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ПЛИСКА
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SIMULATION AND ROBUST MODIFICATIONS OF ESTIMATES IN BRANCHING PROCESSES

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This study is focused on the comparison and modification of different estimates arising in the branching processes. Simulations of models with or without migration are put through. Due to the complexity of the computations the algorithms are designed with the language of technical computing MATLAB. Using the simulations, estimates of the offspring mean of the generated processes are calculated. It is well known in the literature that under certain conditions the asymptotic distribution of the estimates is proved to be normal. Using the asymptotic normality a modified method of maximum likelihood is proposed. The aim is to obtain trimmed maximum likelihood estimates based on several sample paths with the same number of generations. Thus in a natural way the observations, inconsistent with the aprior information about the asymptotic normality are excluded from the model. The computation of the standard error allows the comparison of different types of estimates.

1. Introduction

1.1. The problem

Our work is focused on two main topics, which may be considered separately, but are still in close relationship. The first one is to show how robust statistics can be used for estimating the parameters of some classes of branching processes. As far as we know, this has not been done before, so we have decided to start with the simplest case - the Bienayme-Galton-Watson process and to show that this estimation is reasonable and in some cases may be preferred. The proposed

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weighted least trimmed estimate (WLTE) may be considered as a generalization of the maximum likelihood and needs complex numerical computation. For evaluating its reliability we have carried out several simulations. Here appears the second topic - the development of a software package for simulation and estimation of branching processes in an appropriate computing environment.

Imagine that we have the following situation: one biologist has to find out what is the average number of children of a bacterium of some specific species. He decides that its reproduction law follows the concept of the branching processes theory. So, if he has ten petri (the small dishes used in biology and chemistry) with bacteria, he will get from each of them after an appropriate period of time ten numbers - the estimates of the average number of children. They all will be different. Should he take their average? And what would happen, if some of the observed cases are not measured correctly, or - if we have outliers? These are questions we are trying to answer in the simplest case.

1.2.   Some basic results about the classical estimation of a Bienayme-Galton-Watson process

In this work we consider the estimations of a very simple nonergodic model - the Bienayme-Galton-Watson (BGW) process. We will use the following notation:

Let $\{X_{tj}, \ t = 0, 1, 2, \cdots, j = 0, 1, 2, \cdots\}$ is a double array of independent random variables, distributed according to the reproduction law $\{p_k, \ k = 0, 1, 2, \cdots\}$. We write

$$Z_0 = 1$$

$$Z_{t+1} = \sum_{j=1}^{Z_t} X_{i,j}, \ t = 0, 1, 2, \cdots$$

in the sense that the sequence $\{Z_t\}$ given by this recursion has the same distribution as a BGW process (a sum from 1 to zero is given zero).

Let us also denote by

$$m = \sum_{k=1}^{\infty} k p_k = E Z_1$$

the mean number of children per individual or reproduction mean and by

$$\sigma^2 = \sum_{k=1}^{\infty} k^2 p_k - m^2 = Var Z_1$$

the reproduction variance.

Some of the unusual features arising in the context of the nonergodic model estimation are (see [6]):

- inconsistent maximum likelihood estimates

- nonestimability of many parameters

- nonnormal limit laws with classical type of norming

- conditional asymptotic inference and so on.

If one adopts the Bayessian outlook many of these problems become less important, but are usually replaced by computational difficulties.

Let us pay our attention to the concept of consistency: In classical i.i.d. theory consistency is an important requirement of an estimate. If we have a large sample, any reasonable estimate should be close to the true parameter. In the case of stochastic processes, the large sample is often obtained by letting the observation time get large, i.e. by looking at a whole path of the process. Unless $p_0 = 0$ we can not find any consistent estimate, based on a single infinite realization of a BGW process. The problem is that the process may become extinct, in which case there is not enough information in a path to tell two distinct probability measures apart. In other words even when the observation time becomes large we may not actually make a large number of observations.

