finite a.s., the probability that $\mathbf{X}(t)\cap(a,\infty) = \mathbf{X}^{(\varepsilon)}(t)\cap(a,\infty)$ can be made as close to 1 as we wish by choosing $\varepsilon>0$ sufficiently small. It now follows readily that the temporal branching property of $\mathbf{X}^{(\varepsilon)}$ can be transferred to $\mathbf{X}$ by letting ε tend to 0. □

Corollary 1. *Suppose that f is an excessive function for the growth-fragmentation process $\mathbf{X}$. Then for every $x>0$, the process*

$$\left(\sum_{z\in\mathbf{X}(t)} f(z), t\ge 0\right)$$

is a supermartingale under $\mathbf{P}_x$ in the natural filtration generated by the growth-fragmentation process $\mathbf{X}$.

Proof. This follows readily from the temporal branching property and the very definition of excessive functions for a growth-fragmentation process. □

2.3. A criterion for excessiveness

We now state the main result of this section, which provides a simple criterion for the existence of an excessive function for a growth-fragmentation and is easy to verify in practice.

Theorem 1. *Consider a measurable function $f:(0,\infty)\to[0,\infty)$ which fulfills (1), and agree that $f(\partial)=0$. If for every $x>0$ and $t>0$, there is the inequality*

$$E_x\left(f\big(X(t)\big) + \sum_{0<s\le t} f\big(-\Delta X(s)\big)\right) \le f(x),$$

then f is excessive for the growth-fragmentation process $\mathbf{X}$.

Remarks.

1. *In the pure fragmentation case when the process X has non-increasing sample paths, the identity function $f(x) = x$ obviously fulfills the condition of the statement since $X(t) - \sum_{0<s\le t} \Delta X(s) = X^c(t)$, where X^c denotes the continuous part of X.*
2. *An application of the Markov property shows easily that the condition on the statement is fulfilled if and only if the process*

$$f\big(X(t)\big) + \sum_{0<s\le t} f\big(-\Delta X(s)\big), \qquad t \ge 0$$

is a super-martingale under P_x for every $x > 0$. Whether this holds or not for a given cell process X and a given function f can then be investigated using stochastic calculus (see, e.g., Ether and Kurtz [10] and Jacod and Shiryaev [11]) in the fairly general situation when X is a semi-martingale and the function f smooth enough. See also the forthcoming Lemma 2.

Proof of Theorem 1. We introduce the filtration $(\mathcal{F}_i)_{i\ge 0}$, where $\mathcal{F}_i = \sigma((\mathcal{X}_u, b_u) : |u| \le i)$. We fix t and consider the chain

$$\Sigma(i) = \sum_{|u|\le i, b_u \le t} f\big(\mathcal{X}_u(t - b_u)\big) + \sum_{|v|=i, b_v \le t} \sum_{s \le t - b_v} f\big(-\Delta \mathcal{X}_v(s)\big), \qquad i = 0, 1, \ldots;$$

we shall check that $\Sigma = (\Sigma(i), i \ge 0)$ is an $(\mathcal{F}_i)$-supermartingale. Then $\Sigma(\infty) = \lim_{i\to\infty} \Sigma(i)$ exists a.s., with $\Sigma(\infty) \ge \sum_{\mathbf{X}(t)} f(z)$. It thus follows from Fatou's lemma that

$$\mathbf{E}_x\Big(\sum_{z\in\mathbf{X}(t)} f(z)\Big) \le \mathbf{E}_x\big(\Sigma(0)\big) = E_x\Big(f\big(X(t)\big) + \sum_{0<s\le t} f\big(-\Delta X(s)\big)\Big) \le f(x),$$

where the last inequality derives again from the assumption of the statement.

It thus remains to prove that $\Sigma(i)$ is indeed a super-martingale. We recall first that for every vertex $v \in \mathbb{N}^i$ at generation $i \ge 1$, the birth-time b_v and initial size $\mathcal{X}_v(0)$ of the cell labelled by v are measurable with respect to $(\mathcal{X}_{v-}, b_{v-})$, where $v-$ is the mother of v. The assumption of the statement entails that on the event $b_v \le t$, the conditional expectation given $\mathcal{F}_{i-1}$ of

$$f\big(\mathcal{X}_v(t - b_v)\big) + \sum_{0<s\le t-b_v} f\big(-\Delta \mathcal{X}_v(s)\big),$$

is bounded from above by $f(\mathcal{X}_v(0))$. Recall that (on this event) $\mathcal{X}_v(0) = -\Delta\mathcal{X}_{v-}(b_v - b_{v-})$ and $b_v - b_{v-} \le t - b_{v-}$. Summing over vertices v at generation i, we get that the conditional expectation

$$\mathcal{E}_x\Big(\sum_{|v|=i, b_v\le t} f\big(\mathcal{X}_v(t - b_v)\big) + \sum_{|v|=i, b_v\le t} \sum_{s\le t-b_v} f\big(-\Delta\mathcal{X}_v(s)\big)\big|\mathcal{F}_{i-1}\Big)$$

is bounded from above by

$$\sum_{|v|=i, b_v \le t} f\big(\mathcal{X}_v(0)\big) = \sum_{|u|=i-1, b_u \le t} \sum_{r \le t-b_u} f\big(-\Delta\mathcal{X}_u(r)\big).$$

It thus only remains to add $\sum_{|u|\le i-1, b_u\le t} f(-\Delta\mathcal{X}_u(t-b_u))$ to both sides, and we get

$$\mathcal{E}_x\big(\Sigma(i)|\mathcal{F}_{i-1}\big) \le \Sigma(i-1),$$

which is the desired super-martingale property. □

3. Self-similar growth-fragmentation processes

In this section, we shall study growth-fragmentation processes when the cell process X is self-similar. We first provide some fundamental background on self-similar Markov processes and the approach of Lamperti [13] to the latter, tailored to fit the present framework.

