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COMPARISON BETWEEN NUMERICAL AND SIMULATION METHODS FOR AGE-DEPENDENT BRANCHING MODELS WITH IMMIGRATION

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This work aims to provide and to compare numerical computation and simulation method to estimate the distribution of some relevant variables related to an age-dependent branching model allowing immigration at state zero. Specifically, we analyze the behaviour of the following variables: the extinction time and the waiting time for the beginning of the survival of population forever. They are strongly related to the population and re-population experiments in biology and to the wastewater treatment, as well. Throughout the paper, we illustrate the methods provided by some proper examples.

1. Introduction

In biological treatment of industrial wastewater by cells feeding on a substrate in a bio-reactor, bio-technologists and environmentalists ask about how long takes the final establishment of bacterial cultures in wasted water. This question is directly related to the study of the extinction time of cells feeding and of the number of trials necessary before the bacterial culture starts to grow irreversibly.

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As a convenient tool to treat this problem, Slavtchova-Bojkova (2000, 2004) proposed the use of a special class of branching processes, namely age-dependent branching processes with immigration in the state zero. In these works, implicit equations for the distribution function (d.f.) of both, the life period of a bacterial culture and the total waiting time to the beginning of that population which will survive forever, were determined. However, these equations turned out to be very useful from a practical viewpoint, because the d.f. are not determined in a direct way. That is why, it is reasonable to try to estimate them by means of these equations using numerical method. The goal of the paper is to provide and to compare two different approaches: one by means of a numerical method and another one by means of simulation.

In the next section we define the probability model and fix the notation. In sections 3 and 4, the numerical procedure and Monte-Carlo method for simulation are provided and applied to particular cases, respectively. Finally, in section 5 we compare the proposed methods.

2. The Probability Model

We will first outline an age-dependent branching process $\{Z(t)\}_{t \geq 0}$. Consider a population process starting at time 0 with a single progenitor of age 0 whose life-length τ has distribution $G(t) = P(\tau \leq t)$, $G(0^+) = 0$. With probability p_k , $k \geq 0$, it produces at the end of its life k similar individuals (of age 0), with the same life-length distribution $G(t)$ and reproduction distribution $\{p_k\}_{k \geq 0}$ ($\sum_{k=0}^{\infty} p_k = 1$). The probability generating function (p.g.f.) of the number ξ of offspring, is denoted by

$$f(s) = \sum_{k=0}^{\infty} p_k s^k, \quad |s| \leq 1, \quad p_k = P(\xi = k).$$

Provided that there is at least one descendent, the death-and-reproduction process is repeated, and continues as long as individuals exist.

Let us denote by $Z(t)$ the number of individuals existing in the population at time t or the state of the age-dependent process $\{Z(t)\}_{t \geq 0}$ at time t . Note that a path becomes extinct once $Z(t) = 0$ for some t (and for all t thereafter), and that the above process is “age-dependent” in the sense that the probability an individual living at time t dies in the interval $(t, t + dt)$ is, in general, a non-constant function of t . The process $\{Z(t)\}_{t \geq 0}$ is the so-called Bellman-Harris branching process (see, for example, Athreya and Ney (1972), pp. 137-144). Now, let us introduce the process of interest $\{\tilde{Z}(t)\}_{t \geq 0}$, i. e. every time the process $\{Z(t)\}_{t \geq 0}$ hits the state zero we suppose to have an immigration of one particle from an

outside source. Then, $\{\tilde{Z}(t)\}_{t \geq 0}$ is the process with immigration in the state zero introduced by Mitov and Yanev (1985).

For a branching process with immigration $\{\tilde{Z}(t)\}_{t \geq 0}$ we call life periods (cycles) the intervals $(t_0, t_0 + T_{t_0})$ of maximal length on which $\inf_{t_0 \leq t < t_0 + T_{t_0}} Z(t) > 0$. We denote $T := T_0$. The variable T is improper one with probability $1 - q$, i.e. $P(T < \infty) = q$, where q is the probability of eventual extinction of the process $\{Z(t)\}_{t \geq 0}$. Thus $\{\tilde{Z}(t)\}_{t \geq 0}$ may have several life periods, the last one always being infinite, provided the process is supercritical ($m := f'(1) > 1$). On the set $\{T < \infty\}$ (means that at least once a certain extinction is observed), Slavtchova-Bojkova (2000) obtained that

$$(1) \quad q(t) := P(T \leq t | T < \infty) = \frac{1}{q} \int_0^t f(v(t-u)) dG(u)$$

for $t > 0$, where $v(t) := P(Z(t) = 0)$ and $v(0) = P(Z(0) = 0) = 0$. Moreover

$$E(T | T < \infty) = \frac{1}{q} \int_0^\infty (q - v(t)) dt.$$

Notice that if $q = 1$, then $q(t) = v(t)$ for all $t \geq 0$. It is well known that $v(t) = \int_0^t f(v(t-u)) dG(u)$ (see Athreya and Ney (1972), pp. 138) and is independent of the magnitude of q .

