

Information properties of the nonparametric maximum likelihood estimators in branching processes with random migration

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Abstract: We consider the nonparametric maximum likelihood estimation of single type discrete time branching processes with random migration. These processes occur naturally in situations where besides the random reproduction both emigration and immigration of individuals can be observed in the population. Our aim is to study the behaviour of the estimators by calculating the Fisher information matrix and in particular to present confidence intervals for the migration probabilities and for the offspring and immigration distribution, which to be further examined by simulations and computational results.

Keywords: branching processes, migration, nonparametric estimators, Fisher information matrix, confidence intervals, simulations

I. INTRODUCTION

Controlled branching processes (CBPs) are useful tools when we want to regulate the dynamics of a population. In the 1950s-60s, some works [1, 2] started to introduce the idea of control into the process, but one of the most significant contributions was made by Sevast’yanov and Zubkov in 1974 [3]. They introduced the so-called ϕ -CBP, which used a deterministic control. N. Yanev extended this idea in [4] by allowing a random control in the process.

By incorporating random migration terms, this framework extends the classical Bienaymé-Galton-Watson (BGW) model, offering a more flexible and realistic representation of population dynamics. Such an extension is particularly relevant for biological and ecological applications, where external movement plays a crucial role in shaping population structure, persistence, and variability. These developments not only deepen our theoretical understanding of branching processes but also enhance their practical applicability in modeling complex, real-world systems.

The properties of this model have been extensively examined in studies like [5–11]. These investigations build upon the classical notion of criticality in branching processes, incorporating an additional parameter that accounts for the expected migration of individuals.

We study a submodel of the branching process with random migration (BPRM) that allows only emigration after reproduction (individual emigration), whereas in the original model, emigration is also permitted before reproduction (family emigration). Note that in the BPRM, the evolution of individuals is not independent, unlike in the classical BGW process.

In this paper, we extend our work from [12], by calculating the Fisher information matrix (FIM) and

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constructing confidence intervals for some of the non-parametric estimators obtained there.

A. BPRM: the model

Given that our study was motivated by [13], we have aimed to preserve as much consistency as possible with the notation and terminology introduced there.

We use three mutually independent sets of nonnegative integer valued random variables (r.v.): $X = \{X_{n,i}\}$, $\eta = \{\eta_n\}$ and $I = \{I_n\}$. The variables within each set are independent and identically distributed (i.i.d.). The BPRM $\{Y_n\}$ is then defined as

$$Y_0 \geq 0, \quad Y_{n+1} = \left(\sum_{i=1}^{Y_n} X_{n,i} + M_n \right)^+, \quad n = 0, 1, \dots, \tag{1}$$

where

$$M_n = \begin{cases} -\eta_n, & \text{with probability } p, \\ 0, & \text{with probability } q, \\ I_n, & \text{with probability } r, \end{cases} \tag{2}$$

$p + q + r = 1$, Y_0 is independent of X, η and I and $a^+ = \max\{0, a\}$.

For creating the $(n+1)$ -st generation, we first observe the reproduction of the individuals in the n -th one. Here, $X_{n,i}$ denotes the number of offspring of the i -th individual living in the n -th generation. After that, one of three types of migration occurs: emigration, no migration or immigration, with respective probabilities p, q and r .

In line with the standard classification for single-type discrete-time branching processes, the process is considered subcritical when $\mathbb{E}[X_{1,1}] < 1$, critical when $\mathbb{E}[X_{1,1}] = 1$, and supercritical when $\mathbb{E}[X_{1,1}] > 1$. In addition to this classification, the model incorporates another parameter, $M = \mathbb{E}[M_n | Y_n > 0]$. From a statistical perspective, a negative value of M ($M < 0$) indicates that, on average, emigration exceeds immigration, whereas a positive value ($M > 0$) signifies that immigration dominates the effect of emigration [10].

As can be seen from (1)–(2), the process $\{Y_n\}$ is not absorbed at zero, meaning that it can be regenerated after some time by introducing immigrants into the population. In this case the stay at zero is a random variable ζ , allowing geometric distribution with a parameter r , i.e. $\mathbb{P}(\zeta = k) = r(1-r)^k, k = 0, 1, \dots$. This probability represents the likelihood that the process remains at zero for exactly k generations before an immigration event occurs and the population is renewed.