3.1. Lamperti's representation of self-similar cell processes

Let $\xi = (\xi(t), t \ge 0)$ denote a real-valued Lévy process which starts from 0, has no positive jumps, and is possibly killed at some independent exponential time. Its distribution can be characterized by a quadruple $(\sigma^2, b, \Lambda, k)$, which we shall refer to as the characteristics of ξ, where $\sigma^2 \ge 0$, $b \in \mathbb{R}$, $k \ge 0$ is the killing rate, and Λ a measure on $(-\infty, 0)$, known as the Lévy measure, such that

$$\int_{(-\infty,0)} \big(1 \wedge y^2\big)\Lambda(\mathrm{d}y) < \infty.$$

Specifically, the Lévy–Khintchin formula

$$\Psi(q) := -k + \frac{1}{2}\sigma^2 q^2 + bq + \int_{(-\infty,0)} \big(\mathrm{e}^{qy} - 1 + q\big(1 - \mathrm{e}^{y}\big)\big)\Lambda(\mathrm{d}y) \tag{4}$$

defines a convex function $\Psi : [0, \infty) \to \mathbb{R}$ which is known as the Laplace exponent of ξ, and we have

$$E\big(\exp\big(q\xi(t)\big)\big) = \exp\big(t\Psi(q)\big) \qquad \text{for all } t, q \ge 0,$$

with the convention that $\exp(q\xi(t)) = 0$ when ξ has been killed before time t. In the literature, the Lévy–Khintchin formula is usually written with $q(1-\mathrm{e}^{y})$ replaced by $-qy\mathbf{1}_{y>-1}$ in the integral, but this is unimportant as its only amounts to changing the coefficient of the linear term in Ψ. We further assume that when $k = 0$, ξ drifts to $-\infty$, in the sense that $\lim_{t\to\infty} \xi(t) = -\infty$ a.s. It is well known that the latter is equivalent to assuming that the right-derivative of Ψ at 0 is negative, $\Psi'(0+) \in [-\infty, 0)$, and in terms of the characteristics of ξ, to $b < \int_{(-\infty,0)} (\mathrm{e}^{y} - 1 - y)\Lambda(\mathrm{d}y)$.

Then fix $\alpha \in \mathbb{R}$ and define for every $t \geq 0$

$$\tau_t^{(\alpha)} := \inf\left\{u \geq 0 : \int_0^u \exp\bigl(-\alpha\xi(s)\bigr)\,\mathrm{d}s \geq t\right\}. \tag{5}$$

More precisely, $\tau_t^{(\alpha)}$ is always finite when $\alpha \geq 0$ and $k = 0$; however when $\alpha < 0$ or $k > 0$, the exponential integral $I^{(\alpha)} := \int_0^\infty \exp(-\alpha\xi_s)\,\mathrm{d}s$ is finite a.s. and $\tau_t^{(\alpha)} = \infty$ for all $t \geq I^{(\alpha)}$. For every $x > 0$, we write P_x for the distribution of the process

$$X(t) := x\exp\bigl\{\xi\bigl(\tau_{tx^\alpha}^{(\alpha)}\bigr)\bigr\}, \qquad t \geq 0$$

with the convention that $X(t) = \partial$ if $x^\alpha t \geq I^{(\alpha)}$. Then $X = (X(t), t \geq 0)$ is both Markovian and self-similar, in the sense that for every $x > 0$,

$$\text{the law of } \bigl(xX\bigl(x^\alpha t\bigr), t \geq 0\bigr) \text{ under } P_1 \text{ is } P_x. \tag{6}$$

Of course, X is also a cell process, thanks to the assumptions we made on the Lévy process ξ. More precisely, X has an infinite lifetime if and only if $\alpha \geq 0$ and $k = 0$, and otherwise is killed at time $x^{-\alpha} I^{(\alpha)}$ either by reaching continuously the boundary 0 (if $k = 0$) or by sudden death (if $k > 0$). Conversely, any self-similar cell process can be constructed in this way.

We call a cell system $\mathcal{X}$, or a growth-fragmentation process $\mathbf{X}$, *self-similar* with index α whenever its cell process X fulfills (6), that is when $(X(t), t \geq 0)$ is constructed from a Lévy process with no positive jumps ξ and an index $\alpha \in \mathbb{R}$ as above; the initial value $x > 0$ being chosen arbitrarily. In the theory of self-similar processes, $H := -1/\alpha$ is known as the Hurst exponent; however in order to remain coherent with the literature on self-similar fragmentations, we shall rather refer to α the index of self-similarity (note also that this allows taking $\alpha = 0$). We first observe that the self-similarity property of X propagates to the whole cell system $\mathcal{X}$. Recall that for $u \in \mathbb{U}$, b_u denotes the birth time of the cell labelled by u.

