

**SIMULATION STUDY ON THE OFFSPRING MEAN  
ESTIMATORS IN DISCRETE TIME BRANCHING  
PROCESSES WITH MIGRATION\***

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In the present work we consider two widely used definitions of a branching process with migration, related to the controlled branching processes framework, classical and multiple. We simulate the two processes with equal offspring and migration characteristics and estimate the offspring mean via the weighted conditional least squares estimators based on two sampling schemes – on the generation sizes only and the generation sizes and the migration components. We propose a robust modification of the second estimator in the case when several trajectories of the process are observed.

**Keywords:** branching processes, migration, statistical estimation, simulation, robust estimators

**СИМУЛАЦИОННО ИЗУЧАВАНЕ НА  
ИНДИВИДУАЛНОТО СРЕДНО НА РАЗКЛОНЯВАЩИ СЕ  
МИГРАЦИОННИ ПРОЦЕСИ С ДИСКРЕТНО ВРЕМЕ**

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В настоящата статия разглеждаме две широко използвани дефиниции на разклоняващи се процеси с миграция, класическа и многомерна, които от своя страна са свързани с регулируемите разклоняващи се процеси. Симулираме двата процеса, използвайки едни и същи характеристики за наследниците и мигрантите. Също така, използваме две оценки по метода на претеглените най-малки квадрати. Първата оценка зависи само от размера на поколенията, докато във втората участва и миграционната компонента. Предлагаме и робастна модификация на втората оценка, когато са наблюдавани няколко траектории на процеса.

**Ключови думи:** разклоняващи се процеси, миграция, статистическа оценка, симулация, робастни оценки

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**1. Introduction: history.** Branching processes, a vital mathematical tool for modeling family name extinction dynamics, originated with Irénée-Jules Bienaymé, a pioneering French mathematician [2]. Despite the lack of a formal proof, Bienaymé’s work remained undiscovered until 1972 when Heyde and Seneta brought it to light [6]. Analyzing the mean ratio’s influence on family extinction, Bienaymé explored scenarios where a mean ratio less than unity ( $m < 1$ ) revealed the inevitable decline of families. For ( $m = 1$ ), families faded at a slower pace, and for ( $m > 1$ ), families demonstrated growth, with a positive probability of continued expansion across successive generations. This intricate mathematical dynamic underscores the profound impact of branching processes on understanding the generational fate of family lineages.

Contributions from Francis Galton and Henry Watson further shaped branching processes. Galton’s 1873 problem, published in the *Educational Times*, addressed the population dynamics of a large nation where adult males colonize a district with distinct surnames. Watson initially attempted to solve this problem but made an error in his analysis, incorrectly predicting the extinction of all family lines. Although this proposition was later disproven, Galton, Watson, and Bienaymé are recognized for their contributions to the earliest model of a branching process.

There are many sources where the formulation of the model (for example [1], [5] and [14]) can be found, but we will use the one given in [3, p. 2], which is as follows: Let  $(\Omega, \mathcal{A}, P)$  be a probability space on which an array of non-negative integer-valued random variables  $\{X_n(i) : n = 0, 1, \dots; i = 1, 2, \dots\}$  is given, where  $\{X_n(i)\}$  are independent and identically distributed (i.i.d.) with a common probability mass function (p.m.f.)  $\{p_k\}_{k \geq 0}$  (*offspring distribution*). To avoid trivialities, we assume that  $p_0 > 0$ ,  $p_0 + p_1 < 1$  and therefore  $p_j \neq 1$  for any  $j$ . If any  $p_j$  were equal to 1, it would essentially mean that the corresponding event always happens, which might trivialize the analysis or the model being discussed. The Bienaymé–Galton–Watson (BGW) process is a discrete time homogeneous Markov chain  $\{Z_n\}_{n \geq 0}$  defined inductively by  $Z_0 = 1$  and for  $n = 0, 1, 2, \dots$

$$Z_{n+1} = \begin{cases} \sum_{i=1}^{Z_n} X_n(i), & Z_n > 0, \\ 0, & Z_n = 0. \end{cases}$$

The notation  $Z_{n+1}$  is employed to represent the total number of individuals in the  $(n + 1)$ st generation, while  $X_n(i)$  denotes the number of offspring of the  $i$ th individual living in the  $n$ th generation. The population initiates with a single individual, signified by  $Z_0 = 1$ . In this definition it is not possible to regulate the number of individuals throughout the generations.

