Panjer Randomized Fibonacci Model and Dynamic Instabilities in Population Growth Models

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Abstract. Although Fibonacci's numbers play an important role in modeling phenomena in a wide variety of subjects, their use as descriptors of population growth has clearly been rather restricted after the introduction of the Verhulst logistic model and its numerous modifications and extensions. In fact, in the very unrealistic Fibonacci model neither population extinction nor bounded growth are possible, only quasi-exponential unbounded population growth can result. We present a modified model assuming that the number of direct offsprings of each ancestor is a Bernoulli random variable, hence with positive probability of 0 count, and thus accommodating both extinction and possible sustainable growth. We compare algebraic and numerical treatment of equations using the fixed point method in the framework of instabilities of numerical algorithms for finding roots of equations. On the othe hand, branching processes are natural models for random population growth in many situations. Here we use basic count models whose probability mass function satisfies Panjer iteration, and investigate randomly stopped sums and collective risk when the subordinator random variable and the summands are independent and identically distributed basic count random variables.
Keywords: Fibonacci model, Verhulst model, Bernoulli offsprings, branching processes, fixed point algorithm instabilities, branching processes, Panjer iteration, basic count models.

1 Introduction

Let $N(t)$ denote the size of some population at time t. Two main issues in population dynamics deal with the probability of extinction and with the total size of the progeny of an ancestor.

Fibonacci (c. 1170 – c. 1250) in his *Liber Abaci* posed and solved a problem involving the growth of a population of rabbits based on idealized and very unrealistic assumptions. As a consequence, a population with Fibonacci's growth pattern never dies out, while we know that the total progeny of some ancestor is in many real circumstances finite, cf. for instance Lotka [15] example (p. 123–136) on the extinction of surnames, using branching processes. However, Fibonacci's numbers are still a very active research area, since they (mainly the initial numbers of the sequence) can approximate quite well counts in many natural systems, and have been applied successfully in very diverse situations and areas, namely aesthetic (the golden ratio is pervasive in all form of plastic arts, and is even used by aesthetic surgeons in beauty improvement), including for instance Lindenmayer grammars, cf. Prusinkiewicz and Hanan [20], used by Pestana [18] for an initial investigation of music composition with repetitive structures.

1.1   Fibonacci population growth model

Fibonacci (c. 1170 – c. 1250) in his *Liber Abaci* posed and solved a problem involving the growth of a population of rabbits based on idealized and very unrealistic assumptions. The solution, generation by generation, was a sequence of numbers $\{F_n\}_{n \geq 0}$ later known as Fibonacci numbers, starting with $\{0, 1\}$, such that $F_{n+2} = F_n + F_{n+1}$. Using Binet's formula

$$F_n = \frac{(1 + \sqrt{5})^n - (1 - \sqrt{5})^n}{2^n \sqrt{5}}$$

the computation of any member of the Fibonacci sequence is straightforward.

Although the wide success of Fibonacci's sequence as an approximate model for the first few generations is still praised in many branches of Biology, the very unrealistic assumption that any couple of rabbits gives birth to exactly one couple of rabbits as offsprings, and this in each of exactly two successive mating periods, cannot accommodate important real features in population dynamics, such as sustainable growth or even population extinction, as studied successfully for instance by Lotka [14] using the more realistic sustainable growth logistic model introduced by Verhulst. In fact, rewriting $F_{n+2} = F_n + F_{n+1} = 2\,F_{n+1} - F_{n-1} \implies F_{n+2} - F_{n+1} = F_{n+1} - F_{n-1}$, the closely associated differential equation $\frac{\mathrm{d}}{\mathrm{d}t}\,N(t) = \frac{\partial^2}{\partial t^2}\,N(t)$ shows that Fibonacci's growth is approximately exponential. Indeed, we get an approximate geometric growth with ratio $\frac{1+\sqrt{5}}{2}$. Even for moderate values such as $n = 11$, say, $F_{12} = 144 \approx F_{11}\frac{1+\sqrt{5}}{2} = 144.005$ (recall that $\frac{1+\sqrt{5}}{2}$ is the "golden ratio" limit of $\frac{F_{n+1}}{F_n}$).