Lemma 1. *Consider a self-similar cell system $\mathcal{X} = (\mathcal{X}_u, u \in \mathbb{U})$ with index α. Fix $x > 0$ arbitrary, and define for every $u \in \mathbb{U}$ and $t \geq 0$, $\mathcal{X}'_u(t) = x\mathcal{X}_u(x^\alpha t)$ and $b'_u = x^{-\alpha} b_u$. Then the law of $((\mathcal{X}'_u, b'_u), u \in \mathbb{U})$ under $\mathcal{P}_1$ is the same as the law of $((\mathcal{X}_u, b_u), u \in \mathbb{U})$ under $\mathcal{P}_x$.*

Proof. Indeed, the scaling property (6) shows that $\mathcal{X}'_\varnothing$ has the law P_x. By construction, the sequence of the jump sizes and times of $\mathcal{X}'_\varnothing$ are given, respectively, by $\mathcal{X}'_j(0) = x\mathcal{X}_j(0)$ and $b'_j = x^{-\alpha} b_j$ for $j \in \mathbb{N}$. Applying again the scaling property (6), we deduce that the distribution of $((\mathcal{X}'_u, b'_u), |u| \leq 1)$ under $\mathcal{P}_1$ is the same as that of $((\mathcal{X}_u, b_u), |u| \leq 1)$ under $\mathcal{P}_x$. The proof is completed by iteration of this argument. □

3.2. A criterion for excessiveness of power functions

Throughout this section, we assume that $\mathbf{X}$ is a self-similar growth-fragmentation process with index α, where the self-similar cell process X is related to the spectrally negative Lévy process ξ with characteristics (σ^2, b, Λ) by the Lamperti's transformation. We next state the main result

of this work, which provides a simple criterion for a power function to be excessive for a self-similar growth-fragmentation process. This criterion is expressed in terms of the characteristics of ξ. Introduce first

$$\kappa(q) := \Psi(q) + \int_{(-\infty,0)} \left(1 - \mathrm{e}^{y}\right)^{q} \Lambda(\mathrm{d}y), \qquad q \in \mathbb{R}. \tag{7}$$

Plainly, $\kappa : \mathbb{R}_+ \to (-\infty, \infty]$ is also convex, and since the condition $\int_{(-\infty,0)}(1 \wedge y^2)\Lambda(\mathrm{d}y) < \infty$ entails that $\int_{(-\infty,0)}(1 - \mathrm{e}^{y})^{q}\Lambda(\mathrm{d}y) < \infty$ for every $q \geq 2$, κ takes finite values on $[2, \infty)$.

Theorem 2. *Suppose that there exists $q > 0$ with $\kappa(q) \leq 0$. Then $x \mapsto x^q$ is excessive for the growth-fragmentation process $\mathbf{X}$ and the following properties hold*:

- (Self-similarity). *For every $x > 0$, the distribution of the process $(x\mathbf{X}(x^{\alpha}t), t \geq 0)$ under $\mathbf{P}_1$ is the same as that of $(\mathbf{X}(t), t \geq 0)$ under $\mathbf{P}_x$.*
- (Branching property). *Conditionally on $\mathbf{X}(t) = \{\{x_1, x_2, \ldots\}\}$, the process $(\mathbf{X}(t+s), s \geq 0)$ is independent of $(\mathbf{X}(r), 0 \leq r \leq t)$ and has the same distribution as $(\bigsqcup \mathbf{X}^{(i)}(s), s \geq 0)$, where the $\mathbf{X}^{(i)}$ are independent self-similar growth-fragmentations with respective laws $\mathbf{P}_{x_i}$.*

When the assumptions of Theorem 2 hold, the cell population $\mathbf{X}(t)$ at time t can of course be ranked in the non-increasing order; however, we shall refrain to use the notation $X_1(t) \geq X_2(t) \geq \cdots \geq 0$ for the latter, as it might induce some confusion with the sizes of cells of the first generation. We conjecture that conversely, when the hypothesis of Theorem 2 fails, then the cell population explodes locally with positive probability, in the sense that there is some compact interval $I \subset (0, \infty)$ such that $\mathbf{X}(t)$ has infinitely many elements in I with positive probability for all for $t \geq 0$ sufficiently large.

We now prove the first part of Theorem 2 by checking that the conditions of Theorem 1 are fulfilled.

Lemma 2. *For every $q \geq 0$ such that $\kappa(q) \leq 0$, the process*

$$X^{q}(t) + \sum_{0<s\leq t} \left|\Delta X(s)\right|^{q}$$

is a supermartingale under P_x for every $x > 0$.

Proof. We first establish the statement in the homogeneous case $\alpha = 0$, that is, when the cell process X is simply the exponential of the Lévy process ξ. Recall that the point process of the jumps of ξ is Poisson with intensity $\mathrm{d}t\,\Lambda(\mathrm{d}y)$. It follows that the increasing process

$$\sum_{0<s\leq t} \left|\Delta X(s)\right|^{q} = \sum_{0<s\leq t} \exp\bigl(q\xi(s-)\bigr)\bigl(1 - \exp\bigl(\Delta\xi(s)\bigr)\bigr)^{q}$$

has predictable compensator

$$\left(\int_{(-\infty,0)} \left(1 - \mathrm{e}^{y}\right)^{q} \Lambda(\mathrm{d}y)\right) \int_0^t \exp\bigl(q\xi(s)\bigr)\,\mathrm{d}s.$$

On the other hand, it is well known that

$$\exp\bigl(q\xi(t)\bigr) - \Psi(q)\int_0^t \exp\bigl(q\xi(s)\bigr)\,\mathrm{d}s$$

is a martingale. Merging these two observations, we deduce that

$$X^q(t) + \sum_{0<s\le t} \bigl|\Delta X(s)\bigr|^q - \kappa(q)\int_0^t X(s)^q\,\mathrm{d}s$$

is a martingale, and our claim provided since $\kappa(q) \le 0$.

