

SOME CONTRIBUTIONS TO THE THEORY ON DISCRETE TIME BRANCHING MODELS

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Abstract. In this work, a general summary concerning the main contributions achieved by our research group to the theory on certain classes of discrete time branching models, including controlled, bisexual and some classical branching processes, is provided. Some open questions for future research are also discussed.

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§1. Introduction

Branching processes theory was initially motivated to explain the extinction phenomenon of certain family lines belonging to the European aristocracy. Nowadays it provides appropriate mathematical models to describe the probabilistic evolution of systems whose components (cell, particles, individuals in general) after certain life period reproduce and die. Added to their theoretical interest, these processes have therefore a major practical dimension because of potential applications in such diverse fields as biology, demography, ecology, epidemiology, genetics, medicine and so on. Really, the terminology branching processes was proposed by A.N. Kolmogorov in 1938 when he was interested about their applications in biology. Classical books for their study have been provided, among others, by S. Asmussen and H. Hering [2], K. Athreya and P. Ney [3], P. Guttorp [36], T. Harris [38], P. Jagers [46] or G. Sankaranarayanan [65].

In this work we state a general summary concerning the main contributions achieved by our research group to the theory about some discrete time branching models. In section 2 we consider the contributions to certain classical branching models including the Bienaymè-Galton-Watson process, the Bienaymè-Galton-Watson process with immigration and the controlled process with both deterministic and random control. A brief presentation on these models and the topics which have been investigated about them are previously introduced. Section 3 is devoted to stating the contributions achieved in the class of bisexual branching processes. Particular attention is given to the new bisexual processes introduced and investigated by our group. Finally, some open research lines for future study are discussed in section 4. For technical details about the mentioned contributions we refer the reader to the corresponding cited references.

§2. Contributions to the theory on some classical branching models

2.1. Bienaymè-Galton-Watson model

Introduced by I.J. Bienaymè in 1845 and later formalized by F. Galton and H. Watson, the called Bienaymè-Galton-Watson process is a stochastic model defined in the recursive form:

$$Z_0 = N, \quad Z_{n+1} = \sum_{i=1}^{Z_n} X_{ni}, \quad n = 0, 1, \dots \quad (1)$$

where the convention that the empty sum is 0 is adopted, N is a positive integer and X_{ni} , $n = 0, 1, \dots$; $i = 1, 2, \dots$ are independent and identically distributed (iid), non-negative and integer-valued random variables, their common probability law is called the offspring distribution. Intuitively X_{ni} represents the number of descendants originated by the i -th progenitor in the generation n , being Z_{n+1} the population size in the $(n + 1)$ -th generation. It can be easily verified that $\{Z_n\}_{n \geq 0}$ is a homogeneous Markov chain, 0 being an absorbent state and $k = 1, 2, \dots$ transient states. This model has received considerable interest in the literature and from it, several branching models have been derived. Next we provide some classical results about it. Let $m := E[X_{01}]$ and $\sigma^2 := Var[X_{01}] < \infty$ be the mean and variance of the offspring distribution respectively.

The called criticality theorem, see K. Athreya and P. Ney [3, pp. 4], asserts that if $m \leq 1$ then $P(Z_n \rightarrow 0) = 1$, and if $m > 1$ then $P(Z_n \rightarrow 0) < 1$, being $P(Z_n \rightarrow 0)$ the smallest root of the equation $E[s^{X_{01}}] = s$ in the interval $[0, 1]$. Moreover, it is verified the duality extinction-explosion, namely $P(Z_n \rightarrow 0) + P(Z_n \rightarrow \infty) = 1$.

Its limiting evolution depends strongly of m . In fact, for $m < 1$ (subcritical case) it was proved in [68] that

$$\lim_{n \rightarrow \infty} P(Z_n = k \mid Z_n > 0) = b_k, \quad k = 1, 2, \dots \text{ with } \sum_{k=1}^{\infty} b_k = 1$$

where $\sum_{k=1}^{\infty} k b_k < \infty$ if and only if $\sum_{k=1}^{\infty} k \log(k) P(X_{01} = k) < \infty$. For $m = 1$ (critical case) it was determined (see [48] and [68]) that

$$\lim_{n \rightarrow \infty} P(n^{-1} Z_n \leq x \mid Z_n > 0) = 1 - e^{-2x\sigma^{-2}}, \quad x \geq 0$$

and for $m > 1$ (supercritical case) it was established (see [40], [47] or [66]) the existence of a sequence of positive constants $\{k_n\}_{n \geq 0}$ such that $\{k_n Z_n\}_{n \geq 0}$ converges almost surely to a non-negative, finite and non-degenerate random variable.