Note that in [13] the migration component M_n is defined as

$$M_n = \begin{cases} -\left(\sum_{i=1}^{\eta_{n,1}} X_{n,i} + \eta_{n,2} \right), & \text{with probability } p, \\ 0, & \text{with probability } q, \\ I_n \mathbf{1}_{\{Y_n > 0\}} + I_n^0 \mathbf{1}_{\{Y_n = 0\}}, & \text{with probability } r, \end{cases}$$

where the authors offer the following interpretation of the included variables. The r.v. $\eta_{n,1}$ represents family emigration, that is, the number of families that emigrate before reproduction. In contrast, $\eta_{n,2}$ corresponds to individual emigration, meaning that $\eta_{n,2}$ individuals, randomly chosen from different families, are removed after reproduction. Finally, I_n and I_n^0 represent the state-dependent immigration in the non-zero state and the zero state, respectively. In the submodel (1)–(2) $\eta_n := \eta_{n,2}$ allowing only for individual emigration, and the zero and non-zero state immigration components coincide: $I_n = I_n^0$.

B. BPRM: estimators

In [12], we derived nonparametric maximum likelihood estimators (NMLEs) for migration event probabilities, as well as for the distributions of offspring, emigrants, and immigrants. We use the same notation here as in that work, namely:

- 1) $N_l^{em}, N_l^{null}, N_l^{imm}$: indicator random variables showing whether there is emigration, no migration, or immigration in the l -th generation. For example, if we observed immigration in the 10-th generation then $N_{10}^{em} = 0, N_{10}^{null} = 0$ and $N_{10}^{imm} = 1$.
- 2) $N_l^{off}(u)$: the number of parents in the l -th generation having u offspring. Their offspring contribute to the size of the next generation. For example, suppose, that in the l -th generation, we have a vector of offspring $(1, 2, 2, 1, 3, 1)$. In this vector, position i corresponds to the number of offspring of the i -th individual in the l -th generation. According to our notation, we then have:

$$N_l^{off}(1) = 3, N_l^{off}(2) = 2 \quad \text{and} \quad N_l^{off}(3) = 1.$$
- 3) $N_l^{em}(u)$: indicator of the event that emigration occurs in the l -th generation (after reproduction), with exactly u emigrants removed from the population. That is, $N_l^{em}(u) = 1$ if we have exactly u emigrants and is zero otherwise. These individuals do not participate in the next generation.
- 4) $N_l^{imm}(u)$: indicator of the event that immigration occurs in the l -th generation (after reproduction), with exactly u immigrants added to the population.

These immigrants then participate in the $(l + 1)$ -st generation and reproduce according to the offspring distribution of the process.

- 5) $p_u^\tau, \tau \in \{off, em, imm\}$: the probability mass functions (p.m.f.s) of the number of offspring, emigrants, and immigrants, respectively.

Using the notations above, the NMLEs are:

$$\hat{p} = \frac{\sum_{l=0}^{n-1} N_l^{em}}{n}, \quad \hat{q} = \frac{\sum_{l=0}^{n-1} N_l^{null}}{n}, \quad (3)$$

$$\hat{r} = \frac{\sum_{l=0}^{n-1} N_l^{imm}}{n}, \quad \hat{p}_u^\tau = \frac{\sum_{l=0}^{n-1} N_l^\tau(u)}{\sum_{l=0}^{n-1} \sum_{v=0}^\infty N_l^\tau(v)},$$

where $u = 0, 1, 2, \dots$ and $\tau \in \{off, em, imm\}$.

These estimators are derived from the likelihood function expressed as

$$L = \prod_{l=0}^{n-1} p^{N_l^{em}} q^{N_l^{null}} r^{N_l^{imm}} \times \prod_{u=0}^\infty (p_u^{off})^{N_l^{off}(u)} (p_u^{em})^{N_l^{em}(u)} (p_u^{imm})^{N_l^{imm}(u)}. \quad (4)$$

Additionally, we proved some statistical properties of the obtained estimators and provided simulations for them.