To complete the proof for an arbitrary index of self-similarity $\alpha \in \mathbb{R}$, it suffices to observe that if f fulfills the condition of Theorem 1 for some cell process X, then the optional sampling property of nonnegative super-martingales entails that f also fulfills that condition for any Markov process Y which is obtained from X by a bijective time-substitution. Since a self-similar cell process X with index α is constructed from the exponential of a Lévy process ξ by Lamperti's time-substitution, the proof is complete. □

The branching property stated in Theorem 2 follows immediately from Proposition 2. In turn, self-similarity derives from Lemma 1. Specifically, using the notation there, the multiset

$$\mathbf{X}'(t) := \bigl\{\bigl\{X'_u\bigl(t - b'_u\bigr) : u \in \mathbb{U}, b'_u \le t < b'_u + \zeta'_u\bigr\}\bigr\}$$

can be expressed as

$$\begin{aligned}\mathbf{X}'(t) &= \bigl\{\bigl\{x\mathcal{X}_u\bigl(x^\alpha\bigl(t - x^{-\alpha}b_u\bigr)\bigr) : u \in \mathbb{U}, x^{-\alpha}b_u \le t < x^{-\alpha}(b_u + \zeta_u)\bigr\}\bigr\}\\ &= \bigl\{\bigl\{x\mathcal{X}_u\bigl(x^\alpha t - b_u\bigr) : u \in \mathbb{U}, b_u \le x^\alpha t < b_u + \zeta_u\bigr\}\bigr\}\\ &= x\mathbf{X}\bigl(x^\alpha t\bigr),\end{aligned}$$

which entails the claim.

3.3. Homogeneous growth-fragmentations and compensated fragmentations

We say that a self-similar cell process is *homogeneous* if it has index $\alpha = 0$, that is when it given in the form $X(t) = x\exp(\xi(t))$, with ξ a (possibly killed) spectrally negative Lévy process. The associated cell process and growth-fragmentation are then also called homogeneous. We start by connecting homogeneous growth-fragmentations to another family of fragmentation type processes, namely *compensated fragmentations*, that have been recently introduced in [3]. The distribution of a compensated fragmentation is characterized by three parameters: a Gaussian coefficient $\sigma^2 \ge 0$, a growth rate coefficient $b \in \mathbb{R}$, and a dislocation measure ν. The latter is a measure on the space of mass-partitions

$$\mathcal{P} = \left\{\mathbf{p} = (p_1, p_2, \ldots) : p_1 \ge p_2 \ge \cdots \ge 0 \text{ and } \sum_1^\infty p_i \le 1\right\};$$

roughly speaking, ν describes the rates at which a particle splits into smaller fragments. The necessary and sufficient condition for a measure ν on $\mathcal{P}$ to be the dislocation measure of a compensated fragmentation is

$$\int_{\mathcal{P}} (1-p_1)^2 \nu(\mathrm{d}\mathbf{p}) < \infty.$$

We refer to [3] for background.

We further say that a mass-partition $\mathbf{p} = (p_1, p_2, \ldots)$ is binary if $p_2 > 0$ and $p_1 + p_2 = 1$ (then $p_i = 0$ for $i \geq 3$), and write $\mathcal{P}_2$ for the sub-space of binary mass-partitions. For the sake of simplicity, we identify a binary mass partition $\mathbf{p} = (p_1, 1-p_1, 0, \ldots)$ with the pair $(p_1, 1-p_1)$. We also write $\mathbf{0} = (0, \ldots)$ for the null mass-partition and recall that k denotes the killing rate of ξ. We now claim the following.

Proposition 3. *Suppose that the Lévy measure Λ of the spectrally negative Lévy process ξ has support in $[-\ln 2, 0]$, and write ν_2 for the measure on the space of binary partitions $\mathcal{P}_2$, which is defined as the image of Λ by the map $x \mapsto (\mathrm{e}^x, 1-\mathrm{e}^x)$. Then the homogeneous growth-fragmentation process $(\mathbf{X}(t), t \geq 0)$ associated to the cell process $X(t) = \exp(\xi(t))$ is a compensated fragmentation with characteristics $(\sigma^2, b+k, \nu)$, where $\nu = \nu_2 + k\delta_{\mathbf{0}}$.*