1.2   Verhulst sustainable growth logistic model and extensions

Imposing some natural regularity conditions on $N(t)$, namely that $\frac{\mathrm{d}}{\mathrm{d}t}N(t) = \sum_{k=0}^{\infty} A_k[N(t)]^k$, Verhulst ([27], [28], [29]) used the second order approximation

$\frac{\mathrm{d}}{\mathrm{d}t} N(t) = A_1 N(t) + A_2 [N(t)]^2$, with $A_1 > 0$ and $A_2 < 0$, which can be rewritten as

$$\frac{\mathrm{d}}{\mathrm{d}t} N(t) = r\, N(t) \left[1 - \frac{N(t)}{K} \right], \tag{1}$$

(where $r > 0$ is frequently interpreted as a Malthusian instantaneous growth rate parameter, whenever modeling natural breeding populations, and $K > 0$ as the equilibrium limit size of the population) to develop a broadly successful "logistic" population growth model, much more realistic to model sustainable growth. In fact, an initial period of exponential growth if followed by moderate approximately linear growth, with exponential steep exponential moderation when limitation of natural resources (or success of predators or competing species) ultimately curb down growth to sustainable values.

Moreover, and since in many species there exist periodic mating periods, using Euler's ideas on the interplay of differential equations and difference equations in numerical methods, the associated difference equation

$$x_{n+1} = \alpha\, x_n\, (1 - x_n), \tag{2}$$

(where it is convenient to deal with the assumption $x_n \in [0, 1], \; n = 1, 2, \dots$) made his way in modeling population dynamics.

The equilibrium $x_{n+1} = x_n$ leads to a simple second order algebraic equation with positive root $1 - 1/\alpha$, and to a certain extent it is surprising that anyone would care to investigate its numerical solution using the fixed point method, which indeed brings in many pathologies when a steep curve — i.e., for some values of the iterates $|\alpha\,(1 - 2\,x_n)| > 1$ — is approximated by an horizontal straight line. This numerical investigation, apparently devoid of interest, has however been at the root of many theoretical advances when $\alpha \notin [1, 3]$ (namely Feigenbaum bifurcations and ultimate chaotic behavior), and *a posteriori* led to many interesting breakthroughs in the understanding of population dynamics. Due to its close association with the differential equation (1), whose solution is a logistic function

$$N(t) = \frac{K\, N_0}{N_0 + (K - N_0)\, \mathrm{e}^{-rt}}, \tag{3}$$

the parabola $x\,(1 - x)$ appearing in the discretization (2) is very often called the "logistic parabola".

Up to a multiplicative constant, the logistic parabola is the $Beta(2, 2)$ probability density function. In Aleixo *et al.* [1], and in Rocha *et al.* [23] several extensions of population growth models tied to more general $Beta(p, q)$ densities have been investigated, and in Pestana *et al.* [17] the factor $1 - x$ has been considered the linear truncation of $-\ln x$, so obtaining differential functions whose solution exhibits Paretian tail behaviour and ultimately extreme value models (*Gumbel*, *Fréchet* or *Weibull*) solutions for the associated differential equation $\frac{\mathrm{d}}{\mathrm{d}t} N(t) = r\, N(t)\, (-\ln(N(t))^{1+\gamma}$. Tsoularis [26] and Waliszewski and Konarski [30] must be credited for the *Gompertz* (or *Gumbel*) solution when in the associated differential equation $\gamma = 0$. Tsoularis [26] is a very informative state-of-the-art on population growth models. Brilhante *et al.* ([3], [4]) provide

the connection between the solution of the above extensions of the original Verhulst equation to extreme value and Rachev and Resnick [21] geo-extreme value (i.e., when the original sequence is subject to Rényi's [22] rarefaction, equivalent in its final results to Kovalenko's [12] and Kozubowski's [13] geometric thinning).

1.3   Modified Fibonacci models

We shall discuss, using branching processes, several modifications of the Fibonacci model, so that more realistic possibilities, such as limited growth or even extinction, may occur:

1. A framework very similar to the original description posed by Fibonacci: each ancestor can produce direct offsprings only in the first two consecutive reproducing periods. However, instead of deterministically producing exactly one offspring in each reproducing epoch, the number of offsprings is a random $X \frown Bernoulli(p)$.

2. A simple modification, which has the advantage of affordable algebraic treatment, is to consider that the progeny (it is indifferent whether we count individuals in the case of non-sexual reproduction, or couples in the case of sexual reproduction) is a random $Y \frown Geometric(p)$. The hypothesis that in sexual reproduction we consider that the progeny is solely of couples, and that each of those behaves as a faithful couple, is indeed as unrealistic as what has been taken for granted as an assumption in the original Fibonacci model. But the wider variability of the number of offsprings of each ancestor at each reproducing period, with sensible choices so that the mean value $\mathbb{E}(Y) = (1 - p)/p$ is rather small, can produce more realistic results.
   Observe, further, that while the Bernoulli random variable is underdispersed, i.e $Var(X)/\mathbb{E}(X) < 1$, the Geometric random variable is overdispersed, So, it can accommodate more realistic wider variability.