In 1974, Sevastyanov and Zubkov [9] laid the foundation for controlled branching processes. Two years later, in 1976, N. Yanev introduced a special case of a  $\phi$ -controlled branching process with random control functions [12]. Building upon this, in 1980, N. Yanev and K. Mitov [13], along with independent work by S. Nagaev and L. Khan [7], expanded on the concept by introducing the branching process with random migration.

Beyond its biological modeling origins, it is essential to recognize the broader implications of these processes. Their relevance extends into fields like quantum optics and atomic physics, showcasing the versatility and significance of these concepts across diverse scientific domains.

Building on foundational concepts laid out by Sevastyanov, Yanev, and others, our article serves as an overview of controlled branching processes and branching processes with random migration. We focus on understanding how individual means are estimated within these dynamic systems. By presenting numerical results and metrics evaluating estimation effectiveness, we aim to offer valuable insights into the practical applications of these established models. This analysis contributes to a deeper understanding of controlled branching processes. To guide readers through the paper's structure, Section 2 introduces models and notation, while Section 3 delves into sampling schemes and weighted least squares estimators for the offspring mean. The concluding Section 4 offers a presentation of simulations and the corresponding numerical results.

**2. Models with migration.** There are numerous sources providing the definition of a controlled branching process introduced by Sevastyanov in [9]. For the purpose of this article, we will give the formulation presented in [4].

**Definition 1.** *The multiple controlled branching (MCB) process  $\{Z_n\}_{n \geq 0}$  is defined recursively as*

$$(1) \quad Z_0 = I_0 > 0, \quad Z_{n+1} = \left( \sum_{d \in D} \sum_{i=1}^{\phi_{n,d}(Z_n)} X_{n,d}(i) \right)^+, \quad n = 0, 1, \dots,$$

where  $I_0$  is an integer and  $a^+ = \max\{0, a\}$ .

In this definition,  $D$  is an index set, such that for each  $d \in D$ :  $\{X_{n,d}(i)\}_{n \geq 0, i \geq 1}$  are i.i.d. integer-valued random variables (r.v.), which are independent for different values of  $d$ , and  $\{\phi_{n,d}(k)\}_{n \geq 0}$  are non-negative integer-valued r.v. for fixed values of  $d$  and  $k$  (independent from the previous ones for different values of  $d$ ).

A special case of the MCB process is the one with random migration [4]. Let  $X = \{X_n(i), n = 0, 1, \dots; i = 1, 2, \dots\}$ ,  $\eta = \{(\eta_{n,1}, \eta_{n,2})\}$  and  $I = \{I_n\}$  are independent sets of non-negative integer-valued i.i.d. r.v. Additionally,  $\{\xi_n, n = 0, 1, \dots\}$  are i.i.d. r.v. (independent from the previous ones), with  $P(\xi_n = -1) = p$ ,  $P(\xi_n = 0) = q$ ,  $P(\xi_n = +1) = r$  and  $p + q + r = 1$ .

If  $D = \{1, 2, 3\}$ ,  $X_{n,1}(i) = X_n(i)$ ,  $X_{n,2}(i) = -\eta_{n,2}$  (individual emigration),  $X_{n,3}(i) = I_n$  (immigration),  $\phi_{n,1}(Z_n) = \min\{Z_n, Z_n + \xi_n \eta_{n,1}\}^+$ ,  $\phi_{n,2}(Z_n) = \xi_n^- \mathbf{1}_{\{Z_n > 0\}}$  and  $\phi_{n,3}(Z_n) = \xi_n^+ \mathbf{1}_{\{Z_n > 0\}}$ , where  $\xi_n^- = \max\{0, -\xi_n\}$  and  $\xi_n^+ = \max\{0, \xi_n\}$ . Using this notations in (1), we can write it as:

$$(2) \quad Z_{n+1} = \sum_{i=1}^{\phi_{n,1}(Z_n)} X_n(i) - \sum_{i=1}^{\phi_{n,2}(Z_n)} \eta_{n,2} + \sum_{i=1}^{\phi_{n,3}(Z_n)} I_n$$

In this context,  $\phi_{n,1}(\cdot)$  serves to determine whether family emigration occurs. If it happens, an individual is removed from the population and does not contribute to future reproduction. This action effectively excludes the individual's entire family from the next generation, reflecting a parallel absence in subsequent reproductive cycles.  $\phi_{n,2}(\cdot)$  indicates the occurrence of individual emigration, specifically, emigration after reproduction.  $\phi_{n,3}(\cdot)$  shows if there is an immigration in the  $n$ th generation, i.e. if we add individuals that will take part in the reproductive cycle of the next generation.