Proof. Observe first that

$$\int_{\mathcal{P}} (1-p_1)^2 \nu(\mathrm{d}\mathbf{p}) = k + \int_{[-\ln 2, 0)} \left(1-\mathrm{e}^x\right)^2 \Lambda(\mathrm{d}x) \leq k + \int_{[-\ln 2, 0)} x^2 \Lambda(\mathrm{d}x) < \infty,$$

so ν is the dislocation measure of a compensated fragmentation, say $\mathbf{Z} = (\mathbf{Z}(t), t \geq 0)$ with characteristics (σ^2, b, ν); see Definition 3 in [3]. That is, the point-measure valued process

$$\mathcal{L}(t) := \sum_{i=1}^{\infty} \delta_{\ln Z_i(t)}, \qquad t \geq 0$$

is a branching Lévy process with characteristics (σ^2, b, μ), in the sense of Definition 2 of [3], where μ is the image of ν by the map $\mathbf{p} \mapsto \ln \mathbf{p}$. Equivalently, μ is the image of Λ by the map $x \mapsto (x, \ln(1-\mathrm{e}^x))$. Roughly speaking, this implies that the atoms of $\mathcal{L} = (\mathcal{L}(t), t \geq 0)$ form a particle system in which each particle, say located at $z \in \mathbb{R}$, dies and is replaced by a pair of atoms located at $z + x_1$ and $z + x_2$ at rate $\mu(\mathrm{d}\mathbf{x})$ where $\mathbf{x} = (x_1, x_2)$.

Next, for every $c \geq 0$, denote by $\mathcal{L}^{[c]} = (\mathcal{L}^{[c]}(t), t \geq 0)$ the particle system obtained from $\mathcal{L} = (\mathcal{L}(t), t \geq 0)$ by suppressing for each branching event of the type $z \mapsto (z + x_1, z + x_2)$, the second child $z + x_2$ whenever $x_2 \leq -c$ (see Definition 2 and equation (19) in [3] for a precise construction). According to Lemma 3 in [3], $\mathcal{L}^{[c]}$ is again a branching Lévy process with characteristics $(\sigma^2, b, \mu^{[c]})$ in the sense of Definition 1 of [3], where $\mu^{[c]}$ is the image of μ by the map $(x_1, x_2) \mapsto (x_1, x_2^{[c]})$, with $x^{[c]} = x_2$ if $x_2 > -c$, and $x^{[c]} = -\infty$ if $x_2 \leq -c$.

For $c = 0$, $\mathcal{L}^{[0]}(t)$ has a single atom located at $\xi_*(t)$, which is referred to as the selected atom. According to Corollary 1 in [3], the process of the selected atom ξ_* is a spectrally negative Lévy

process with Laplace exponent Ψ_* given by

$$\Psi_*(q) = \frac{1}{2}\sigma^2 q^2 + bq + \int_{\mathscr{P}} \big(p_1^q - 1 + q(1-p_1)\big)\nu(\mathrm{d}\mathbf{p})$$
$$= -k + \frac{1}{2}\sigma^2 q^2 + (b+k)q + \int_{\mathscr{P}_2} \big(p_1^q - 1 + q(1-p_1)\big)\nu_2(\mathrm{d}\mathbf{p}).$$

It is immediately seen that $\Psi_* = \Psi$, and thus the selected atom has the same distribution as ξ.

For every $c \geq 0$, the branching Lévy process $\mathcal{L}^{[c]}$ has a discrete genealogical structure, and since $x_2 = \ln(1 - \mathrm{e}^{x_1})$ for μ-almost every $\mathbf{x} = (x_1, x_2)$, Definition 1 and Lemma 3 of [3] entail that its evolution can be described as follows. The system starts with an atom at the origin, which evolves according to the law of the distinguished fragment ξ_*. At the first instant τ when this atom has a jump of size $y < \ln(1 - \mathrm{e}^{-c})$, that is such that $\ln(1 - \mathrm{e}^{y}) > -c$, a new particle is born at location $\xi_*(\tau-) + \ln(1 - \mathrm{e}^{y})$. After this first birth event, the mother and the daughter particles evolve independently one of the other, according to the same dynamics as ξ_*, until the first instant when one of those two particles has another jump of size a jump of size less than $\ln(1 - \mathrm{e}^{-c})$. Then a third particle is born, etc. Thus, if we map the atoms of $\mathcal{L}^{[c]}$ into $(0, \infty)$ by the exponential function $z \mapsto \mathrm{e}^z$, we obtain the following particle system. The exponential of the selected atom is viewed as the size of Eve cell, it size thus evolves according to the process $\mathcal{X}_\varnothing = \exp(\xi_*)$. Each time τ when the size of the Eve cell has a jump with $\mathcal{X}_\varnothing(\tau) < (1 - \mathrm{e}^{-c})\mathcal{X}_\varnothing(\tau-)$, that is equivalently, when $\xi_*(\tau) - \xi_*(\tau-) < \ln(1 - \mathrm{e}^{-c})$, a daughter cell with size $\mathcal{X}_\varnothing(\tau-) - \mathcal{X}_\varnothing(\tau)$ is born. Daughter cells evolve independently one of the other, again with the same random transitions as $\mathcal{X}_\varnothing = \exp(\xi_*)$, and in turn give birth to grand-daughter cells each time their sizes drop suddenly by factor smaller than $1 - \mathrm{e}^{-c}$, and so on and so forth.