Results about its accumulated progeny, namely $Y_n = \sum_{i=0}^n Z_i$, $n = 0, 1, \dots$, were provided in [37], [42] and [63], and its inferential theory was developed, between others, in [14], [37], [40], [41] or [60]. In 1922, R. Fisher considered this model under a genetic context and after 1940 its interest increased due to its several applications in the physical and biological sciences, mainly to nuclear chain reactions and particles cascades (see [7], [8], [11] or [64]).

Remark 1. We have considered subcritical Bienaymè-Galton-Watson models with some classical offspring distributions (Poisson, binomial and negative binomial laws) and we have investigated in [6] the probabilistic evolution of the variables $T := \min\{n > 0 : Z_n = 0\}$ and

$Y_T := \sum_{k=0}^{T-1} Z_k$, namely the extinction time and the total progeny until the extinction. Through simulation, a comparative study has been also provided.

2.2. Bienaymè-Galton-Watson model with immigration

Initially studied by C.R. Heathcote [39] and A.G. Pakes [62] as a modification of the standard model (1), the Bienaymè-Galton-Watson process with immigration is a branching model which allows the incorporation, in each generation, of individuals from another populations. From the general setting given in (1) its mathematical formal definition is:

$$Y_0 = N, \quad Y_{n+1} = \sum_{i=1}^{Y_n} X_{ni} + I_{n+1}, \quad n = 0, 1, \dots$$

where I_{n+1} represents the number of immigrants in the $(n + 1)$ -th generation, $\{I_n\}_{n \geq 1}$ being a sequence of iid non-negative and integer-valued random variables independent of $\{X_{ni}, n = 0, 1, \dots; i = 1, 2, \dots\}$.

Under some conditions it has been established, see G. Sankaranarayanan [65, pp. 195] that $\{Y_n\}_{n \geq 0}$ suitably normalized converges in distribution to certain random variable Y . Supposed that $E[X_{01}] = 1$ it was proved, see P. Jagers [46, pp. 56], that Y has a Gamma distribution. However when $E[X_{01}] < 1$ or $E[X_{01}] > 1$ the limiting distribution of Y is not sufficiently determined.

Remark 2. Our main contribution to the theory on this branching model has been to identify the Pearson's distribution type associated to Y by using the first cumulants of both, the offspring and the immigration laws (see [50]).

2.3. Controlled model with deterministic control function

The controlled branching process with deterministic control function was defined by B.A. Sevast'yanov and A.M. Zubkov [67] in the form:

$$Z_0 = N, \quad Z_{n+1} = \sum_{i=1}^{\phi(Z_n)} X_{ni}, \quad n = 0, 1, \dots$$

where the intuitive interpretation of the variables X_{ni} and Z_n is the same that in (1) but now, the novelty is the incorporation of the control function ϕ whose mission is to determine, in each generation, the number of progenitors who intervene in the subsequent reproduction process. Really, for those values of Z_n such that $\phi(Z_n) < Z_n$ we have that $Z_n - \phi(Z_n)$ individuals are removed from the population and therefore they do not participate in the future evolution of the process. For the values of Z_n such that $\phi(Z_n) > Z_n$ a total of $\phi(Z_n) - Z_n$ new individuals (immigrants) of the same type are added to the population participating in the reproduction process under the same conditions as the others. Finally, no control is applied on the population when $\phi(Z_n) = Z_n$.

With respect to this model, two questions have fundamentally been investigated, the problem of its possible extinction, i.e. the study of conditions which guarantee that the evolution of the population finishes from a certain generation (see [67] and [70]) and, supposing that the extinction has not happened, the problem of investigating its probable future evolution (see [5] and [70]).