As noted in [12] the BPRM process defined by (1)–(2) can also be considered as a special case of a controlled branching process with random control function, defined by the migration component. Hence the estimators of the offspring probabilities p_u^{off} have the same form as the estimators of the offspring probabilities for the general controlled branching process, proposed and studied in [14]. In our setting, however, one can directly estimate the probabilities for migration and the distributions of the immigration and the emigration components, which otherwise remain hidden within the overall CBP migration component.

C. New results

In this section, we continue the work presented in the previous two subsections by investigating the FIM, (Section II) and constructing confidence intervals (CI) for the parameters (Section III).

For clarity and readability, matrix and vector dimensions are omitted throughout the paper once they have been specified.

II. FISHER INFORMATION MATRIX

We consider the parameter vector $\theta \in \mathbb{R}^{3+\nu}$, where $\nu = j + k + w$, defined as

$$\theta = (p, q, r, p_0^{off}, \dots, p_j^{off}, p_0^{em}, \dots, p_k^{em}, p_0^{imm}, \dots, p_w^{imm})^T, \quad (5)$$

with respect to which the FIM will be derived.

The first and second derivatives of the log-likelihood function

$$\log L = \sum_{l=0}^{n-1} \left(N_l^{em} \log p + N_l^{null} \log q + N_l^{imm} \log r \right) + \sum_{l=0}^{n-1} \sum_{u=0}^\infty \left(N_l^{off}(u) \log p_u^{off} + N_l^{em}(u) \log p_u^{em} + N_l^{imm}(u) \log p_u^{imm} \right), \quad (6)$$

are computed with respect to the parameters, following the order given in (5).

Remark 1. It is important to note that in Section I-B we theoretically allowed all of the p.m.f.s to have support from zero to infinity. However, in real-world applications they are not infinite, which is why we restrict them to finite values in (5).

The Hessian matrix of the log-likelihood function (6) is

$$\mathbf{H}_{(3+\nu) \times (3+\nu)}(\theta) = -\text{diag}(\mathbf{A}, \mathbf{B}, \mathbf{C}, \mathbf{D}), \quad (7)$$

where all the component matrices are also diagonal and they are as follows:

$$\mathbf{A}_{3 \times 3} = \text{diag} \left(\frac{\sum_l N_l^{em}}{p^2}, \frac{\sum_l N_l^{null}}{q^2}, \frac{\sum_l N_l^{imm}}{r^2} \right), \quad (8)$$

$$\mathbf{B}_{j \times j} = \text{diag} \left(\frac{\sum_l N_l^{off}(0)}{(p_0^{off})^2}, \dots, \frac{\sum_l N_l^{off}(j)}{(p_j^{off})^2} \right), \quad (9)$$

$$\mathbf{C}_{k \times k} = \text{diag} \left(\frac{\sum_l N_l^{em}(0)}{(p_0^{em})^2}, \dots, \frac{\sum_l N_l^{em}(k)}{(p_k^{em})^2} \right), \quad (10)$$

$$\mathbf{D}_{w \times w} = \text{diag} \left(\frac{\sum_l N_l^{imm}(0)}{(p_0^{imm})^2}, \dots, \frac{\sum_l N_l^{imm}(w)}{(p_w^{imm})^2} \right). \quad (11)$$

To obtain the FIM we take the expectation of the matrix \mathbf{H} , which is computed by taking the expectation of each of its individual elements (matrices).

For the expectation of matrix \mathbf{A} we have

$$\mathbb{E}[\mathbf{A}] = \text{diag} \left(\frac{n}{p}, \frac{n}{q}, \frac{n}{r} \right), \quad (12)$$

which is easily obtained by noting that the sums involve indicator random variables that do not depend on the size of the generation.

The situation is different when calculating expectations involving $N_l^{off}(j)$, since it depends on the size of the current generation.

For example, let's consider $N_l^{off}(0)$, the number of parents in the l -th generation that have zero offspring.