3. An almost similar framework as the one described in item 1 is investigated explicitly assuming removing each progenitor from the system after two reproduction periods, using randomly stopped sums.

Aside from presenting models allowing for extinction and limited growth, and hence more realistic than the unlimited quasi-exponential growth of the original Fibonacci model, our aim is to compare whenever possible algebraic solutions to numerical solutions using the fixed point method. These indeed exhibit instabilities whenever the function is too steep in a neighborhood of the root we wish to calculate.

Although those instabilities are qualitatively quite different from the celebrated Feigenbaum bifurcations and ultimate chaos that the discretization of the Verhulst model brought to the limelights of the structural investigation of dynamical systems, it seems worthwhile to discuss them, since the philosophical controversy whether pathologies observed in the numerical solution of equations $x = f(x)$ using the fixed point algorithm are an essential feature or solely an inherent consequence of instabilities to be expected when $|f'(x)| > 1$ in the vicinity of the equation root is far from being settled.

In this first paper, we shall discuss in depth the Bernoulli randomized model described in item 1, postponing for a second part other randomizations.

2   Modified Randomized Fibonacci Models: Bernoulli(p) Offsprings in Each Reproduction Epoch

Let us assume that the process starts with one ancestor (single or couple, according to the reproduction characteristics of the species). In each of the two initial reproduction epochs each unit produces $X \frown Bernoulli(p)$ offsprings, and is removed from the process after the the second reproduction epoch. On the other hand, each offspring becomes an ancestor in the next step, behaving exactly in the some fashion.

Let Z_1 denote the number of units in the system in the first step of the process, i.e. exactly when the initial ancestor is removed from the system:

$$Z_1 = \begin{Bmatrix} 0 & 1 & 2 & 3 \\ (1-p)^2 & p(1-p)(2-p) & 2p^2(1-p) & p^3 \end{Bmatrix} \tag{4}$$

The probability generating function is

$$\mathcal{G}_{Z_1}(t) = (1-p)^2 + p(1-p)(2-p)t + 2p^2(1-p)t^2 + p^3 t^3, \tag{5}$$

and hence the mean value, expressed as a function of p, is

$$\mathbb{E}(Z_1) = p(1-p)(2-p) + 4p^2(1-p) + 3p^3, \tag{6}$$

which is greater than 1 for $p \in (\sqrt{2} - 1, 1] \approx (0.414214, 1]$.

If $\mathbb{E}(Z_1) < 1$, extinction is almost sure.

If $\mathbb{E}(Z_1) > 1$, defining iteratively $x_n = \mathcal{G}_{Z_1}(x_{n-1})$, with initial value $x_1 = \mathbb{P}[Z_1 = 0] = (1-p)^2$, x_n is the probability that the process terminates at or before the n-th generation, cf. Feller [5], Theorem p. 297.

The sequence $\{x_n\}$ is increasing, its limit $x \leq 1$ being the solution of the equation

$$x = \mathcal{G}_{Z_1}(x)$$

In the model at hand, the probability of extinction is therefore

$$x \equiv x_p = \min \left\{ 1, \frac{(p-2)p^2 + \sqrt{p^3(4 - 4p + p^3)}}{2 p^3} \right\}, \tag{7}$$

On the other hand, the total number os descendants from the initial ancestor up to the n-th generation is $Y_n = 1 + Z_1 + Z_2 + \cdots + Z_n$, where Z_k denotes de number of units in the k-th generation. Following Good [7] (an argument that inspired Feller [5], XII.5), $R_1(t) = t\,\mathcal{G}(t)$ and iteratively $R_n(t) = t\,R_{n-1}(t)$, we obtain the probability generating functions for the successive generations.

This is a decreasing sequence, whose limit $\rho(s)$ satisfies $\rho(s) = s\,\mathcal{G}(\rho(s))$ and which may be found solving $t = s\,\mathcal{G}(t)$. Each coefficient r_k in the MacLaurin's expansion of $\rho(s)$ is the probability that the total progeny consists of k elements, and therefore if $\sum r_k = \rho(1) < 1$, this is the probability of extinction.
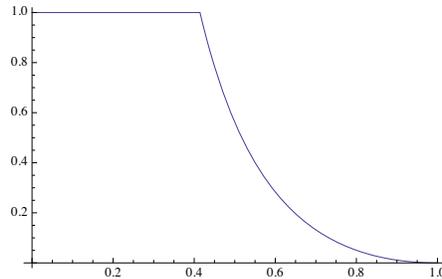
Fig. 1. Extinction probability x_p, in (7), as a function of p in the Bernoulli(p) off-springs randomized Fibonacci model.