A fundamental difference between the branching process case and the i.i.d. model is the structure of the tail σ-field. In the i.i.d case it is trivial (Kolmogorov's 0-1 law) but for a branching process it contains the extinction set $B = \{Z_t = 0 \ for \ some \ t\}$, which has nonzero probability whenever $p_0 > 0$. Thus tail-measurable random variables will not in general be trivial. Since consistency of a sequence of estimates is a tail property it can only be achieved in models with trivial tail σ-fields. Such models are often called ergodic.

It is proved that we may be able to estimate the offspring mean consistently on the explosion set $A = \bar{B}$. In our work we will use the following two estimates:

$$\bar{m}_t = \begin{cases} \frac{Z_t}{Z_{t-1}}, & Z_{t-1} > 0 \\ 1, & Z_{t-1} = 0 \end{cases},$$

known as Lotka-Nagaev estimate and

$$\hat{m}_t = \frac{Z_1 + Z_2 \cdots + Z_t}{Z_0 + Z_1 + \cdots + Z_{t-1}},$$

known as Harris estimate.

The following results are well-known (see f.e. [6]) and describe the asymptotic behaviour of the estimates in the supercritical case. The Lotka-Nagaev estimate is obtained by the conditional method of moments and has the following properties:

Theorem 1. Let $1 < m < \infty$ and $Z_0 > 0$. Then as $t \to \infty$

a) $\bar{m}_t \to m$ a.s. on the explosion set A.

b) if $0 < \sigma < \infty$ then

$$\frac{\sqrt{Z_t}}{\sigma}(\bar{m}_t - m) \to N(0,1)$$

in distribution on A.

The Harris estimate is a nonparametric maximum likelihood estimate, for which we have the following :

Theorem 2. Let $1 < m < \infty$. Then as $t \to \infty$, conditionally upon nonextinction (set A)

a) $\hat{m}_t \to m$ a.s. , i.e. $\hat{m}_t$ is strongly consistent.

b) $E\hat{m}_t < m$, $E\hat{m}_t \to m$, i.e. $\hat{m}_t$ underestimates m, but is asymptotically unbiased.

c) if $0 < \sigma < \infty$ then

$$\frac{\sqrt{U_t}}{\sigma}(\hat{m}_t - m) \to N(0,1)$$

in distribution, where $U_t = Z_0 + \cdots + Z_{t-1}$.

2.   Statistical model

A robust extension of the Maximum Likelihood Estimates (MLE) that possesses a high breakdown point was introduced by Vandev and Neykov (1993). This modification considers the likelihood of individual observations as residuals and applies the basic idea of the Least Trimmed Squares (LTS) estimates of Rousseeuw (1984) using appropriate weights.

Generally speaking, Vandev and Neykov (1998) defined the $WLTE(k)$ estimates, $\widehat{\theta}$, for the unknown parameter $\theta \in \Theta^p$ as

$$\widehat{\theta} = \underset{\theta \in \Theta^p}{argmin} \sum_{i=1}^{k} w_i f_{\nu(i)}(\theta),$$

where $f_{\nu(1)}(\theta) \leq f_{\nu(2)}(\theta) \leq \cdots \leq f_{\nu(n)}(\theta)$ are the ordered values of $f_i = -\log \varphi(x_i, \theta)$ at θ, $\varphi(x_i, \theta)$ is a probability density, θ is an unknown parameter and $\nu = (\nu(1), \cdots, \nu(n))$ is the corresponding permutation of the indices, which may depend on θ. The weights $w_i \geq 0$, $i = 1, \cdots, k$, are such that an index $k = \max\{i : w_i > 0\}$ exists.

Vandev and Neykov (1998) proved that the finite sample breakdown point of the $WLTE(k)$ estimates is not less than $(n-k)/n$ if $n \geq 3d$, $(n+d)/2 \leq$

$k \leq n - d$, when Θ^p is a topological space and the set $F = \{f_i(\theta), i = 1, \cdots, n\}$ is d-full. A finite set F of n functions is called d-full, according to Vandev (1993), if for each subset of cardinality d of F, the supremum of this subset is a subcompact function. A real valued function $g(\theta)$ is called subcompact, if its Lesbegue sets $L_g(C) = \{\theta : g(\theta) \leq C\}$ are compact for any constant C (see Vandev and Neykov, 1993).