Remark 3. Our contributions to this class of controlled models have mainly been:

- Assuming a control function ϕ verifying that $\phi(x_1 + x_2) \geq \phi(x_1) + \phi(x_2)$, $x_1, x_2 \in \mathbb{R}^+$ we have studied properties on its stochastic monotony and we have obtained some results about its extinction probability and limiting behaviour (see [21]).
- We have determined non-parametric estimators for the offspring distribution and its associated mean and variance. For the proposed estimators, some moments and asymptotic properties as consistency and limit theorems have been obtained (see [34] and [35]).

2.4. Controlled model with random control function

Consider on the same probability space the independent sets of non-negative integer-valued random variables $\{X_{ni} : n = 0, 1, \dots; i = 1, 2, \dots\}$ and $\{\phi_n(k) : n, k = 0, 1, \dots\}$, where X_{ni} are iid and, for $n = 0, 1, \dots$, the sequences $\{\phi_n(k)\}_{k \geq 0}$ are independent and with identical one-dimensional probability distributions. The controlled branching process with random control function, introduced by N.M. Yanev [69], is defined in the form:

$$Z_0 = N, \quad Z_{n+1} = \sum_{i=1}^{\phi_n(Z_n)} X_{ni}, \quad n = 0, 1, \dots$$

As in (1), X_{ni} represents the number of descendants originated by the i -th individual in the generation n and Z_{n+1} is the population size in the $(n+1)$ -th generation. Each individual, independently of all others, gives rise to new individuals with the same probability distribution but, unlike the Bienaymè-Galton-Watson process, the population size in the $(n+1)$ -th generation is determined by a random process. Actually, if $Z_n = k$ the random variable $\phi_n(k)$ will determine the number of progenitors in the n -th generation. Thus, it is deduced that this branching model could describe the probabilistic evolution of populations in which taking into account some environmental, social or another factors a random mechanism establishes the number of progenitors who participate in each generation.

Assuming that $\phi_n(k) = \alpha_n k(1 + o(1))$ almost surely, where $\{\alpha_n\}_{n \geq 0}$ is a sequence of iid non-negative random variables, sufficient conditions for the extinction or non-extinction of such a process were determined in [69]. With similar requirements about the control variables $\phi_n(k)$ but omitting the assumption of independence in the sequence $\{\alpha_n\}_{n \geq 0}$, sufficient conditions for the extinction were provided in [9] and imposing certain hypotheses on the α -th absolute moments ($1 < \alpha \leq 2$) of the offspring distribution and the control variables, a limiting result was established in [61]. Finally, using some specific control variables, certain inferential questions were considered in [15].

Remark 4. Our research group has studied this branching model under a more general context, assuming asymptotically linear growth of the expectation of the control variables, and we have investigated its extinction probability and probabilistic evolution. More concretely, our contributions to the theory of this model have been (see [27], [28], [30], [31], [32] and [33]) the following:

- To study the transition properties between its states.
- To obtain some results about its accumulated progeny.

- To determine some necessary and sufficient conditions for its almost sure extinction or its non-extinction with a positive probability.
- To establish, in analogy with the Bienaymè-Galton-Watson process, an appropriate classification for this process in subcritical, critical and supercritical case.
- To investigate, in accordance with the classification established, its limiting behaviour suitably normalized.

§3. Contributions to the theory on bisexual branching models

In the Symposium held in 1966 at the Wistar Institute of Anatomy and Biology of Philadelphia, S.M. Ulam in his presentation title *How to formulate mathematically problems of rate of evolution?* pointed out that *"There is a very nice and simple mathematical technique for describing processes starting with a single object, which then duplicates and gives 0, 1, 2 or more descendants. It is called the theory of branching processes. It deals with asexual reproduction and gives methods to calculate the number of existing particles, of various kinds, in future generations, and other questions of this sort. I would like to stress that a corresponding theory for branching with sex, where particles get together, say at random and then produce offspring, i.e., a combination of a binary process of mating and reproduction, is mathematically much more difficult and no exact theory exists as yet"*. Two years later, D.J. Daley [12] introduced the following two-sex stochastic model:

3.1. Daley bisexual model

$$Z_0 = N, \quad (F_{n+1}, M_{n+1}) = \sum_{i=1}^{Z_n} (f_{ni}, m_{ni}), \quad Z_{n+1} = L(F_{n+1}, M_{n+1}), \quad n = 0, 1, \dots \quad (2)$$

where the empty sum is considered to be $(0, 0)$, N is a positive integer, $\{(f_{ni}, m_{ni}), n = 0, 1, \dots; i = 1, 2, \dots\}$ is a sequence of iid non-negative, integer-valued random variables, their common probability law is called offspring distribution, and the mating function $L : \mathbb{R}^+ \times \mathbb{R}^+ \rightarrow \mathbb{R}^+$ is assumed to be monotonic non-decreasing in each coordinate, integer-valued on integer arguments and such that $L(x, y) \leq xy$. Intuitively (f_{ni}, m_{ni}) represents the number of females and males produced by the i -th mating unit in the n -th generation, hence by (2), (F_{n+1}, M_{n+1}) will be the total number of females and males in the $(n + 1)$ -th generation. These females and males form $Z_{n+1} = L(F_{n+1}, M_{n+1})$ couples (mating units), which reproduce independently of all other mating units with the same offspring distribution for each generation. It can be proved that $\{(F_n, M_n)\}_{n \geq 1}$ and $\{Z_n\}_{n \geq 0}$ are homogeneous Markov chains.

The Daley's process is a reasonable model to describe the probabilistic evolution of populations with sexual reproduction, it has received some attention in the literature (see [1], [4], [10], [12], [13], [16], [43], [44] or [64]) and a survey about it has been recently published by D. Hull [45]. Next we provide some information on this model.

Definition 1. The Daley's process is said to be superadditive when its mating function verifies,

for $k = 2, 3, \dots$, that

$$L\left(\sum_{i=1}^k x_i, \sum_{i=1}^k y_i\right) \geq \sum_{i=1}^k L(x_i, y_i), \quad x_i, y_i \in \mathbb{R}^+, \quad i = 1, \dots, k.$$

Notice that superadditivity is an intuitive and logic condition. It is not a serious restriction, most of the mating functions considered are superadditive.

Definition 2. We define the mean growth rates per mating unit as:

$$r_k := k^{-1}E[Z_{n+1}|Z_n = k], \quad k = 1, 2, \dots$$

It is clear that the extinction of this process occurs when for some n it is verified that $Z_n = 0$. The most important result about its extinction probability was provided in [13] for a superadditive Daley's model. In fact, it was proved that $P(Z_n \rightarrow 0 | Z_0 = k) = 1$, $k = 1, 2, \dots$ if and only if $r := \lim_{k \rightarrow \infty} r_k \leq 1$. This fact motivated its classification in subcritical ($r < 1$), critical ($r = 1$) and supercritical ($r > 1$) case.

Considering the mating function $L(x, y) = \min\{x, y\}$ some results about the limiting behaviour of the sequences $\{r^{-n}F_n\}_{n \geq 1}$ and $\{r^{-n}M_n\}_{n \geq 1}$ were established in [4], and assuming some additional conditions on the mating function and offspring distribution belonging to the power series family of distributions, maximum likelihood estimators for the offspring mean vector and the growth rate r were determined in [16].

Remark 5. Our research group has investigated several questions about this bisexual model and some contributions to its probabilistic and inferential theory have been provided in [17], [18], [19], [20], [24], [29] and [52]. To sum up, considering a superadditive Daley's model we have obtained:

- Some necessary and sufficient conditions for the almost sure, L^1 and L^2 convergence of the sequences $\{r^{-n}Z_n\}_{n \geq 0}$, $\{r^{-n}F_n\}_{n \geq 1}$ and $\{r^{-n}M_n\}_{n \geq 1}$ to non-degenerate limits.
- Properties about its stochastic monotony and some results concerning its accumulate progeny.
- Non-parametric and bayesian estimators for the offspring distribution, the mean vector and the growth rate.
- Some applications, for example the probabilistic evolution of certain variables in ecological problems.