In the supercritical case, we denote by M the last instant of immigration, i.e. the “birth time” of that process which will finally survive forever. It is verified that $P(M = 0) = 1 - q$, $P(M < \infty) = 1$ and on the event $\{M > 0\}$, i.e. at least one immigration is necessary or equivalent the first life cycle is finite ($T < \infty$), Slavtchova-Bojkova (2004) obtained that

$$(2) \quad P(M \leq t | T < \infty) = (1 - q)(\delta_{t0} + \sum_{i=1}^\infty q^i v^{*i}(t)),$$

where $\delta_{t0} = 1$ if $t = 0$ or 0 if $t \neq 0$ and $v^{*(i+1)}(t) = \int_0^t v^{*i}(t-u) dv(u)$, with $v^{*0}(t) = 1$, $v^{*1}(t) = v(t)$. Moreover

$$E(M) = \frac{q}{1 - q} E(T | T < \infty).$$

Although, the equations (1) and (2) show a mathematical relation of the variables T and M , it is not possible to obtain explicitly an equation for each variable. In the next sections we provide two computational procedures, one numerical and another one by simulation, which concern the estimation of the conditional (given ultimate extinction) distribution of the life-length cycle T and of the conditional distribution of so called total waiting time M to the beginning of the successful experiment.

3. Numerical Method

In what follows we will describe the idea of the computational procedure and the two concrete examples we applied it to. Let l be the maximum number of offspring an individual can have, r be the greatest age an individual can live to, and $g(\cdot)$ be the life-length density. There are two mutually exclusive ways a trajectory can become extinct by time t : the progenitor dies by time t with probability $1 - G(t)$ and leaves no offspring, or the progenitor dies at time $1 \leq s < t$ with probability $g(s)$, having had $1 \leq k \leq l$ offspring and each of the k offsprings' lines becomes extinct by time t . To compute the probability of extinction $v(t)$ by time t of the Bellman-Harris branching process $\{Z(t)\}_{t \geq 0}$ we will use the following recurrence equations

$$v(t) = p_0 G(t) + \sum_{s=1}^{t-1} \sum_{k=1}^l p_k v^k(t-s) g(s), \quad \text{if } t < r$$

and

$$v(t) = p_0 + \sum_{s=1}^r \sum_{k=1}^l p_k v^k(t-s) g(s), \quad \text{if } t \geq r,$$

obtained after time discretization of the renewal type integral equation satisfied by $v(t)$, i.e.

$$v(t) = \int_0^t f(v(t-u)) dG(u).$$

It is relevant to remark that as $q(t) = q^{-1}v(t)$, then approaching $v(t)$, $q(t)$ is also obtained.

To study the implications of the above method we compute the conditional distribution of a life cycle T of an age-dependent branching process with immigration and of the total waiting time M when adopting as a probability density