It depends on the current population size, Y_l , since it is not possible to have more parents with that number of offspring than the total number of individuals. Additionally, it follows a $Bi(Y_l, p_0^{off})$ distribution and

$$\mathbb{E}[N_l^{off}(0)|Y_l] = Y_l p_0^{off}. \tag{13}$$

For the purposes of our analysis, Y_l is treated as a known quantity and is not substituted with its theoretical mean, as the full structure of the family tree is available for reference.

Taking into account (9) and (13), we obtain

$$\mathbb{E}[\mathbf{B}] = \text{diag}\left(\frac{\sum_l Y_l}{p_0^{off}}, \dots, \frac{\sum_l Y_l}{p_j^{off}}\right), \tag{14}$$

where l is from 0 to $n - 1$.

For $\mathbb{E}[\mathbf{C}]$ we do not have a close form at present, because its computation requires a more detailed investigation of the distribution of emigrants under truncation or censoring. Therefore, we leave it in the following form:

$$\mathbb{E}[\mathbf{C}] = \text{diag}\left(\frac{\sum_l \mathbb{E}[N_l^{em}(0)]}{(p_0^{em})^2}, \dots, \frac{\sum_l \mathbb{E}[N_l^{em}(k)]}{(p_k^{em})^2}\right). \tag{15}$$

The expectations in (15) have a more complex form because one should take into consideration that they depend not only on the size of the current generation but also on the truncation effect: we cannot remove more individuals than are present. For example, if the population size is $Y_l = 5$ and the r.v. η_l has support up to 20, the actual number of possible immigrants is $\min(\eta_l, Y_l)$. Therefore the terms $\mathbb{E}[N_l^{em}(k)]$ must account for this minimum and cannot be replaced by the unconditional mean of η_l without further assumptions. This is due to the fact that the evolution of the objects are not independent as in a classical branching process without emigration.

The last matrix to be calculated is $\mathbb{E}[\mathbf{D}]$. For this, we consider the expectation of $N_l^{imm}(w)$. Unlike emigration, in the case of immigration the number of immigrants does not depend on the size of the generation. However, we must take into account that immigration is observable only when it occurs, so to calculate the expectation we use the law of total expectation:

$$\mathbb{E}[N_l^{imm}(w)] = \mathbb{E}[\mathbb{E}[N_l^{imm}(w)|M_n]],$$

taking into account (2), we have that

$$\mathbb{E}[N_l^{imm}(w)] = r p_w^{imm}.$$

Therefore, $\mathbb{E}[\mathbf{D}]$ takes the form

$$\mathbb{E}[\mathbf{D}] = \text{diag}\left(\frac{nr}{p_0^{imm}}, \dots, \frac{nr}{p_w^{imm}}\right). \tag{16}$$

Using (12), (14), (15) and (16) in the expectation of (7), we obtain the FIM as follows:

$$\mathcal{I}(\boldsymbol{\theta}) = \mathbb{E}[-\mathbf{H}(\boldsymbol{\theta})] = \text{diag}(\mathbb{E}[\mathbf{A}], \mathbb{E}[\mathbf{B}], \mathbb{E}[\mathbf{C}], \mathbb{E}[\mathbf{D}]). \tag{17}$$

The above matrix is diagonal, and therefore its inverse is also diagonal. Each diagonal element of the inverse is the reciprocal of the corresponding diagonal element of the original matrix.

Under regularity conditions [15], the MLEs (3) are asymptotically normal. That is

$$\sqrt{n}(\hat{\boldsymbol{\theta}}_n - \boldsymbol{\theta}) \xrightarrow[n \rightarrow \infty]{d} \mathcal{N}(0, \mathcal{I}^{-1}(\boldsymbol{\theta})),$$

where $\boldsymbol{\theta}$ is (5) and $\mathcal{I}^{-1}(\boldsymbol{\theta})$ is the inverse matrix of (17).

III. CONFIDENCE INTERVALS

In many studies, intervals are preferred over point estimates. Based on the FIM obtained in the previous section and our results discussed in Section I, we can now construct confidence intervals (CI) for all parameters, except for p_u^{em} .