A simpler and easier to apply criterion for subcompactness is given in the following theorem (see [2]):

Theorem 3. The real valued continuous function $g(\theta)$, defined on an open subset of $D \in R^n$, is subcompact if and only if for any sequence $\theta_i \to \theta_0$ where θ_0 belongs to the boundary of D, $g(\theta_i) \to \infty$ when $i \to \infty$.
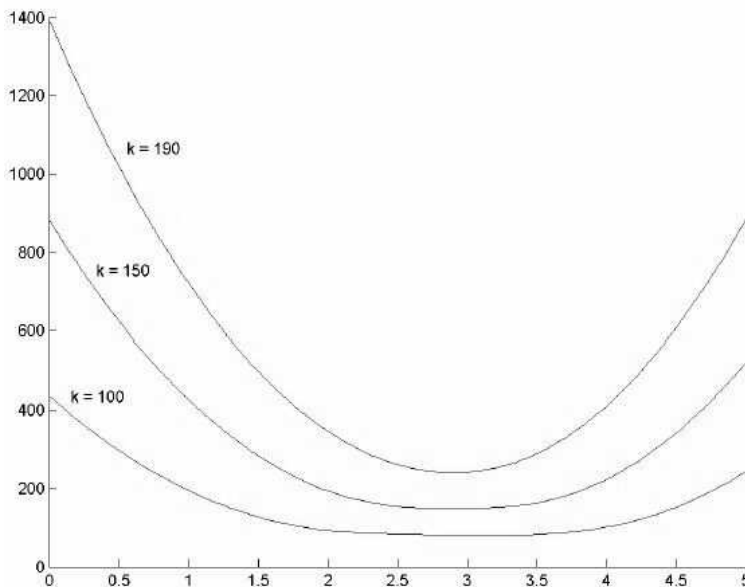
The likelihood function over 200 observations for different values of the trimming factor based on normal subcompact likelihood curves.

For the sake of completeness, we draw the attention to the fact that the finite sample breakdown point of an estimator T, at the finite sample $X = \{x_i; i = 1, \cdots, n\}$, is defined as the largest fraction m/n for which the $\sup_{\tilde{X}} \left\| T(X) - T(\tilde{X}) \right\|$ is finite, where $\tilde{X}$ is a sample obtained from X by replacing any m of the points in X by arbitrary values (see Hampel et al. 1986, Rousseeuw and Leroy, 1987).

Thus, if one wants to study the breakdown point of the $WLTE(k)$ estimates for a particular distribution, one has to find out the index d of fullness of the

corresponding set of log-density functions.

We will apply this concept for estimating the offspring mean in some discrete time branching processes. This study is focused on the well known estimates of Lotka-Nagaev and Harris. Let us suppose that we have a set of sample paths of a branching process. Using this set and the estimates mentioned above we can obtain a number of values for the offspring mean (for any sample path we have one offspring mean estimate). It is well known that, under certain conditions, these values are asymptotically normally distributed. If these conditions are not satisfied the estimated value is far from the real value of the offspring mean.

The aim is to apply the theory of robustness in order to eliminate the cases, which do not satisfy these conditions, and to obtain an estimate of the offspring mean closer to the real value.

The study of the robustness of the estimates of the offspring mean will be based on the breakdown properties of the $WLT(k)$ estimates.

Let us define a robust estimate of offspring mean over the set of sample paths $S = \{S_1, \cdots, S_n\}$ as

$$(1) \qquad \bar{M} = \underset{\mu \in R}{argmin} \sum_{i=1}^{k} -w_i f(Est(S_{\nu(i)}, \mu)),$$

where k is the trimming factor, $f(x)$ is the logarithm of the density function of the standard normal distribution, ν is a permutation of the indexes, such that $f(Est(S_{\nu(1)}, \mu)) \geq f(Est(S_{\nu(2)}, \mu)) \geq \cdots \geq f(Est(S_{\nu(n)}, \mu))$.

With $Est(S_i, \mu)$ we note the transformation of the offspring mean estimate, which gives us asymptotic normality.