Moreover, in order to describe the probabilistic evolution of more complicated sexual reproduction populations, from the Daley's model general context, we have introduced and investigated some new bisexual branching models. Next, we provide the mathematical formal definition and some information about them:

3.2. Bisexual model with immigration of females and males

Introduced in [22], the bisexual process with immigration of females and males is defined in the form:

$$Z_0 = N, \quad (F_{n+1}, M_{n+1}) = \sum_{i=1}^{Z_n} (f_{ni}, m_{ni}) + (F_{n+1}^I, M_{n+1}^I),$$

$$Z_{n+1} = L(F_{n+1}, M_{n+1}), \quad n = 0, 1, \dots$$

where $\{(F_n^I, M_n^I)\}_{n \geq 1}$ is a sequence of iid non-negative, integer-valued random variables independent of $\{(f_{ni}, m_{ni}), n = 0, 1, \dots; i = 1, 2, \dots\}$. Intuitively (F_n^I, M_n^I) represents the number of immigrant females and males in the n -th generation.

The classification of its states, relations among its probability generating functions and some inferential results have been established in [22]. On the other hand, some limiting theorems about it have been obtained in [23] and [26].

3.3. Bisexual model with immigration of mating units

This branching model was also defined in [22] in the following manner:

$$Z_0 = N, \quad (F_{n+1}, M_{n+1}) = \sum_{i=1}^{Z_n} (f_{ni}, m_{ni}), \quad Z_{n+1} = L(F_{n+1}, M_{n+1}) + I_{n+1}, \quad n = 0, 1, \dots$$

where $\{I_n\}_{n \geq 1}$ is a sequence of iid non-negative, integer-valued random variables independent of the random vectors $\{(f_{ni}, m_{ni}), n = 0, 1, \dots; i = 1, 2, \dots\}$. The variable I_n represents the number of immigrant mating units in the n -th generation.

Results concerning the classification of its states and some relations about its probability generating functions have been provided in [22] and its limiting behaviour suitably normalized has been investigated in [25].

3.4. Bisexual model with population-size dependent mating

This branching model has been formally defined in [53] as follows:

$$Z_0 = N, \quad (F_{n+1}, M_{n+1}) = \sum_{i=1}^{Z_n} (f_{ni}, m_{ni}), \quad Z_{n+1} = L_{Z_n}(F_{n+1}, M_{n+1}), \quad n = 0, 1, \dots$$

where $\{L_k\}_{k \geq 0}$ is a sequence of mating functions. We have extended the classical condition of superadditivity usually imposed to mating function considering that $L^* : \mathbb{Z}^+ \times \mathbb{R}^+ \times \mathbb{R}^+ \rightarrow \mathbb{R}^+$ defined by $L^*(k, x, y) = L_k(x, y)$ is a superadditive function. Sufficient conditions which guarantee this requirement have been established in [59] where, under this condition, some stochastic monotony properties and several results about its accumulated progeny have been also investigated. On the other hand, results concerning its extinction probability and limiting behaviour have been derived in [53] and [57].

3.5. Bisexual model in varying environments

Introduced in [54], this branching process is defined in the form:

$$Z_0 = N, \quad (F_{n+1}, M_{n+1}) = \sum_{i=1}^{Z_n} (f_{ni}, m_{ni}), \quad Z_{n+1} = L(F_{n+1}, M_{n+1}), \quad n = 0, 1, \dots$$

where, for every $n = 0, 1, \dots$, $\{(f_{ni}, m_{ni})\}_{i \geq 1}$, is a sequence of iid non-negative, integer-valued random vectors. Consequently, it is deduced that for this process, unlike Daley's model, the offspring probability distribution varies from generation to generation and therefore, it is derived that in general $\{(F_n, M_n)\}_{n \geq 1}$ and its associated sequence of mating units $\{Z_n\}_{n \geq 0}$ are non-homogeneous Markov chains. This lack of homogeneity establishes an important difference with the previous bisexual processes. It can be an interesting model for description of the probabilistic evolution of sexual reproduction populations in which for some environmental, social or another reasons, the probability distribution associated to the reproduction changes in each generation. Relations among its underlying probability generating functions and some necessary and sufficient conditions for its almost sure extinction have been determined in [54] and [55]. Results about its limiting behaviour suitably normalized have been obtained in [56] and [58].