So, the image by the exponential function of the atoms of $\mathcal{L}^{[c]}$ have the same dynamics as a cell system associated to the cell process $X = \exp(\xi)$ in which each daughter cell uj (together with its descent) for $u \in \mathbb{U}$ and $j \in \mathbb{N}$ is killed whenever her size at birth is less than or equal to e^{-c} times the size of her mother immediately before the birth event, that is, whenever $\mathcal{X}_{uj}(0) < \mathrm{e}^{-c}\mathcal{X}_u(b_{uj}-)$. Letting c increase to ∞, we conclude by monotonicity (see Definitions 2 and 3 in [3]) that the compensated fragmentation $\mathbf{Z}$ has the same law as the growth-fragmentation process $\mathbf{X}$. □

Remark. *So we have now two constructions of compensated fragmentations with binary dislocation measures. That in* [3] *takes essentially the point of view of branching random walk and Lévy processes, it is given in physical time. The present one is described in terms of cell processes associated to the exponential of a spectrally negative Lévy process, and adopts the setting of Crump–Mode–Jagers branching processes for the genealogy. The present construction is simpler to make, nonetheless the one in* [3] *is probably better suited to the analysis. We also point out that the construction in* [3] *does not require dislocations to be binary, nor X to converge; however its scope is restricted to the homogenous situation. In particular, the approach in* [3] *does not apply to the general Markovian growth-fragmentation processes which are constructed in the present work. A further important feature is that, as we already mentioned, the distribution of a compensated fragmentation is determined uniquely by the characteristics (σ^2, b, ν); however*

different spectrally negative Lévy processes may generate the same compensated fragmentation process (*cf. Shi* [15]).

We next make the easy observation that Lamperti's transformation for the self-similar cell process can be shifted to the entire cell system. Specifically, consider a homogeneous cell process given in the form $X^{(0)}(t) = x\exp(\xi(t))$, *with* ξ *a spectrally negative Lévy process. Then let* $\mathcal{X}^{(0)} = (\mathcal{X}_u^{(0)}, u \in \mathbb{U})$ *be a* (*homogeneous*) *cell system based on* $X^{(0)}$, *and for each* $u \in \mathbb{U}$, *define the Lamperti transforms*

$$\mathcal{X}_u^{(\alpha)}(t) := \mathcal{X}_u^{(0)}\big(T_u^{(\alpha)}(t)\big),$$

where

$$T_u^{(\alpha)}(t) := \inf\left\{r \geq 0 : \int_0^r \big(\mathcal{X}_u^{(0)}(s)\big)^{-\alpha}\,\mathrm{d}s \geq t\right\}.$$

Corollary 2. *The process* $\mathcal{X}^{(\alpha)} = (\mathcal{X}_u^{(\alpha)}, u \in \mathbb{U})$ *is a cell system based on the self-similar cell process*

$$X^{(\alpha)}(t) = x\exp\big\{\xi\big(\tau^{(\alpha)}_{tx^\alpha}\big)\big\},$$

where $\tau^{(\alpha)}$ *is defined in* (5).

It is a special case of Proposition 3 that when ξ is the negative of a subordinator, then the cell population process $\mathbf{X}^{(0)}$ associated to the cell system $\mathcal{X}^{(0)}$ can be viewed as a homogeneous fragmentation process with a binary conservative dislocation measure. See Pitman and Winkel [14], who investigate in particular the family of subordinators which give rise to the same homogeneous fragmentation. In this framework, Corollary 2 essentially rephrases the connection between self-similar fragmentations with the same dislocation measure and distinct indices of self-similarity which is stated as Theorem 3.3 in [2].

We now conclude this section with an extinction property of self-similar growth-fragmentations with a negative index, which extends the well-known one in the case of pure fragmentation (see, e.g., Section 1.3 in [2]).

Corollary 3. *Assume that the cell process* X *is self-similar with index* $\alpha < 0$ *and that* $\kappa(q) < 0$ *for some* $q \geq 0$. *Then the extinction time*

$$\inf\big\{t \geq 0 : \mathbf{X}(t) = \varnothing\big\}$$

is finite $\mathbf{P}_x$*-a.s. for every* $x > 0$.

Proof. Consider the homogeneous cell process $X^{(0)} = \exp(\xi)$ and let $\mathcal{X}^{(0)} = (\mathcal{X}_u^{(0)}, u \in \mathbb{U})$ denote the corresponding cell-system. We define the self-similar cell-system $\mathcal{X}^{(\alpha)} = (\mathcal{X}_u^{(\alpha)}, u \in \mathbb{U})$ as in Corollary 2. For every $u \in \mathbb{U}$ and $\gamma = 0, \alpha$, we write $b_u^{(\gamma)}$ for the birth-time of the cell labelled by u in $\mathcal{X}^{(\gamma)}$, and by $\zeta_u^{(\gamma)} := \inf\{t \geq 0 : \mathcal{X}_u^{(\gamma)}(t) = 0\}$ for its lifetime. We have to check that

$$\sup_{u\in\mathbb{U}}\big(b_u^{(\alpha)} + \zeta_u^{(\alpha)}\big) < \infty, \qquad \text{almost surely.} \tag{8}$$