In the case of Lotka - Nagaev estimate $Est(S_i, \mu)$ can be presented as follows:

$$Est(S_i, \mu) = \frac{\sqrt{Z_t^i}}{\sigma}(\bar{m}_t^i - \mu), \mu \in R$$

where $\bar{m}_t^i$ is Lotka-Nagaev estimate for the $i-$th sample path . Here Z_t^i are the number of individuals in t-th generation in the sample path S_i. The fixed parameter σ represents the variance of the offspring distribution.

By analogy, in the case of Harris estimate, we have

$$Est(S_i, \mu) = \frac{\sqrt{U_t^i}}{\sigma}(\hat{m}_t^i - \mu), \mu \in R$$

where $U_t^i = Z_0^i + \cdots + Z_{t-1}^i$.

Proposition. The estimate $\bar{M}$ defined with (1) exists and its breakdown point is not less than $(n-k)/n$ if $n \geq 3$, $(n+1)/2 \leq k \leq n-1$.

P r o o f. To prove this proposition we have to find out the index of fullness of the set $F = \{f(Est(S_i, \mu)), i = 1, \cdots, n\}$.

Let us consider the function

$$g(\mu) = f(Est(S_i, \mu))$$

for a given sample path S_i. We have

$$g(\mu) = \log \frac{1}{\sqrt{2\pi}} - \frac{Est(S_i, \mu)}{2} =$$

$$= \log \frac{1}{\sqrt{2\pi}} - \frac{C^2(\bar{m}_t^i - \mu)^2}{2},$$

where the constant $C = \frac{\sqrt{Z_t^i}}{\sigma}$ in the case of Lotka - Nagaev estimate and $C = \frac{\sqrt{U_t^i}}{\sigma}$ in the case of Harris estimate.

It is obvious that the function $g(\mu)$ satisfies the conditions of Theorem 3, so it is subcompact on $\mu \in R$. Therefore, according to Vandev (1993), the index of fullness of the set F is equal to 1. That way the estimate $\bar{M}$ exists and the breakdown point is not less than $(n-k)/n$ if $n \geq 3$ and $(n+1)/2 \leq k \leq n-1$.

To calculate the value of the estimate, defined with (1), we will use an algorithm considered in [1]. The algorithm can be summarized as follows:

1. Setting the initial value for the unknown parameter $\mu = \mu_0 \in (0, \infty)$

2. Sorting the observations according to the log-density function at the current value of the unknown parameter : $f_{\nu(1)}(\mu) \leq f_{\nu(2)}(\mu) \leq \cdots \leq f_{\nu(n)}(\mu)$

3. The weights are equal to 1

4. Finding the value which satisfies (1)

5. If the exit conditions are not satisfied than go back to 2

The optimization algorithm in 4 is based on Golden Section search, parabolic interpolation and Nelder-Mead simplex (direct search) method (see [9]).

3.   A system for simulation and estimation of branching processes

The software system BPEngine is developed to simulate different models branching processes and to estimate various parameters of these processes. The simulation algorithm is based on the following definition of the branching process with random migration (BPRM):

Let us have on the probability space three independent sets of integer-valued random variables, i.i.d. in each set, $X = \{X_{t,i}\}$, $\eta = \{\eta_{t,1}, \eta_{t,2}\}$, $I = \{(I_t, I_t^0)\}$. Then we define

$$Z_t = \left(\sum_{i=1}^{Z_{t-1}} X_{t,i} + M_t \right)^+, \ t = 1, 2, \cdots,$$

$$Z_0 \geq 0,$$

where

$$M_t = \begin{cases} - \left(\sum\limits_{i=1}^{\eta_{t,1}} X_{t,i} + \eta_{t,2} \right), & \textit{with probability } p, \\ 0, & \textit{with probability } q \\ I_t \mathbf{1}_{\{Z_{t-1}>0\}} + I_t^0 \mathbf{1}_{\{Z_{t-1}=0\}}, & \textit{with probability } r. \end{cases}$$

Here $p+q+r = 1$ and Z_0 is independent of X, η and I. As usual $a^+ = \max(0, a)$.