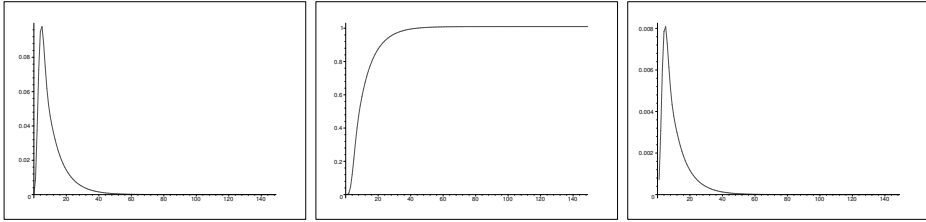


Figure 1: Numerical results for parametrised offspring distribution

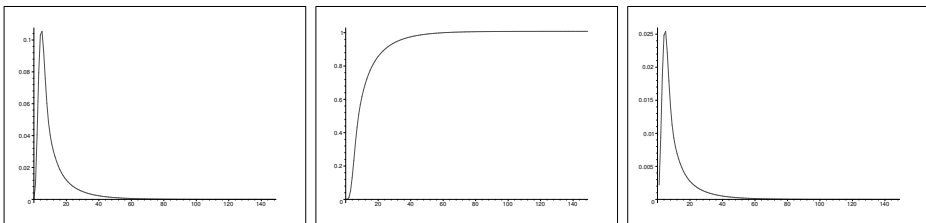


Figure 2: Numerical results for geometric offspring distribution

function (p.d.f.) for cell generation times the $\Gamma(\alpha, \beta)$ form for this distribution with density, $h(x) = \frac{e^{-x\beta} \beta^\alpha x^{\alpha-1}}{\Gamma(\alpha)}$, for $x > 0$, and mean $\lambda = \frac{\alpha}{\beta}$, where $\alpha = 6$ and $\beta = 1$. We consider two cases for the offspring distribution. First we suppose the offspring distribution to belong to the family of p.g.f. $h_p(s) = p + 0.4s + (0.6-p)s^2$, parameterized by $p = P\{\text{the initial progenitor dies without any offspring}\}$. The computational results for $p = 0.05$ (which corresponds to a supercritical case with $m = 1.5$ and $q = 0.09$) are presented in the Figure 1, where we show the conditional density function of the life-period T given that $T < \infty$ (left graphic), $q(t)$ (central graphic) and conditional density function of the total waiting time M given that $M > 0$ (right graphic). In addition, we obtained for the conditional expected value of T on the event of certain extinction, i.e. $E(T|T < \infty) = 11.92$ and for the unconditional $E(M) = 1.17$ in this case.

Secondly, we implemented the computation when the offspring distribution is geometrical one with $p = 2/5$ (which corresponds to a supercritical case with $m = 1.5$ and $q = 0.66$). The obtained results are shown on the Figure 2. We obtain in this case, that $E(T|T < \infty) = 12.46$ and $E(M) = 24.2$.

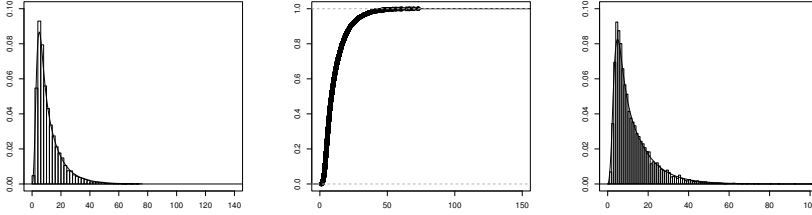


Figure 3: Monte Carlo results for parametrised offspring distribution

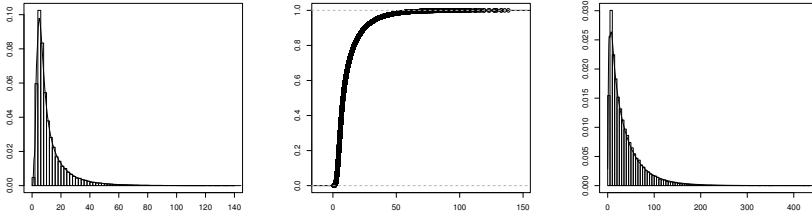


Figure 4: Monte Carlo results for geometric offspring distribution

4. Simulation Method

In this section we apply the Monte-Carlo method to approach the behaviour of the variables T and M , and estimate the density functions using a Gaussian kernel. For the variable T , we simulate the process $\{Z(t)\}_{t \geq 0}$ whereas the process $\{\tilde{Z}(t)\}_{t \geq 0}$ is considered to study the variable M .

For the examples of the previous section, we have simulated 100000 paths of each one. In Figure 3 and Figure 4 we show the estimate density functions for the variables T (left graphic) and M (right graphic), and the estimate cumulative distribution function $q(t)$ (central graphic), both of them given that $T < \infty$, for example 1 and 2 respectively. From the simulation for example 1 we estimate the probability of extinction by 0.09154 with 95% confidence interval (0.08971, 0.09329). Moreover, the sample mean for $T|T < \infty$ is 11.43823 with 95% confidence interval (11.25729, 11.61917) and for M and $M|M > 0$ the sample mean are 1.0955 and 12.25531 with 95% confidence interval (12.05606, 12.45457) and (1.06745, 1.12355), respectively.

For example 2 we estimate the probability of extinction by 0.66349 with 95% confidence interval (0.66056, 0.66642). The sample mean for $T|T < \infty$ is 11.93946 with 95% confidence interval (11.85343, 12.02550) and for M and $M|M > 0$ the sample mean are 23.9818 and 35.89016 with 95% confidence interval (23.77459, 24.18902) and (35.62259, 36.15773), respectively.

5. Discussion

First, we would like to point out that both methods applied for the estimation of the distribution of the life-cycle T and of the total waiting time M lead to similar results. For the numerical procedure we only use Newton-Raphson method (see Jacobson, 1985) for the integral equation satisfied by the extinction probability and the theoretical results for the Bellman-Harris branching processes. As a disadvantage here we would point out that for an arbitrary probability offspring distribution, actually we have to use truncated distribution.

In addition, applying the above mentioned time-discretization computation procedure we need to impose some restrictions: fix the maximal age an individual can live to and a maximal number of offspring an individual can have.

On the other side, using simulation method to have more accurate estimates we need more and more simulations. Another problem which we face is that we need to make a decision in advance when it is reasonable to stop in order to assure that the process “will survive forever”. However, this method allow us to estimate the errors through confidence intervals.

Finally, we would like to point out, that as illustrated by the two examples, the variable M strongly depends on the magnitude of q , nevertheless both examples have the same reproduction mean. On the other hand, the behaviour of the variable T is very similar in both cases.

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