In addition, in [12] we obtained numerical results for the estimators by simulating the model, using the following distributions and probabilities: $p = 0.5797$, $q = 0.3530$, $r = 0.0673$, $X_{n,i} \in Bi(2, 0.55)$, $\eta_n \in Bi(4, 0.2)$ and $I_n \in Bi(5, 0.4)$. We will use the estimations from there here to see whether the confidence intervals perform well for the simulated data. We will present results only for 50 and 100 generations, since the others can be calculated in the same manner.

The CI for the probability of emigration is

$$p \in \left(\hat{p} + z_{\frac{\alpha}{2}} \sqrt{\hat{p}/n}, \hat{p} + z_{1-\frac{\alpha}{2}} \sqrt{\hat{p}/n}\right),$$

where, as usual, $z_{\alpha/2}$ is the $\alpha/2$ -ith quantile of the standard normal distribution. The CI for q and r have the same form, with \hat{p} replaced by their respective estimators.

As we can see from Tables 1 and 2, with an increasing number of generations the CIs become narrower, and all of them include the true value if the estimated parameter.

For the probabilities involved in the offspring distribution, we obtained the following CIs:

$$p_j^{off} \in \left(\hat{p}_j^{off} + z_{\frac{\alpha}{2}} \sqrt{\frac{\hat{p}_j^{off}}{\sum_l Y_l}}, \hat{p}_j^{off} - z_{1-\frac{\alpha}{2}} \sqrt{\frac{\hat{p}_j^{off}}{\sum_l Y_l}}\right). \tag{18}$$

We can see from (18) that we need additional information not directly used so far, namely $\sum_{l=0}^{n-1} Y_l$,

Prob.	Real value	Est. value	95% CI
p	0.5797	0.7200	(0.4848, 0.9552)
q	0.3530	0.2000	(0.0760, 0.3240)
r	0.0673	0.0800	(0.0016, 0.1584)

Table 1: CI for the migration probabilities, $n = 50$.

Prob.	Real value	Est. value	95% CI
p	0.5797	0.6900	(0.5272, 0.8528)
q	0.3530	0.2700	(0.1682, 0.3718)
r	0.0673	0.0400	(0.0246, 0.1354)

Table 2: CI for the migration probabilities, $n = 100$.

Prob.	Real value	Est. value	95% CI
p_0^{off}	0.2025	0.2057	(0.1970, 0.2144)
p_1^{off}	0.4950	0.4913	(0.4779, 0.5047)
p_2^{off}	0.3025	0.3030	(0.2924, 0.3136)

Table 3: CI for the offspring probabilities, $n = 50$.

which is the total size across all generations up to the $(n - 1)$ -st.

The estimations and CIs for the offspring probabilities, Tables 3 and 4, are really close to the true values. This is because, in this simulation, the process is supercritical and we observe an exponential growth, which results in a large sample size across generations and, consequently, tighter confidence intervals.

Finally we present a CI for the immigration distribution:

$$p_w^{imm} \in \left(\hat{p}_w^{imm} + z_{\frac{\alpha}{2}} \sqrt{\frac{\hat{p}_w^{imm}}{n\hat{r}}}, \hat{p}_w^{imm} + z_{1-\frac{\alpha}{2}} \sqrt{\frac{\hat{p}_w^{imm}}{n\hat{r}}} \right).$$

There, as is shown in Table 5, we did not observe all of the possible values, mainly for two reasons: the unobserved values are the least probable ones, and the overall probability of immigration is very small in this simulation. We can also see that the CIs perform poorly in this case, again due to the reasons mentioned above.

Because of the low immigration probability, $r = 0.0673$, up to the 50th generation immigration occurs only four times, and none is observed between the 50th and 100th generations, as can be seen in Fig. 1A. Therefore, there is no point in presenting the numerical results for $n = 100$. However, we have slightly improvement in the case of $n = 200$, Fig. 1B, so we show those results in Table 6.

Prob.	Real value	Est. value	95% CI
p_0^{off}	0.2025	0.2024	(0.2016, 0.2032)
p_1^{off}	0.4950	0.4948	(0.4935, 0.4961)
p_2^{off}	0.3025	0.3028	(0.3018, 0.3038)

Table 4: CI for the offspring probabilities, $n = 100$.