We refer to the random variables, defined above, by the following way: $X_{t,i}$ is the offspring in the t-th generation of the i-th individual which exists in the $(t-1)$-th generation. In the t-th generation the following three situations are possible:

(i) with probability p: $\eta_{t,1}$ families emigrate (*family emigration*) - that is $\eta_{t,1}$ individuals are eliminated in the $(t-1)$-th generation (before reproduction) and do not take part in the further evolution; additionally after the reproduction in the $(t-1)$- th generation $\eta_{t,2}$ individuals emigrate from the t-th generation who can be chosen randomly from different families (*individual emigration*);

(ii) with probability q: the reproduction is according to the Bienayme - Galton - Watson process (BGW), i.e. without any migration;

(iii) with probability r: state dependent immigration of new individuals is possible - I_t individuals in the non-zero states or I_t^0 in the state zero.

Many particular cases can be obtained from this model. When $q = 1$ the process Z_t, $t = 0, 1, \cdots$ is a classical BGW process. When $r = 1$ and I_t and I_t^0 are identically distributed , the process is a branching process with immigration (BGWI). The process with $p = 1$, i.e. the process with pure emigration was studied for $\eta_{t,2} = 0$ a.s. by Vatutin (1977) and Kaverin (1990) and for $\eta_{t,1} = 0$ a.s. by Grey (1988). Some results for the general process are obtained by Yanev

and Yanev (1995, 1996, 1997). Models with nonhomogeneous migration, i.e.$p = p_t$, $q = q_t$, and $r = r_t$ were investigated by Yanev and Mitov(1985).

In the program the simulation of each model is determined by some basic parameters. They are the probability distributions of the random variables, which the process consists of; the initial number of particles (the ancestors) Z_0; the length of the simulated path (the number of generations).

The system allows to use the most popular discrete distributions - Poisson, Binomial, Geometric, Hypergeometric, Negative Binomial and Discrete Uniform. The user can also give an arbitrary discrete distribution.

The system shows also a graphic presentation of the sample path. That enables the user to have a visual idea about the progress of the process.

Further, the program estimates the basic parameters of the process. The sample $Z_0, Z_1, \cdots, Z_t$, according to which the estimates are computed, consists of generation sizes. In this way many of the well known non-parametric estimates for different models branching processes are obtained. To compute other estimates is possible to use other sets of observations like the three of generations, two successful generations Z_{t-1}, Z_t; the initial and another observation Z_0, Z_t; censored observations $Z_L(n), Z_{L+1}(n), \cdots, Z_{L+T}(n)$. For instance, for the classical BGW and the BGW process with random number of ancestors we can obtain the following estimates: Heyde, Lotka-Nagaev and Harris estimates for the offspring mean, the estimates of the offspring variance when the mean is known and when using the last three estimates; for the BGWI we have estimates of the offspring mean and immigration mean, proposed first by Heyde and Seneta (1972), which use the conditional least squares method and the estimates, proposed by Wei and Winnicki (1998) and so on.

The system can be considered as a new development of the system presented by Nicheva and Yanev (2000). The main difference is in the computing environment MATLAB which we have used. There are several reasons for this decision. First of all, we wanted to coordinate our system with the existing procedures for robust estimates. MATLAB gives us a very useful and flexible way for development of such software. And the last, but not least reason - it is a very convenient tool in the educational process in courses such as Stochastic and Branching processes.

Finally, we would like to mention that all results from the system BPEngine can be obtained very easily and quickly by the user.

In the future the system will be developed for more complicated models of branching processes.

4.   Computational Results

To illustrate the advantages of the robust estimate, defined above, we did a number of simulations of discrete time branching processes with known offspring mean and variance. Then we used the computational procedure, considered in [1], to obtain an estimated value of the offspring mean. This value is compared with the average of Lotka - Nagaev (or Harris) estimates for the simulated set of sample paths.

We set all the weights in (1) equal to 1. In this way we obtained a Least Trimmed Estimate. As is shown in [1], in this case we have a faster and more simple algorithm and a smaller value of the standard error of the estimate.