For every $u = (u_1, \dots, u_j) \in \mathbb{U}$ and $t \geq 0$, we define $u^{(\gamma)}(t)$ as the youngest ancestor of the cell u in the system $\mathcal{X}^{(\gamma)}$ which is alive at time t. That is $u^{(\gamma)}(t) = u$ whenever $t \geq b_u^{(\gamma)}$ and $u^{(\gamma)}(t) = (u_1, \dots, u_{i-1})$ if $b^{(\gamma)}_{(u_1,\dots,u_{i-1})} \leq t < b^{(\gamma)}_{(u_1,\dots,u_i)}$ for some $i = 1, \dots, j$. We then define the path

$$\mathcal{Y}_u^{(\gamma)}(t) = \mathcal{X}^{(\gamma)}_{u^{(\gamma)}(t)}\big(t - b^{(\gamma)}_{u^{(\gamma)}(t)}\big), \qquad t \geq 0$$

which is obtained by the concatenation of the portions of paths of the ancestors of u. Plainly, we have

$$\inf\big\{t \geq 0 : \mathcal{Y}_u^{(\alpha)}(t) = \partial\big\} = b_u^{(\alpha)} + \zeta_u^{(\alpha)},$$

and on the other hand, Corollary 2 entails that $\mathcal{Y}_u^{(\alpha)}$ and $\mathcal{Y}_u^{(0)}$ are related by the Lamperti transformation. In particular, the lifetime of $\mathcal{Y}_u^{(\alpha)}$ can also be expressed as

$$\inf\big\{t \geq 0 : \mathcal{Y}_u^{(\alpha)}(t) = \partial\big\} = \int_0^\infty \big(\mathcal{Y}_u^{(0)}(t)\big)^{-\alpha}\,\mathrm{d}t.$$

On the other hand, we deduce from Corollary 3 in [3] and Proposition 3 that the process

$$\exp\big(-\kappa(q)t\big)\sum_{u\in\mathbb{U}}\big(X_u^{(0)}(t)\big)^q, \qquad t \geq 0$$

is a martingale (as a matter of fact, Corollary 3 in [3] assumes $q \geq 2$, but the argument works as well for $q > 0$ provided that $\kappa(q) < \infty$). As a consequence, if $X_*^{(0)}(t)$ denotes the size of the largest cell in the population $\mathbf{X}^{(0)}(t)$

$$\omega := \sup\big\{\exp\big(-t\kappa(q)/q\big)X_*^{(0)}(t), t \geq 0\big\} < \infty \qquad \text{a.s.}$$

Since $\mathcal{Y}_u^{(0)}(t) \leq X_*^{(0)}(t)$, we conclude that for all $u \in \mathbb{U}$,

$$b_u^{(\alpha)} + \zeta_u^{(\alpha)} \leq \omega^{-\alpha}\int_0^\infty \exp\big(-t\alpha\kappa(q)/q\big)\,\mathrm{d}t < \infty \qquad \text{a.s.}$$

Since $\alpha < 0$ and $\kappa(q) < 0$, the right-hand side is a.s. finite, which establishes (8). □

3.4. The genealogical branching random walk and some applications

In Section 2.1, we have seen that the genealogy of cell systems is described by a general branching process. In this final section, we start by observing that in the self-similar case, we can view process of the families of the logarithm of the sizes of cells at birth, indexed by generations, as a branching random walk. Specifically, for every integer $n \geq 0$, introduce

$$\mathcal{Z}(n) := \big\{\big\{\ln \mathcal{X}_u(0) : u \in \mathbb{N}^n\big\}\big\}.$$

The self-similarity property of the cell process entails that for every $x > 0$, the distribution of $\mathcal{Z}(1)$ under $\mathcal{P}_x$ is the same as that of $\ln x + \mathcal{Z}(1)$ under $\mathcal{P}_1$, and then the genealogical branching

property (cf. Proposition 1) readily yields that the process $(\mathcal{Z}(n) : n \geq 0)$ is a branching random walk. In words, $(\mathcal{Z}(n) : n \geq 0)$ is a Markov chain such that the conditional distribution of $\mathcal{Z}(n+1)$ given $\mathcal{Z}(n)$ is the law of the random multi-set $\bigsqcup_{z\in\mathcal{Z}(n)}(z+\bar{\mathcal{Z}}_z)$ which is obtained by replacing each element z of $\mathcal{Z}(n)$ by $z+\bar{\mathcal{Z}}_z$, where each $\bar{\mathcal{Z}}_z$ denotes an independent copy of $\mathcal{Z}(1)$ under $\mathcal{P}_1$. In the rest of this section, we shall implicitly rule out the degenerate case when the cell process X is continuous a.s.

We point out that the mean Laplace transform of $\mathcal{Z}(1)$,

$$m(q) := \mathcal{E}_1\Big(\sum_{z\in\mathcal{Z}(1)} \exp(qz)\Big), \qquad q > 0,$$

can be computed explicitly in terms of the Laplace exponent Ψ of the underlying Lévy process ξ, which is given by (4), and the function κ, which has been defined in (7).

Lemma 3. *For every $q > 0$ with $\kappa(q) < \infty$, one has*

$$m(q) = \begin{cases} 1 - \kappa(q)/\psi(q), & \text{if } \Psi(q) < 0, \\ \infty, & \text{otherwise.} \end{cases}$$

As a consequence, $m(q) < 1$ if and only if $\kappa(q) < 0$, and then

$$\mathcal{E}_1\Big(\sum_{u\in\mathbb{U}} \mathcal{X}_u^q(0)\Big) = \frac{\psi(q)}{\kappa(q)} < \infty.$$

Proof. Because cell systems corresponding to self-similar cell processes having the same underlying Lévy process ξ are related one to the other by Lamperti's time substitution (see Corollary 2), and because such a time substitution does not modify neither the genealogy of cells nor their sizes at birth, we may assume without loss of generality that the index of self-similarity is $\alpha = 0$. In this setting, the cell process is $X(t) = \exp(\xi(t))$ and we have therefore

$$\mathcal{E}_1\Big(\sum_{z\in\mathcal{Z}(1)} \exp(qz)\Big) = E\left(\sum_{t\geq 0} \exp\big(q\xi(t-)\big)\big(1 - \exp\big(\Delta\xi(t)\big)\big)^q\right).$$