The total progeny is finite whenever the expected value $\mu = \mathbb{E}(Z_1) < 1$. Therefore, as $\mathbb{E}(Z_n) = \mu^n$, it follows that the expected value of the total progeny is $\sum_{n=0}^{\infty} \mu^n = \frac{1}{1-\mu}$.

In this randomized Bernoulli Fibonacci modified model, from solving $t = s\,\mathcal{G}(t)$ we get

$$\rho(s) = \frac{2(-p^2 s + p^3 s)}{3\,p^3 s} - \frac{(1 - \mathrm{i}\sqrt{3})A(s)}{32^{2/3}\,p^3 s\,\left((B(s) + \sqrt{4A^3(s) + B^2(s)})\right)^{1/3}} - \frac{(1 + \mathrm{i}\sqrt{3})}{62^{1/3}\,p^3 s}\left((B(s) + \sqrt{4A^3(s) + B^2(s)})\right)^{1/3} \tag{8}$$

where $A(s) = -3p^3 s + (2p^4 - p^5 - p^6)s^2$, and $B(s) = 18(1-p)p^5 s^2 + (7p^6 - 12p^7 + 3p^8 + 2p^9)s^3$.

Plotting the the real part of the above function $\rho(s)$, in (8), for $s = 1$, which indeed coincides with (7), we obtain a visual grasp of the probability of extinction as a function of p, exactly the one given in Fig. 1, using now a more complex definition of the function to be plotted.

Observe that the equilibrium point $p = \rho(p)$ is 0.513376. The observation that this is approximately the proportion of male offsprings in the observed equilibrium of human reproduction is surely circumstantial, or at least we do not devise any bond tying that empirical observation.

On the other hand, $\mu < 1$ for $p < \sqrt{2} - 1 \approx 0.414214$. Below, in Table 1 we register for a few values of p the expected size of the total progeny:

We now compare this analytic solution with the numerical results defining iteratively $x_n = \mathcal{G}_{Z_1}(x_{n-1})$, the probability that extinction does occur at or before the n-th generation, with initial value $x_1 = \mathbb{P}[Z_1 = 0] = (1-p)^2$.

The successive repeated compositions of a function with itself can be computed using for instance the command "Nest" in *Mathematica*, and the corresponding evaluation at the appropriate point can then generate a list of coordinates with the command "Flatten".

In Table 2 we illustrate the result for the choices 0.1(0.1)0.9, and also for the extreme choices 0.01 and 0.99, and finally for the equilibrium value 0.513376 (using 200 points and 300 iterated compositions of the function with itself.

p	μ	Expected size $\frac{1}{1-\mu}$
0.1	0.21	1.26582
0.2	0.44	1.78571
0.3	0.69	3.22581
0.4	0.96	25
.41421	0.99999...	99246.7

Table 1. Expected total progeny when $\mu < 1$ in the modified Bernoulli randomized Fibonacci model.
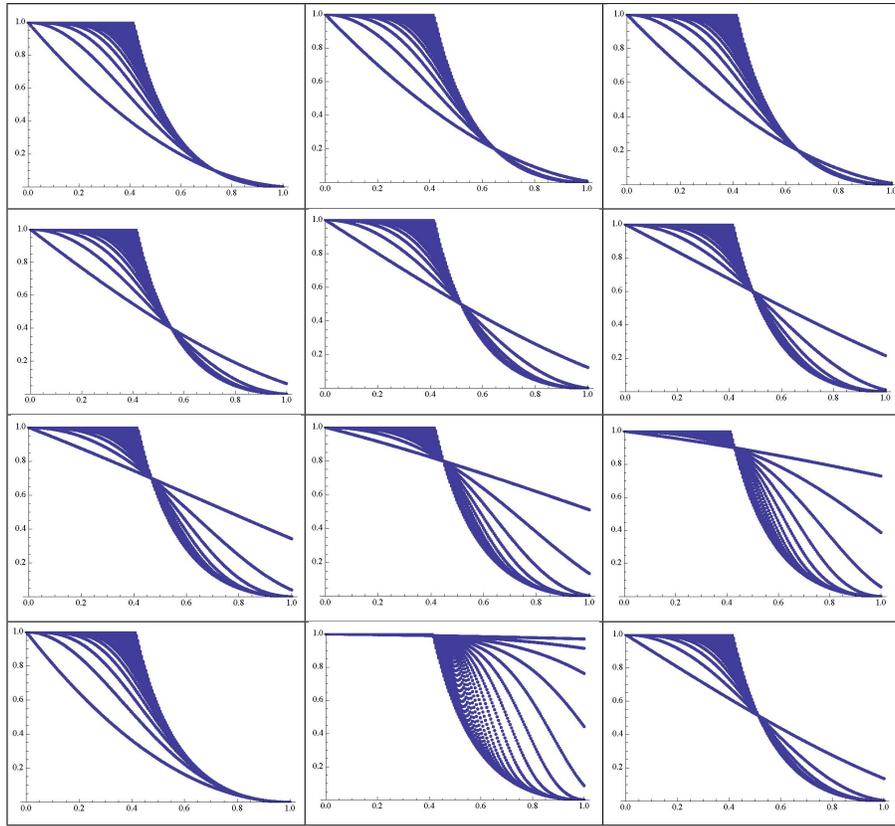

