Comparison between Numerical and Simulation Methods for Age-dependent Branching Models with Immigration

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Abstract

This work aims to compare numerical computation and simulation results of an age-dependent branching model allowing immigration. In general, main idea originated from the problem of estimating the waiting time to a successful experiment in population and re-population experiments with different species, which have disappeared for some reason. We provide different approaches to estimate the distribution of some relevant variables appearing in this model.

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1 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 τ 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

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

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 $\{Z(t)\}_{t\geq 0}$ 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 that 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 $\{\widetilde{Z}(t)\}_{t\geq 0}$, 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, $\{\widetilde{Z}(t)\}_{t\geq 0}$ is the process with immigration in the state zero. Foster (1971) and Pakes (1975) first studied the discrete-time version of these processes.

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

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

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

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

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

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

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

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

In this paper we provide two computational procedures, one numerical and another one by simulation, which concern the estimation of the extinction probability $q(t)$ at time t, the estimation of the conditional (given ultimate extinction) distribution of the life-length cycle T and of the conditional and unconditional distribution of so called total waiting time M for the beginning of the successful experiment. Finally, we compare the advantages and disadvantages of the proposed methods.

2 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 $g(.)$ be the mortality 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.

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

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 for the case when adopting as a probability density function (p.d.f.) for cell generation times the $\Gamma(\alpha, \beta)$ form for this distribution with p.d.f., $f(x) = \frac{e^{-x\beta}\beta^{\alpha}x^{\alpha-1}}{\Gamma(\alpha)}$, for $x > 0$, and mean $\lambda = \frac{\alpha}{\beta}$, where $\alpha = 6, \quad \beta = 1$. 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 $p = 0.1$ (which corresponds to the supercritical case) are presented on the Figure 1, where we show the conditional density function of the life-period T given that $T < \infty$ (left graphic) and conditional density function of the total waiting time M (right graphic).

Secondly, we implemented the computation when the offspring distribution is geometrical one with $p = 2/5$. The obtained results are shown on the Figure 2.

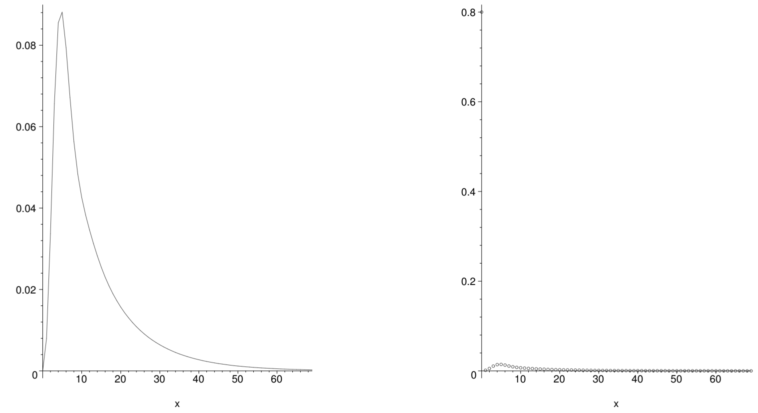

Figure 1.

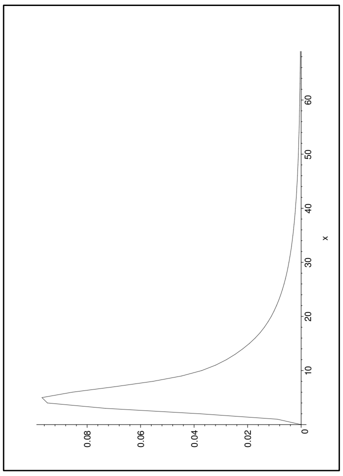

Figure 2.

3 Simulation Method

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 $\{\widetilde{Z}(t)\}_{t\geq 0}$ is considered to study the variable M.

For the example of the previous section, we have simulated 100000 paths. In Figure 2, we show the estimate density function for the variable T (left graphic) and the estimate cumulative distribution function (right graphic), both given that $T < \infty$. We notice that 19952 paths verified that $T < \infty$, and consequently we use these ones to estimate T. Moreover, the sample mean is 13.09936 with 95% confidence interval $(12.94386, 13.25486)$.

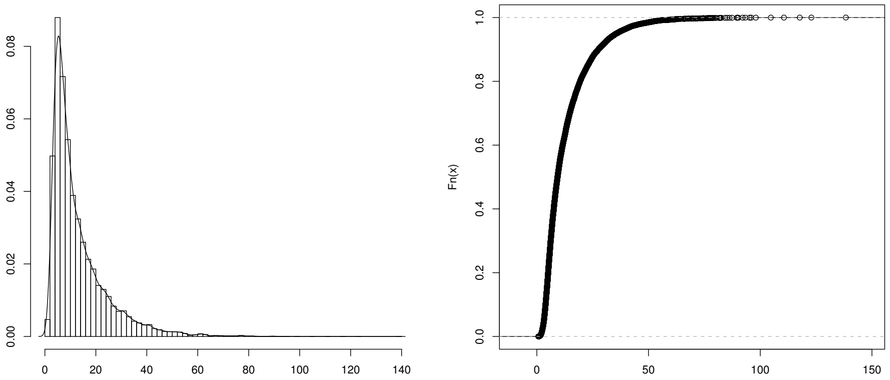

Figure 3.

On the other hand, in Figure 3, we show the histogram for the numbers of immigration (left graphic) and the estimate density function for the variable M given that $T < \infty$ (right graphic). In this case, 19985 paths satisfy this condition and the sample mean is 3.281064 with 95% confidence interval $(3.223889, 3.338257)$.

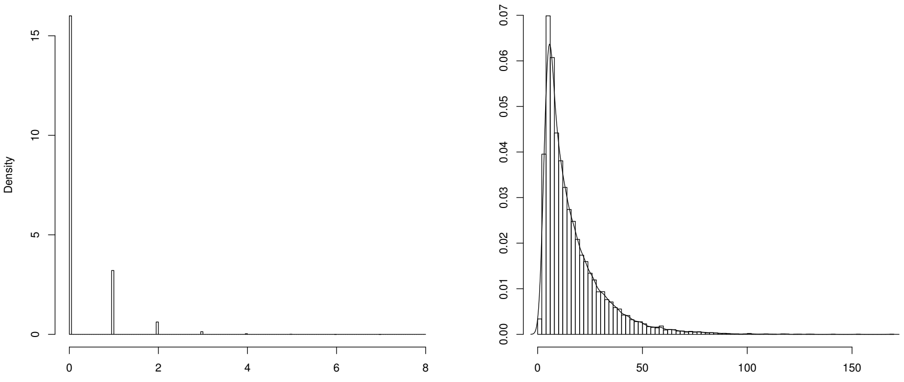

Figure 4.

4 Advantages and Disadvantages of Different Methods

First, we would like to point out thatby both methods applied for the estimation of the distribution of the life-cycle T and of the total waiting time M, we obtain 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 fact, 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 procedure allow us to obtain the conditional distribution for the variable M and to extract additional information for the considered characteristics.

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