Classical arguments based on the Lévy–Itô decomposition of Lévy processes and the compensation formula for Poissonian integrals show that the right-hand side equals

$$E\left(\int_0^\infty \exp\big(q\xi(t)\big)\,\mathrm{d}t\right)\int_{\mathbb{R}_-}\big(1-\mathrm{e}^x\big)^q\,\Lambda(\mathrm{d}x),$$

where Λ denotes the Lévy measure of the underlying Lévy process ξ. This quantity is finite if and only if $\Psi(q) < 0$ and is then given by

$$-\frac{1}{\Psi(q)}\int_{\mathbb{R}_-}\big(1-\mathrm{e}^x\big)^q\,\Lambda(\mathrm{d}x).$$

The formula for $m(q)$ in the statement then follows from the definition (7) of κ by substitution.

Assume now that $\kappa(q) < 0$ for some $q > 0$. The definition (7) shows that $\Psi(q) < \kappa(q) < 0$, so that $m(q) < 1$ by the first part, and the conserve is immediate. The fact that $(\mathcal{Z}(n) : n \geq 0)$ is a branching random walk entails that the mean Laplace transform of $\mathcal{Z}(n)$ is

$$\mathcal{E}_1\Big(\sum_{z\in\mathcal{Z}(n)} \exp(qz)\Big) = m(q)^n$$

and thus

$$\mathcal{E}_1\Big(\sum_{u\in\mathbb{U}} \mathcal{X}_u^q(0)\Big) = \mathcal{E}_1\Big(\sum_{n=0}^{\infty}\sum_{z\in\mathcal{Z}(n)} \exp(qz)\Big) = \frac{1}{1-m(q)} = \frac{\psi(q)}{\kappa(q)}. \qquad \square$$

We next point at the following reinforcement of Lemma 3. Introduce the maximal size of each cell

$$\mathcal{X}_u^* := \sup_{t\geq 0} \mathcal{X}_u(t), \qquad u \in \mathbb{U}.$$

We also write $\mathcal{L}_{\mathbb{U}}^q$ for the space of q-summable families indexed by $\mathbb{U}$, endowed with the usual norm.

Corollary 4. *Suppose that there exists $q > 0$ with $\kappa(q) < 0$. Then we have*

$$\mathcal{E}_1\Big(\sum_{u\in\mathbb{U}} (\mathcal{X}_u^*)^q\Big) < \infty.$$

As a consequence, the process $\mathbf{X} = (\mathbf{X}(t), t \geq 0)$ has càdlàg paths in $\mathcal{L}_{\mathbb{U}}^q$, a.s.

Remark. *Because for any $q' > q$, convergence in $\mathcal{L}_{\mathbb{U}}^q$ implies convergence in $\mathcal{L}_{\mathbb{U}}^{q'}$, $\mathbf{X}$ is thus also càdlàg in $\mathcal{L}_{\mathbb{U}}^{q'}$.*

Proof. We first recall that $\sup_{t\geq 0} \xi(t)$ has the exponential distribution with parameter ϱ, where $\varrho > 0$ is the strictly positive solution to $\Psi(q) = 0$; see for instance Corollary VII.2(ii) in [1]. Therefore, for every $r \in (0, \varrho)$, we have

$$\mathcal{E}_1\big((\mathcal{X}_u^*)^r\big) = \frac{\varrho}{\varrho - r}\mathcal{E}_1\big((\mathcal{X}_u(0))^r\big).$$

Let now $q > 0$ with $\kappa(q) < 0$. Since Ψ remains nonnegative on $[\varrho, \infty)$ and $\kappa \geq \Psi$, we see that $q < \varrho$, and we conclude from Lemma 3 that

$$\mathcal{E}_1\Big(\sum_{u\in\mathbb{U}} (\mathcal{X}_u^*)^q\Big) = \frac{\varrho}{\varrho - q}\mathcal{E}_1\Big(\sum_{u\in\mathbb{U}} \mathcal{X}_u^q(0)\Big) < \infty.$$

Then, consider a sequence $(\mathbb{U}_n : n \in \mathbb{N})$ of finite subsets of $\mathbb{U}$ with $\mathbb{U}_n \subseteq \mathbb{U}_{n+1}$ and $\bigcup_{n\in\mathbb{N}} \mathbb{U}_n = \mathbb{U}$. Because each cell process X_u has càdlàg paths and $\mathbb{U}_n$ is finite, the process $t \mapsto (1_{\mathbb{U}_n}(u)X_u(t) : u \in \mathbb{U})$ has also càdlàg paths in $\mathcal{L}^q_{\mathbb{U}}$, a.s. We deduce from the first part that

$$\lim_{n\to\infty} \mathcal{E}_1\Big(\sum_{u\in\mathbb{U}\setminus\mathbb{U}_n} \big(\mathcal{X}^*_u\big)^q \Big) = 0$$

and it follows easily that $(\mathbf{X}(t), t \geq 0)$ has càdlàg paths in $\mathcal{L}^q_{\mathbb{U}}$, a.s. □

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