Table 2. Graphical representation of 300 compositions of the generating function with itself; from left to right and top to bottom, initial 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 0.01, 0.99, 0.513376.

From those graphics it is obvious that the use of the fixed point method leads to instabilities, that seem quite different in nature from the Feigenbaum bifurcations encountered in the discretization of the Verhulst model and its various extensions we have mentioned. Further research is needed to interpret those pathologies in the context of dynamical models.

3 Randomizing the Fibonaccy Population Growth Model Via Branching Processes

Let $\{f_n\}_{n \in \mathcal{S}_X}$ denote the probability mass function (pmf) of a discrete random variable (rv) X with support $\mathcal{S}_X \subset \mathbb{N}$. The corresponding probability generating function (pgf) is $m_X(t) = E(t^X) = \sum_{n=0}^{\infty} f_n t^n$.

If N is a discrete rv, $X_0 = 0$ and $X_1, X_2, \ldots$ independent replicas of X, with N and X_k independent, and we define the "compound" rv $Y = \sum_{k=0}^{N} X_k$, then

$$m_Y(t) = \sum_{j \in \mathcal{S}_Y} m_X^j(t)\, \mathbb{P}[N = j] = m_N(m_X(t)). \qquad (9)$$

From this, we may easily compute mean value and variance of the rv Y. An alternative designation for the concept of compounding rv's is the concept of randomly stopped sums, which can have the advantage of explicitly indicating the type of the subordinator rv.

If in particular X_k, $k = 1, 2, \ldots$ are independent replicas of a count rv X modeling the number of direct descendants of each individual (or each female) in the population, and we define

$$Y_0 = 1, \qquad Y_1 = X_1, \qquad Y_2 = \sum_{k=0}^{Y_1} X_k, \quad \ldots \quad Y_{n+1} = \sum_{k=0}^{Y_n} X_k, \quad \ldots \qquad (10)$$

we may interpret Y_k as the number of direct offsprings in the k-th generation, and $Z_n = \sum_{j=0}^{n} Y_j$ as the total progeny of some ancestor until the n-th generation. Let us denote $m(t) = m_1(t)$ the pgf of $Y_1 \overset{\mathrm{d}}{=} X$, $m_n(t)$ the pgf of Y_n; then $m_n(t) = m(m_{n-1}(t) = m^{\otimes(n)}(t)$, where $m^{\otimes(n)}$ denotes the n-fold composition of m with itself.

Following Good [7] (an argument that inspired Feller [5], XII.5), $m_{Z_1}(t) = t\, m_X(t)$ and iteratively $m_{Z_n}(t) = t\, m_{Z_{n-1}}(t)$, we obtain the probability generating functions for the number of descendants up to each successive generation.

This is a decreasing sequence, whose limit $\rho(s)$ satisfies $\rho(s) = s\, m_X(\rho(s))$ and which may be found solving $t = s\, m_X(t)$. Each coefficient r_k in the MacLaurin's expansion of $\rho(s)$ is the probability that the total progeny consists of k elements, and therefore if $\sum r_k = \rho(1) < 1$, this is the probability of extinction.

$\{Y_0, Y_1, ...\}$ is usually called a Galton–Watson branching process, or a cascade process. Simple examples of branching processes, and basic results on important problems such as extinction probability and size of a population can be found in Feller [5]. Namely, in what concerns extinction:

Theorem 1. *If* $\mathbb{E}(Y) = \mu \leq 1$*, the process almost surely dies out, and its expected size is* $\dfrac{1}{1 - \mu}$ *when* $\mu < 1$*, and infinite when* $\mu = 1$*. If* $\mu > 1$*, the probability* f_n *that the process terminates at or before the n-th generation tends to the unique root* $x < 1$ *of the equation* $x = m_Y(x)$*.*

And, in what concerns the total progeny:

Theorem 2. *Denoting* ρ_k *the probability that the total progeny has k individuals,*

1. *the extinction probability is* $\displaystyle\sum_{k=1}^{\infty} \rho_k$*.*

2. *The pgf* $\rho(s) = \displaystyle\sum_{k=1}^{\infty} \rho_k s^k$ *is given by the unique positive root of* $t = s\, m_Y(t)$*, and* $\rho(s) \leq x$*.*

More extensive monographies on branching processes, with deeper results, are Harris [8], Athreya and Ney [2] or Jaegers [10]. Gnedenko and Korolev [6] present interesting examples of random infinite divisibility and random stability using branching processes, and they establish necessary and sufficient conditions for the convergence of randomly stopped sums, and limit theorems for super-critical (i. e., $\mu = \mathbb{E}(X) > 1$) Galton–Watson processes.