Prob.	Real value	Est. value	95% CI
p_0^{imm}	0.0778	—	—
p_1^{imm}	0.2592	0.2500	(-0.2400, 0.7400)
p_2^{imm}	0.3456	0.2500	(-0.2400, 0.7400)
p_3^{imm}	0.2304	0.5000	(-0.1930, 1.1930)
p_4^{imm}	0.0768	—	—
p_5^{imm}	0.0102	—	—

Table 5: CI for the migration probabilities, $n = 50$.

Prob.	Real value	Est. value	95% CI
p_0^{imm}	0.0778	—	—
p_1^{imm}	0.2592	0.1429	(-0.0551, 0.3409)
p_2^{imm}	0.3456	0.5000	(0.1296, 0.8704)
p_3^{imm}	0.2304	0.3571	(0.0441, 0.6701)
p_4^{imm}	0.0768	—	—
p_5^{imm}	0.0102	—	—

Table 6: CI for the migration probabilities, $n = 200$.

As shown in Table 6, the CIs are almost reasonable, except for the one corresponding to p_1^{imm} . The estimation of rare events is always difficult and challenging task.

Additionally, from a statistical point of view, 50 generations should be sufficient to obtain reliable results. However, in the context of branching processes, even in the simplest model, the required number of generations is much larger [16, 17], sometimes exceeding a thousand.

IV. CONCLUSION

In this paper, we derived the Fisher information matrix for branching processes with random migration and constructed confidence intervals for the corresponding nonparametric maximum likelihood estimators. The results demonstrate that even with relatively small sample sizes, reliable estimation is possible for offspring and migration probabilities. However, further investigation is required in cases involving emigration or when the probability of any migration type is very low.

Beyond their theoretical importance, our results provide practical tools for analyzing real-world systems in biology and ecology, where migration influences population dynamics. Future research may focus on

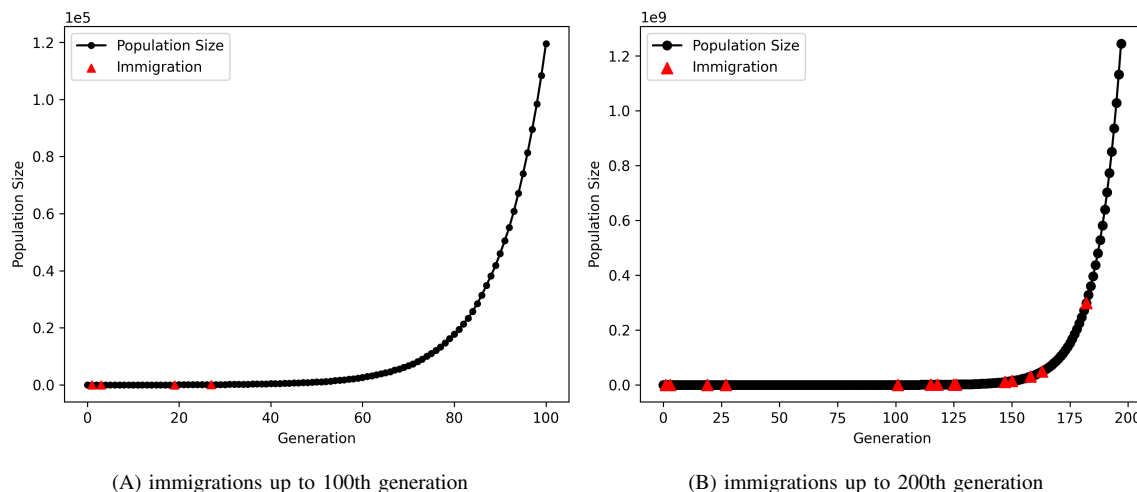


Fig. 1: Population size across generations with immigration events.

improved methods for rare event estimation, such as Bayesian techniques, resampling-based confidence intervals, or simulating multiple realizations of the family tree and then calculating the standard errors of the proposed estimators.

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