It is easy to check that (2) gives us:

**Definition 2.**

$$(3) \quad Z_0 > 0, \quad Z_{n+1} = \left( \sum_{i=1}^{Z_n} X_n(i) + M_n \mathbf{1}_{\{Z_n > 0\}} \right)^+, \quad n = 0, 1, \dots,$$

where

$$M_n = \begin{cases} -\sum_{j=1}^{\eta_{n,1}} X_n(j) - \eta_{n,2}, & \text{with probability } p \\ 0, & \text{with probability } q \\ I_n, & \text{with probability } r \end{cases},$$

with  $\sum_{k=1}^x = 0$  if  $x \leq 0$ .

This model closely resembles the one defined in [8], with a key distinction that in [8] 0 is not an absorbing state (if 0 is an absorbing state, the process concludes once it reaches zero), but  $I = \{(I_n, I_n^0)\}$  and with probability  $r$ ,  $M_n = I_n \mathbf{1}_{\{Z_n > 0\}} + I_n^0 \mathbf{1}_{\{Z_n = 0\}}$ , i.e

**Definition 3.**

$$(4) \quad Z_0 \geq 0, \quad Z_{n+1} = \left( \sum_{i=1}^{Z_n} X_n(i) + M_n \right)^+, \quad n = 0, 1, \dots,$$

where

$$M_n = \begin{cases} -\sum_{j=1}^{\eta_{n,1}} X_n(j) - \eta_{n,2}, & \text{with probability } p \\ 0, & \text{with probability } q \\ I_n \mathbf{1}_{\{Z_n > 0\}} + I_n^0 \mathbf{1}_{\{Z_n = 0\}}, & \text{with probability } r \end{cases}.$$

In both Definition 2 and Definition 3, the condition  $p + q + r = 1$  holds true.

A simpler variant of model (3), introduced above, is presented in [3], where emigration and immigration take place before the reproduction phase.

**Definition 4.** The CB process  $\{Z_n\}_{n \geq 0}$  is defined recursively as

$$(5) \quad Z_0 = I_0 > 0, \quad Z_{n+1} = \sum_{i=1}^{\phi_n(Z_n)} X_n(i), \quad n = 0, 1, \dots$$

Here, the control function dictates three possible scenarios:

- $Z_n - \phi_n(Z_n)$  individuals are removed from the population if  $\phi_n(Z_n) < Z_n$  and do not participate in the evolution of the process;
- $\phi_n(Z_n) - Z_n$  are added to the population before reproduction if  $\phi_n(Z_n) > Z_n$ ;
- No individual are removed or added if  $\phi_n(Z_n) = Z_n$ .

This model provides a more straightforward framework where migration events precede the reproductive phase.

**3. Estimators for the offspring mean.** Understanding the offspring distribution in branching processes is fundamental to reveal the overall behavior of the process. Estimating the offspring mean,  $m = E[X_1(1)]$ , is an important step toward grasping the

dynamics across generations in various scenarios. We will explore two types of conditional weighted least squares (CWLS) estimators connected to the processes introduced earlier.

Using the CWLS method, Yanev and Nitcheva, [8], proposed the following estimator for the offspring mean of the process defined in (4)

$$(6) \quad \tilde{m}_n = \frac{\sum_{i=1}^n Z_i \sum_{i=1}^n \frac{1}{1 + Z_{i-1}} - n \sum_{i=1}^n \frac{Z_i}{1 + Z_{i-1}}}{\sum_{i=1}^n (1 + Z_{i-1}) \sum_{i=1}^n \frac{1}{1 + Z_{i-1}} - n^2}.$$

We see that the only thing we need for the estimator is the number of individuals in each generation, although that is not always an easy task. Furthermore, conducting an analytical analysis of the estimator presents challenges and is a subject for future work.