§4. Some open research lines for future study

Nowadays we have open different research lines about branching processes. Next we provide information about some of them:

4.1. To complete the probabilistic and inferential theory concerning some classes of branching models previously mentioned

With respect to the class of controlled branching models, some questions for future research are for example:

- (a) To complete the probabilistic theory about the controlled model with random control function. For instance, two interesting problems are:

- (a.1) For $k = 1, 2, \dots$, let $\tau(k) := k^{-1}E[X_{01}]E[\phi_0(k)]$ which is intuitively interpreted as the expected growth rate per individual when, in certain generation, there is k individuals. In order to obtain conditions for the almost sure extinction, in [27] have been considered different possible behaviours for the sequence $\{\tau(k)\}_{k \geq 1}$ with respect to 1. In particular, the cases $\limsup_{k \rightarrow \infty} \tau(k) < 1$ and $\liminf_{k \rightarrow \infty} \tau(k) > 1$, called subcritical and supercritical, respectively, have been investigated. An open question is to consider a controlled process with random control function under the complementary situation, i.e.

$$\liminf_{k \rightarrow \infty} \tau(k) \leq 1 \leq \limsup_{k \rightarrow \infty} \tau(k)$$

referred as critical case and to investigate its extinction probability and, for some suitably chosen norming constants, its limiting evolution.

- (a.2) The controlled branching process with random control function defined in (2) can be generalized by introducing of multi-type random control function in the following way:

$$Z_0 = N, \quad Z_{n+1} = \sum_{i \in I} \sum_{j=1}^{\phi_{n,i}(Z_n)} X_{n,i}(j), \quad n = 0, 1, \dots \quad (3)$$

where I is an index set (finite or infinite), for each $i \in I$ fixed $X_{n,i}(j)$ are iid non-negative and integer-valued random variables, independent of the set of control variables $\{\phi_{n,i}(k), n = 0, 1, \dots; k = 0, 1, \dots; i \in I\}$, being $\{\phi_{n,i}(k), k = 0, 1, \dots; i \in I\}$, $n = 0, 1, \dots$ independent random fields with identical one dimensional probability distributions. The particular case of (3) where $\phi_{n,i}(k) \equiv \phi_i(k)$ almost surely, ϕ_i being a deterministic control function was firstly investigated by A.M. Zubkov [70]. Our purpose is to investigate the extinction probability and the limiting behaviour of the general model (3) assuming linear growth of the mathematical expectation corresponding to the multi-type random control variables.

- (b) To develop, from a classical and a bayesian point of view, the inferential theory about the controlled model with random control function.
- (c) To develop their potential applications.

Concerning to the class of bisexual branching models some open questions are:

- (a) To complete their probabilistic theory. For example, two possibilities are, to study the L^α -convergence, $1 \leq \alpha \leq 2$ for the model with population-size dependent mating and, in order to obtain some new results about the limiting behaviour of the model in varying environments, to investigate another possible sequences of norming constants.
- (b) To develop their inferential theory considering both the classical and the bayesian outlook.
- (c) To develop their potential applications.

4.2. To introduce and investigate new discrete time branching models

In order to describe the probabilistic evolution of more complex populations we are also interested in to introduce and investigate new branching models. A possibility is for example:

Let $\{X_{n,i}(j) : i = 1, \dots, m; n = 0, 1, \dots; j = 1, 2, \dots\}$ be a sequence of m -dimensional non-negative, integer-valued and independent random vectors defined on the same probability space, and such that for each type $i \in \{1, \dots, m\}$ are identically distributed. The basic multi-type branching model is then introduced as the m -dimensional process $\{Z(n)\}_{n \geq 0}$ defined in the recursive form:

$$Z(0) = N, \quad Z(n+1) = \sum_{i=1}^m \sum_{j=1}^{Z_i(n)} X_{n,i}(j), \quad n = 0, 1, \dots \quad (4)$$

where N is a m -dimensional vector of non-negative integers, the positive integer m denotes the number of different types of individuals and the random vector $X_{n,i}(j)$ informs us about the number of descendants of each type originated by the j -th progenitor of type i in the n -th generation. Thus, $Z(n)$ represents the total number of individuals of each type in the generation n . The process is initiated with the vector of progenitors N . A good exposition about the results investigated on this multi-type model can be seen in the book by C. Mode [49]. In order to consider more complicated multi-type situations, our research group is interested in to develop new multi-type branching models. Taking into account (4), we have introduced the following model:

For each m -dimensional non-negative and integer-valued vector z let $\{Y_{n,i}(z) : i = 1, \dots, m; n = 0, 1, \dots\}$ be a sequence of m -dimensional non-negative and integer-valued random vectors which are defined on the same probability space where:

- (i) If n and \tilde{n} are non-negative integers such that $n \neq \tilde{n}$, then the m^2 -dimensional random vectors $(Y_{n,1}(z), \dots, Y_{n,m}(z))$ and $(Y_{\tilde{n},1}(\tilde{z}), \dots, Y_{\tilde{n},m}(\tilde{z}))$ are independent for any z and \tilde{z} .
- (ii) For every z , the random vectors $(Y_{n,1}(z), \dots, Y_{n,m}(z))$, $n = 0, 1, \dots$ are iid.