We generated 10 sample paths with 15 generations for offspring mean equal to 0.8, 1.0, 1.2, 1.5 and 1.7. The trimming factor was set to 7. Than we calculated the average of the offspring mean estimates using Lotka - Nagaev or Harris estimate. The obtained value was compared with the value calculated using (1). The results are shown in the next two tables, where in columns *Lotka-Nagaev* and *Harris* the average of estimations for corresponding estimates are shown and the robust estimations are given in columns $\bar{M}_{LN}$ and $\bar{M}_{Hr}$ (with correspondent standard error SE).

Offspring mean	Lotka-Nagaev	$\bar{M}_{LN}$	SE_{LN}
0.8	1	2	∞
1.0	1.02	1.200	0.2357
1.2	1.1174	1.1372	0.0477
1.5	1.3479	1.4940	0.0070
1.7	1.55	1.6993	0.0020

Table 1. Lotka - Nagaev estimates

| Offspring mean	Harris	$\bar{M}_{Hr}$	SE_{Hr}
0.8	0.3923	0.7586	0.1661
1.0	0.6137	1.0524	0.0690
1.2	0.7499	1.2244	0.0212
1.5	1.0521	1.5031	0.0049
1.7	1.3574	1.6996	0.0017

Table 2. Harris estimates

Let us first consider Table 1. The Lotka - Nagaev estimate uses only the last two generations from the sample path and its value for extinct sample paths is

artificially defined as 1. That way we do not have much information to use in the robust estimate. This is seen in the first three rows where the offspring mean is near 1. For instance, in the first row all sample paths have become extinct and all Lotka-Nagaev estimates are equal to 1. Thus the idea of the asymptotic normality cannot be applied. For the values of the offspring mean bigger than 1.2 the robust estimates are obviously closer to the real value.

The situation in Table 2 is completely different. Because of the fact that the Harris estimate uses all the information from the sample path, we obtain very good estimates even in the subcritical cases. Although in the subcritical cases the extinction is almost sure, the estimates, based on some sample paths, may be also considered to have an approximately normal distribution. The most interesting result is in the third row where we are in the supercritical case, the robust estimate is correct and very close to the true value, but the Harris estimate is smaller than 1 and suggests a subcritical situation.

On Fig.1 the theoretical vs estimated offspring mean is compared.
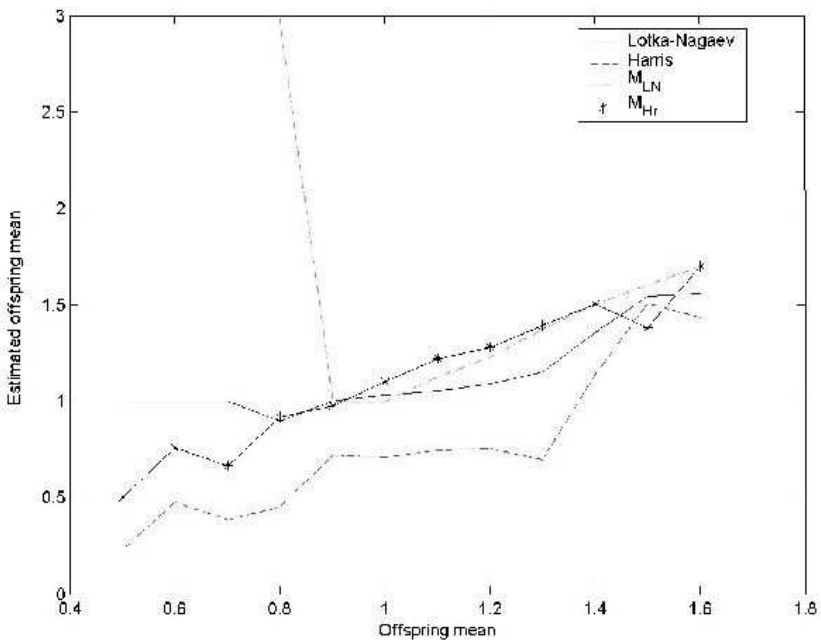
Here is seen that the classical Harris estimate underestimates the offspring mean, but the robust modification estimates the parameter correctly. This is very important in the cases when the offspring mean is higher than 1, but Harris estimate is less than 1.

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