To obtain this estimator, the method involves minimizing the sum of squared weighted residuals with respect to two parameters,  $m$  and  $M$  (representing the migration mean, which is currently not of our interest). This method is also applied in [10] for the offspring mean of the process defined in (5). The resulting estimator is given by:

$$(7) \quad \hat{m}_n = \left( \sum_{i=1}^n \frac{Z_i \varepsilon(Z_{i-1})}{\varepsilon(Z_{i-1}) + 1} \right) \left( \sum_{i=1}^n \frac{\varepsilon^2(Z_{i-1})}{\varepsilon(Z_{i-1}) + 1} \right)^{-1},$$

where  $\varepsilon(Z_{i-1})$  is the expectation of the control function, denoted as  $\varepsilon(k) = E[\phi_n(k)]$ . The asymptotic behavior of (7) has been studied with respect to the criticality of the process, and it has been proven that the estimator exhibits asymptotic normality and consistency. It is noteworthy that in this case, the minimization is solely with respect to  $m$ , assuming prior knowledge of  $\varepsilon(k)$  for each generation. Consequently, obtaining more information about the family tree becomes crucial. However, in [10], they also mentioned that if  $\varepsilon(k)$  is not known, it can be replaced  $\varepsilon(Z_{i-1})$  with  $\phi_{i-1}(Z_{i-1})$  and the modified estimator is:

$$(8) \quad \hat{m}_n = \left( \sum_{i=1}^n \frac{Z_i \phi_{i-1}(Z_{i-1})}{\phi_{i-1}(Z_{i-1}) + 1} \right) \left( \sum_{i=1}^n \frac{\phi_{i-1}^2(Z_{i-1})}{\phi_{i-1}(Z_{i-1}) + 1} \right)^{-1}.$$

**4. Simulation study.** We present the outcomes of simulations, each including 1000 paths, spanning across different generations ( $n = 10, 50, 100$ ) for both the processes detailed in (4) and (5). In the first model, emigration can occur both before and after reproduction, while in the second, it is only possible before. Another significant distinction is that immigration in (4) happens after the new individuals are produced, but in (5), it occurs before.

To generate the offspring distribution, as well as the distributions for emigrants and immigrants, Python is employed to randomize the values (also it is used for simulating the models). The resulting distributions are presented in the following three tables.

The following graphics, Figure 1 and Figure 2, display only a single path, providing a basic understanding of the two processes.

From both figures, we observe that up to the 50th generation, the two processes exhibit very similar behavior. However, in the third plots, we notice that process (5) demonstrates more rapid growth. This difference arises because we allow very few emi-

Table 1. Offspring distribution

0	1	2
0.0718	0.7571	0.1711

Table 2. Emigrant distribution

1	2	3
0.1979	0.5996	0.2025

Table 3. Immigrant distribution

1	2	3
0.2951	0.0243	0.6806

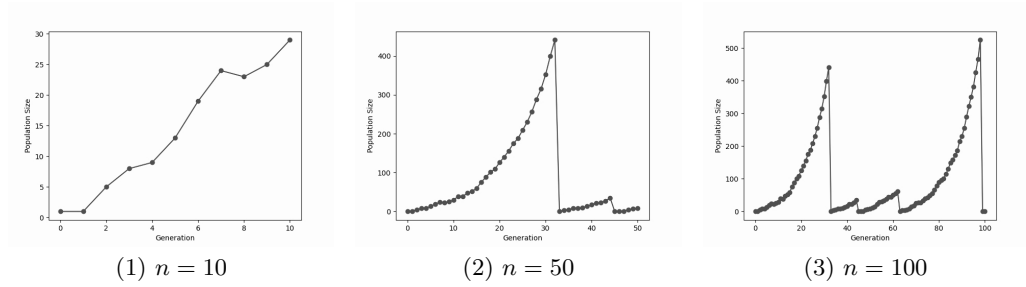


Fig. 1. Process with migration, model (4)

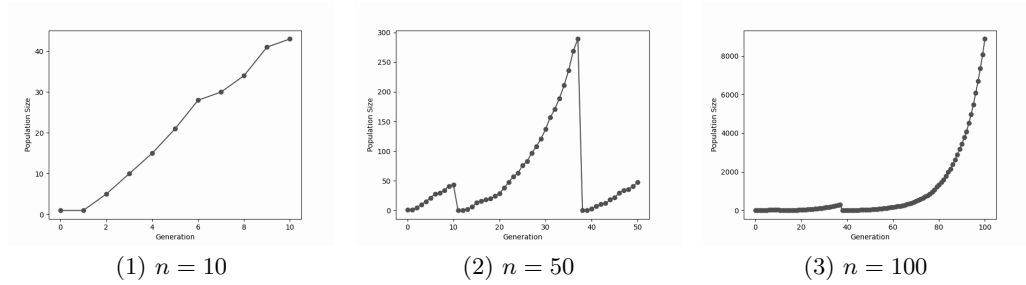


Fig. 2. Process with migration, model (5)

grants before reproduction, and at some point, they become insignificant for (5). On the contrary, (4) shows slower growth because this process involves individual emigration, meaning that certain individuals are removed after reproduction and do not participate to the next generation.