Then, we define the called population-size dependent generalized multi-type process in the form:

$$Z(0) = N \quad Z(n+1) = \sum_{i=1}^m Y_{n,i}(Z(n)), \quad n = 0, 1, \dots$$

It is easy to verify that (4) is a particular case of this model. Our interest will be focused in the study of its probabilistical and inferential theory.

4.3. To develop the theory about continuous time bisexual branching models

Note that the previous branching models considered are discrete time processes. We have also initiated a new research line on continuous time bisexual models. In fact, we have formulated the following general continuous time bisexual process (see [48]):

Let us consider the sets of random variables on a common probability space:

- (i) $\{(\eta_{nk}; f_{nk}, m_{nk}), k = 1, 2, \dots\}$, $n = 0, 1, \dots$, are iid vectors, where $\{\eta_{nk}\}_{k \geq 0}$ are iid non-negative random variables and $\{(f_{nk}, m_{nk})\}_{k \geq 0}$ are iid non-negative integer-valued random vectors.
- (ii) $\{\tau_f(n, k; i)\}$ and $\{\tau_m(n, k; i)\}$, $n = 0, 1, 2, \dots; k = 1, 2, \dots; i = 1, 2, \dots$, are independent sets of non-negative iid random variables.
- (iii) The random point process $\{S_n\}_{n \geq 0}$, with $S_0 = 0 < S_1 < S_2 < \dots < S_n < \dots$

Intuitively, one can interpreted S_n as a moment of a mating of the n -th generation of the mating units. Hence, for $k = 1, 2, \dots$, $T_k = S_k - S_{k-1}$ will represent the k -th period of forming of the k -th generation of the mating units.

Then $(\eta_{nk}; f_{nk}, m_{nk})$ can be interpreted as the evolution of the k -th mating unit which is formed in the n -th generation, where η_{nk} is the life-period of the unit and (f_{nk}, m_{nk}) is the offspring of f_{nk} female and m_{nk} male individuals born at zero-age in the end of the life-period.

The evolutions of the individuals are assumed independent. The variable $\tau_f(n, k; i)$ (or $\tau_m(n, k; i)$) can be interpreted as a life-period of the i -th female (or male) born by the k -th unit of the n -th generation.

It is proposed that the process starts by $N \geq 1$ mating units at zero-age, i.e. $Z(0) = Z_0 = N$ is the 0-generation.

Then each mating unit evolves according to $(\eta_{0k}; f_{0k}, m_{0k})$, $k = 1, 2, \dots, N$ and it is not difficult to see that the number of the females and males at the moment S_1 can be presented as follows:

$$F_1 = F(S_1) = \sum_{k=1}^{Z_0} 1_{\{S_0 < \eta_{0k} \leq S_1\}} \sum_{i=1}^{f_{0k}} 1_{\{\tau_f(0,k;i) \geq S_1 - \eta_{0k}\}},$$

$$M_1 = M(S_1) = \sum_{k=1}^{Z_0} 1_{\{S_0 < \eta_{0k} \leq S_1\}} \sum_{i=1}^{m_{0k}} 1_{\{\tau_m(0,k;i) \geq S_1 - \eta_{0k}\}}$$