The $Y \frown Geometric(p)$ model for the number of direct descendants, with pmf $\{f_n = p\,(1 - p)^n\}_{n \in \mathbb{N}}$, provides an algebraic simple treatment. In fact, writing $q = 1 - p$, $m_Y(t) = \dfrac{p}{1 - qt}$, and

$$m_{Y_n}(t) = \begin{cases} p\,\dfrac{q^n - p^n - (q^{n-1} - p^{n-1})\,q\,t}{q^{-1}n - p^{n-1} - (q^n - p^n)\,q\,t} & p \neq q \\[4ex] \dfrac{n - (n-1)t}{n + 1 - nt} & p = q = \frac{1}{2} \end{cases} \tag{11}$$

is easily computed.

Both the $Bernoulli(p)$ and the $Geometric(p)$ pmf's satisfy the recursive expression

$$f_{n+1} = \left(a + \frac{b}{n+1}\right) f_n, \quad \forall n \geq k, \quad f_n = 0 \text{ for } 0 \leq n \leq k - 1 \tag{12}$$

(in the case of $X \frown Bernoulli(p)$, $a = \dfrac{p}{p-1}$ and $b = \dfrac{2p}{1-p}$, and in the case of $X \frown Geometric(p)$, $a = q$ and $b = 0$). As we shall state in the following section, the above recursive expression is valid for the pmf of a broad class of rv's, known as Panjer rv's, that play an important role on the theory of collective risk. We investigate some consequences of using simple Panjer direct progeny models in branching processes.

4 Basic Count Models

We shall say that X is a Panjer rv if its pmf $\{f_n\}_{n \in \mathcal{S}_X}$ satisfies the recursive expression

$$f_{n+1} = \left(a + \frac{b}{n+1}\right) f_n, \ \forall n \geq k, \quad f_n = 0 \text{ for } 0 \leq n \leq k-1. \quad (13)$$

We denote $Panjer(a, b, k)$ the class of all pmf's satisfying (13).

This expression has been used by several authors, with $k = 0$, before Panjer [16], but it was in this seminal paper that the consequences for the iterative computation of the density of the collective risk process have been established.

In fact, Panjer [16] considered only the case $k = 0$ — for which the non degenerate types are the underdispersed binomial, the overdispersed negative binomial, and the Poisson in between —, but immediatly Sundt and Jewell [25] published the extension for $k = 1$, with the logarithmic and the extended negative binomial solutions.

Finally Hess *et al.* [9] defined the general class, with the recursion starting with $k \geq 0$, the $f_0, ..., f_{k-1}$ being free parameters (for $k = 0$, f_0 can be considered the starting jump of a hurdle process); it is also known as the class of basic count distributions, or class of basic claim distributions. For more details, cf. Rolsky *et al.* [24], Klugman *et al.* [11], and Pestana and Velosa [19].

Theorem 3. *Let $\{f_n\}_{n \in \mathcal{S}_X}$ be the pmf of a non degenerate count rv X. For $a, b \in \mathbb{R}$ the statements that follow are equivalent:*

(a) $\{f_n\}_{n \in \mathcal{S}_X}$ is a $Panjer(a, b; k)$ pmf.
(b) for $\ell \in \mathbb{N}^+$, the pgf $m_X(t) = \sum_{n=0}^{\infty} f_n t^n$ satisfies the differential equations

$$(1 - at)h^{(\ell)}(t) = (\ell a + b)h^{(\ell-1)}(t) + f_k \binom{k}{\ell} \ell! \, t^{k-1},$$

$t \in [0, 1)$ and $h^{(j)}(0) = 0$ for $j \leq k - 1$.
(c) m_X satisfies the differential equation

$$(1 - at)h^{(k+1)}(t) = ((k+1)a + b)h^{(k)}(t),$$

$t \in [0, 1)$ and $h^{(j)}(0) = 0$ for $j \leq k - 1$.

Further, $Q = Panjer(a, b; k) \implies (k+1)\, a + b > 0$, and on the other hand $a + b \geq 0 \Rightarrow a < 1$ and $a + b < 0 \Rightarrow a \leq 1$.