Additionally, we provide corresponding estimators for  $m$  as given by equations (6) and (8). For each case, we calculate the mean of the estimated  $m$ -s in every path and present the resulting value (the same approach is used in [8]), i.e.

$$avg_N(\tilde{m}) = \frac{1}{N} \sum_{j=1}^N \tilde{m}_n(j), \quad avg_N(\hat{m}) = \frac{1}{N} \sum_{j=1}^N \hat{m}_n(j),$$

where  $N$  is the number of simulated paths, which, in our case, is set to  $N = 1000$  for each scenario.

For the simulation of (5), we once again assume that  $p$ ,  $q$ , and  $r$  represent the probabilities of emigration, no migration, and immigration, respectively. This is analog of

Gawton-Watson process with migration defined in [3], in which the control function is a random variable, depending on  $p$ ,  $q$  and  $r$ . Here  $p = 0.03$ ,  $q = 0.2046$ ,  $r = 0.7654$  and the offspring mean is  $m \approx 1.0993$ , starting from  $Z_0 = 1$ . The results are presented in Table 4.

Table 4. Values of  $avg_N(\tilde{m})$  and  $avg_N(\hat{m})$

$n$	$avg_N(\tilde{m})$	$avg_N(\hat{m})$
10	0.9963	1.0418
50	1.0245	1.0168
100	1.0172	1.0019

The simulation results indicate the effective performance of both methods. However, an interesting question for a future work is whether it is possible to employ a similar estimator as (8) for a process that involves three control functions, such as (2).

The simulated process is supercritical. This allows us to use the asymptotic normality of the estimator (8). According to [3], Theorem 5.7,  $\sqrt{A_n}(\hat{m}_n - m) \xrightarrow{d} N(0, \sigma^2)$  as  $n \rightarrow \infty$ , where  $A_n = \sum_{i=1}^n \frac{\varepsilon^2(Z_{i-1})}{\varepsilon(Z_{i-1}) + 1}$  and  $\sigma^2 > 0$  is a constant. Having observed  $N$  trajectories  $\{S_1, \dots, S_N\}$  of the process, carrying information about the generation sizes and the value of the migration function, and supposing that some of the trajectories contain outliers (“contaminated” data which influence the correct estimation of the offspring mean), robust modifications of the estimators (8) can be constructed. Following the methodology, described in [11], the weighted least trimmed modification of (8) is defined as

$$\bar{m}(k) = \arg \min_{m \in R} \sum_{i=1}^k -w_i f(Est(S_{\nu(i)}, m))$$

where  $k$  is the trimming factor,  $f(x)$  is the logarithm of the density function of the standard normal distribution,  $\nu$  is a permutation of the indexes, such that  $f(Est(S_{\nu(1)}, m)) \geq f(Est(S_{\nu(2)}, m)) \geq \dots \geq f(Est(S_{\nu(n)}, m))$ . With  $Est(S_i, m) = \frac{\sqrt{A_n}}{\sigma} (\hat{m}_n^{(i)} - m)$  we note the transformation of the offspring mean estimator, which asymptotically behaves like a standard normal r.v. The weights  $w_i \geq 0$ ,  $i = 1, \dots, k$ , are such that an index  $k = \max\{i : w_i > 0\}$  exists. Following the steps in [11], Theorem 1, it can be proved that this estimator exists and its breakdown point is not less than  $(N - k)/n$  if  $n \geq 3$ ,  $(N + 1)/2 \leq k \leq N - 1$ . Hence the estimator  $\bar{m}(k)$  is robust and it incorporates only the most “probable” or “typical” trajectories of the process. The trajectories leading to untypical for the standard normal distribution values  $Est(S_i, m)$  are indicated as “outlier trajectories” and are excluded from the final form of the estimator  $\bar{m}(k)$ .

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