Hence the first generation of the units can be determined by the condition $Z_1 = L(F_1, M_1)$, where $L(x, y)$ is a mating function. The new mating units have a zero-age and evolve independently of each other according to $(\eta_{1k}; f_{1k}, m_{1k})$, $k = 1, 2, \dots, Z_1$. The new born females have a zero-age and a life-period $\tau_f(1, k; i)$, $i = 1, 2, \dots, f_{1k}$. Similarly for the males with a life-period $\tau_m(1, k; i)$, $i = 1, 2, \dots, m_{1k}$. Then the numbers of the females and males which exist at the moment S_2 can be calculated as follows:

$$F_2 = F(S_2) = \sum_{k=1}^{Z_0} 1_{\{S_1 < S_0 + \eta_{0k} \leq S_2\}} \sum_{i=1}^{f_{0k}} 1_{\{\tau_f(0,k;i) \geq S_2 - (\eta_{0k} + S_0)\}}$$

$$+ \sum_{k=1}^{Z_1} 1_{\{S_1 < S_1 + \eta_{1k} \leq S_2\}} \sum_{i=1}^{f_{1k}} 1_{\{\tau_f(1,k;i) \geq S_2 - (\eta_{1k} + S_1)\}},$$

$$M_2 = M(S_2) = \sum_{k=1}^{Z_0} 1_{\{S_1 < S_0 + \eta_{0k} \leq S_2\}} \sum_{i=1}^{m_{0k}} 1_{\{\tau_m(0,k;i) \geq S_2 - (\eta_{0k} + S_0)\}}$$

$$+ \sum_{k=1}^{Z_1} 1_{\{S_1 < S_1 + \eta_{1k} \leq S_2\}} \sum_{i=1}^{m_{1k}} 1_{\{\tau_m(1,k;i) \geq S_2 - (\eta_{1k} + S_1)\}}$$

Hence the second generation of the units is $Z_2 = L(F_2, M_2)$ and so on.

Similarly, if the first n generations $(F_k, M_k; Z_k)$, $k = 1, 2, \dots, n$ are determined, then it is not difficult to obtain the next generation

$$F_{n+1} = F(S_{n+1}) = \sum_{j=0}^n \sum_{k=1}^{Z_j} 1_{\{S_n < S_j + \eta_{jk} \leq S_{n+1}\}} \sum_{i=1}^{f_{jk}} 1_{\{\tau_f(j,k;i) \geq S_{n+1} - (\eta_{jk} + S_j)\}},$$

$$M_{n+1} = M(S_{n+1}) = \sum_{j=0}^n \sum_{k=1}^{Z_j} 1_{\{S_n < S_j + \eta_{jk} \leq S_{n+1}\}} \sum_{i=1}^{m_{jk}} 1_{\{\tau_m(j,k;i) \geq S_{n+1} - (\eta_{jk} + S_j)\}} \quad (5)$$

where $Z_0 = N$, and $Z_{n+1} = L(F_{n+1}, M_{n+1})$, $n = 0, 1, 2, \dots$

It is not difficult to realize that the continuous time bisexual branching process, namely $\{B(t)\}_{t \geq 0}$, where $B(t) = (F(t), M(t); Z(t))$, can be determined by the process $\{B_n\}_{n \geq 0}$, where $B_n = (F_n, M_n; Z_n)$, defined by (5) with $B_0 = (0, 0; N)$.

Indeed, let $\{\nu(t)\}_{t \geq 0}$, where $\nu(t) = \max\{n : S_n \leq t\}$, be the corresponding renewal process. Then taking into account (i) – (iii) and (5) it follows that for $t \geq 0$:

$$Z(t) = \sum_{j=0}^{\nu(t)} \sum_{k=0}^{Z_j} 1_{\{\eta_{jk} \geq t - S_j\}},$$

$$F(t) = \sum_{j=0}^{\nu(t)} \sum_{k=1}^{Z_j} 1_{\{S_{\nu(t)} < S_j + \eta_{jk} \leq t\}} \sum_{i=1}^{f_{jk}} 1_{\{\tau_f(j,k;i) \geq t - \eta_{jk} - S_j\}},$$

$$M(t) = \sum_{j=0}^{\nu(t)} \sum_{k=1}^{Z_j} 1_{\{S_{\nu(t)} < S_j + \eta_{jk} \leq t\}} \sum_{i=1}^{m_{jk}} 1_{\{\tau_m(j,k;i) \geq t - \eta_{jk} - S_j\}}$$
(6)

From (5) and (6) it follows that, in general, the processes $\{B_n\}_{n \geq 0}$ and $\{B(t)\}_{t \geq 0}$ are non-markovian and also non-homogeneous in time. A questions for a future research is to develop its probabilistic and inferential theory.

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