From this it is easy to conclude that the Panjer class has the following non degenerate elements:

1. The $Binomial(\nu, p)$, $\nu \in \mathbb{N}^+$, $p \in (0,1)$, which is $Panjer(\frac{p}{p-1}, \frac{(\nu+1)\,p}{1-p}, 0)$.

   Its variation index $\mathcal{I}(X) = \dfrac{\mathrm{var}(X)}{\mathbb{E}(X)} = 1 - p < 1$, i.e., X is underdispersed.

2. The $Poisson(\mu)$, $\mu > 0$ is $Panjer(0, \mu, 0)$. Its dispersion index is 1.

3. The overdispersed $NegativeBinomial(\alpha, p)$, $\alpha > 0$, $p \in (0,1)$, with pmf $\left\{ \binom{\alpha+n-1}{n} p^n (1-p)^\alpha \right\}_{n \in \mathbb{N}}$, is $Panjer(p, (\alpha-1)\,p, 0)$.

4. The $ExtendedNegativeBinomial(\alpha, p, k)$, $\alpha \in (-k, -k+1)$, $p \in (0,1), k \in \mathbb{N}^+$, with pmf

$$f_n = \frac{\dbinom{\alpha+n-1}{n} p^n}{(1-p)^{-\alpha} - \displaystyle\sum_{j=0}^{k-1} \dbinom{\alpha+j-1}{j} p^j}, \quad n = k, k+1, ..., \qquad (14)$$

   in the support $\mathcal{S}_X = \{k, k+1, \dots\}$, is $Panjer(p, (\alpha-1)\,p, k)$. In the expression above the extended binomial coefficients $\dbinom{\alpha+n-1}{n}$ are defined as $\dbinom{\alpha+n-1}{n} = \dbinom{-\alpha}{n} = \dfrac{\Gamma(\alpha+n)}{\Gamma(\alpha)\,n!}$.

5. The $ExtendedLogarithmic(p, k)$, $p \in (0,1), k \in \mathbb{N}^+$, with pmf

$$f_n = \frac{\dfrac{p^n}{\dbinom{n}{m}}}{\displaystyle\sum_{j=m}^{\infty} \dfrac{p^j}{\dbinom{j}{m}}}, \quad n = k, k+1, ..., \qquad (15)$$

   is $Panjer(p, -kp, k)$.

6. If $X \frown Panjer(a, b, k)$, truncating $\{k, k+1, ..., \ell-1\} \subset \mathcal{S}_X$ we obtain a truncated rv $X^* \frown Panjer(a, b, \ell)$.

The special "unit" cases $Bernoulli(p) \equiv Binomial(1, p)$, $Geometric(p) \equiv NegativeBinomial(1, p))$, $ExtendedNegativeBinomial(\alpha, p, 1)$ whose pmf has the simple form $\dfrac{1 - (1 - q\,t)^{-\alpha}}{1 - p^{-\alpha}}$, $t \le \frac{1}{q}$), and $Panjer(p, -p, 1)$ or $Logarithmic(p)$ (or $ExtendedLogarithmic(1, p)$, with pgf $\dfrac{\ln(1 - pt)}{\ln(1 - p)}$), do have specially nice properties in each of the corresponding subclasses.

   In particular, $NegativeBinomial(\alpha, p)$ — and hence, as a special case $Geometric(p)$ — that result from a $Gamma$ randomization of the $Poisson(\Lambda)$, i.e., an hierarchic model with $\Lambda \frown Gamma(\alpha, 1)$ — are successfully used to

model the descendance of populations when the distribution of direct offsprings exhibits large variation, and both the the $ExtendedNegativeBinomial(\alpha, p, 1)$ and the $Logarithmic(p)$ distributions have been used to provide close fit to some natural populations.

In Table 2 below we sumarize results, indicating also the pgf $m_Q(t)$:

Table 3. Panjer distributions.

X	a	b	k	$m_Q(t)$
$Binomial(m, p)$	$\frac{p}{p-1}$	$\frac{(m+1)p}{1-p}$	0	$(1 - p + pt)^m$
$Poisson(\mu)$	0	μ	0	$e^{\mu(t-1)}$
$NegativeBinomial(\alpha, p)$	p	$(\alpha - 1)p$	0	$\left(\frac{1-pt}{1-p}\right)^{-\alpha}$
$ExtendedNegativeBinomial(\alpha, p, k)$	p	$(\alpha - 1)p$	k	$\frac{(1-pt)^{-\alpha} - \sum_{j=0}^{k-1} \binom{\alpha+j-1}{j}(pt)^j}{(1-p)^{-\alpha} - \sum_{j=0}^{k-1} \binom{\alpha+j-1}{j}p^j}$
$ExtendedLogarithmic(p, k)$	p	$-kp$	k	$\frac{\sum_{n=k}^{\infty} \binom{n}{k}^{-1}(pt)^n}{\sum_{n=k}^{\infty} \binom{n}{k}^{-1}p^n}$

5   Randomly Stopped Sums with Panjer Subordinator

The importance of the Panjer class is a consequence of the implications that the recursive expression (13) has on the recursive computation of the density of randomly stopped sums subordinated by Panjer rv's. This results from the following theorem:

Theorem 4. *Let $\{q_n\}_{n\in\mathbb{N}}$ be the pmf of a count distribution Y, and $\{f_n\}_{n\in\mathbb{N}}$ denote the pmf of a claim number distribution X whose support is a subset of the positive integers, i. e. $f_0 = 0$. Consider the randomly stopped sum $T = \sum_{n=\inf \mathcal{S}_Y}^{Y} X_n$, with Y and the replicas X_n of X independent.*
Then the following statements are equivalent:

1. $Y \frown Panjer(a, b, k)$;
2. *For any claim number rv X and any $\ell \geq 1$, m_T satisfies the differential equation*

$$(1 - a \, m_X(t)) h^{(\ell)}(t) = \sum_{i=1}^{\ell} \binom{\ell}{i} (a + b \frac{i}{\ell}) \, h^{(\ell-i)}(t) \, m_X^{(i)}(t) + q_k \, m_T^{(\ell)}(t),$$

$t \in [0, 1)$, *with the initial conditions $h^{(j)}(0) = 0$ for $j \leq k - 1$.*

From this, we can compute the pmf of a compound rv T with Panjer subordinator Y and count summands independent replicas of X, as defined above, by observing that for $\ell \geq 1$

$$(1 - a \, m_X(t)) \, m_T^{(\ell)}(t) = \sum_{i=1}^{\ell} \binom{\ell}{i} \left(a + b \frac{i}{\ell} \right) m_T^{(\ell-i)}(t) \, m_X^{(i)}(t) + q_k \, [m_X^k(t)]^{(\ell)}.$$

In fact, the main consequence of Panjer's theory is the following result:

Theorem 5. *Let $\{q_n\}_{n \in \mathbb{N}}$ be the pmf of a count distribution Y, and $\{f_n\}_{n \in \mathbb{N}}$ denote the pmf of a claim number distribution X whose support is a subset of the positive integers. Consider the randomly stopped sum $T = \sum\limits_{n \in \mathcal{S}_Y} X_n$, with Y and the replicas X_n of X independent. Then*

$$\mathbb{P}[T = n] = g_n = \begin{cases} m_Y(m_X(0)) = m_T(f_0) & n = 0 \\ \dfrac{1}{1 - a \, f_0} \left[\displaystyle\sum_{i=1}^{n} \left(a + b \frac{i}{n} \right) g_{n-i} f_i \right] + q_k f_n^{*k} & n \geq 1 \end{cases} \tag{16}$$

where f_n^{*k} stands for the k-th iterated convolution of the sequence $\{f_n\}$ with itself.

(There exists a simple extension for the density when the summands are absolutely continuous, but it is not relevant in the context of branching processes.)

6   Discussion and Conclusions

With the exception of *Poisson* or of *Geometric* subordinator — i.e., of a $Panjer(0, \mu, 0)$ or a $Panjer(p, 0, 0)$, respectively, cf. Pestana and Velosa [19] on the simplicity of these cases when compared to the complexity of others — we couldn't obtain any close expressions for the n-fold composition of the pgf for any other Panjer subordinators. Aside from those two cases, the only one for which we got more promising results has been — as predictable — the

Logarithmic(p). Moreover, when the aim is to extend the Fibonacci sequence using branching randomization, in case we want to remove individuals from the population after two mating epochs, we have the extra burden of subtracting, the two rv's used being dependent.

Happily, compound pgf's are amenable to compute mean values and variances, and in what concerns the mean value we have the extra facility that the mean value of the difference is the difference of the means values, regardless whether the random variables are dependent or independent. So, it is easy to follow the process on average, and the relation of the sequence of expected values to the sequence of Fibonacci numbers simple.

The quantities of interest — extinction probability and expected total size in the supercritical case, size of the n-th generation, total size of the population up to the n-th generation — can be dealt with computationally. When the fixed point method is used to compute roots of some equation $F(x) = x$, numerical instabilities are a rule whenever F is too steep, and the sufficient convergence conditions are not met.

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