1. ABSTRACT

In this research project we introduce a model of branching stochastic process which takes into account the incubation period of the life of individuals. We demonstrate that such processes may be treated as a two-type age-dependent branching process with a periodic mean matrix. In the case when the Malthusian parameter exists we derive the extinction probability and the asymptotic behavior of the mean number of individuals. Exact formulas for the expected extinction time and for the distribution of the number of generations to extinction are obtained. Applications in determining of the optimal vaccination rate in SIR epidemics are also demonstrated. In the case when the Malthusian parameter does not exist study of the process requires additional restrictions on the life and incubation time distributions which define so called sub-exponential family. We obtain certain new properties of sub-exponential distributions, in particular, describe a subclass, which is closed with respect to convolution. Using these results we derive asymptotic behavior of the first and second moments and of the probability of non-extinction. We also prove a limit theorem for the process conditioned on non-extinction.

AMS 2000 Subject Classification: Primary 60J80, Secondary 62M05.
Key Words: incubation period, branching process, ultimate extinction, time to extinction, Malthusian parameter, SIR epidemic.

2. INTRODUCTION AND DEFINITION OF THE PROCESS

In applications of branching processes one may have a situation, when new individuals are born not only during life time or at time of death of the parent, but also some period of time (called incubation period) after her death or departure from a given region. For example, in fish or turtle populations the individuals lay a large number of eggs during the spawning period and leave the spawning ground. After an incubation period which depends on the weather, water temperature and other factors, these eggs generate new individuals. Another example can be found in plant populations, where the plants produce a large number of seeds, which generate new plants after an incubation period. The last example relates to the spreading of infectious diseases, where the time span elapsing from the time of infection to the development of symptoms is referred to as the incubation period (see Mode and Sleeman[14], p. 23). In this project we study a modification of the branching stochastic process which takes into account the incubation period of individual's life time.

We consider a population of individuals of the same type who colonize a region. Assume that at time zero we have a single individual (ancestor) of age zero labelled I. This individual lives a random time L_I. At the end of the time interval L_I the individual dies or leaves the region (emigrate) after laying a random number ν_I of eggs (seeds). Each egg E, after a random incubation period τ_E, independently of the others generates ξ_E individuals of age zero, with $P\{\xi_E = 1\} = 1 - P\{\xi_E = 0\} = p$. This means that each egg generates one individual with probability p and will be "destroyed" with probability $q,\ 0 \leq q < 1,\ p + q = 1$. These new individuals, independently of each other, behave in the same manner as the initial ancestor, i.e. live a random period of time and lay a random number of eggs, before they die or emigrate, and so on. In branching processes the "life-history" of an individual is associated with its life span and offspring size. In our process the life-history of individual I is given by the pair (L_I, ν_I) and, similarly, the life-history of egg E is given by (τ_E, ξ_E). The key assumption in branching processes is independence of lives of distinct individuals, which means in our process that the pairs (L_I, ν_I) and (τ_E, ξ_E) are independent and, for distinct I and E, are independent copies of some pairs (L, ν) and (τ, ξ) respectively.

It is known that "susceptible-infectious-removed" (SIR) epidemic model can be approximated by branching processes, when the initial number of susceptible individuals is large (see Andersson and Britton[1], p. 22). More

precisely, in SIR epidemic models it is assumed that individuals are at first susceptible, if they get infected, they become infectious and remain so for some time, after which they recover and become immune. An individual is said to be removed, if he (or she) has recovered and is immune or dies, and does not further participate in the epidemic. In the framework of the epidemic models L and ν may be understood as the infectious period and the number of contacts during the infectious period of a single infective individual. Naturally, the variable τ is the incubation period and q may be considered as immune rate or as the rate of vaccination. We assume that $p > 0$ to exclude the trivial case, when the process will extinct in the first generation.

Branching processes have been used to approximate the stochastic models of the epidemic ever since Bartlett[4] and Kendall [13]. Recent work on the subject have been done by Ball and Donnelly[3], Farrington and Grant[5] and Farrington *et al.*[6] . In Chapter 3 of Andersson and Britton[1] a systematic study of SIR epidemic models, based on the branching approximation is presented. The recent monograph by Mode and Sleeman[14] is an excellent source on applications of stochastic processes in epidemiology. In particular, in Chapter 2 of this monograph, possible distributions of the incubation period are discussed.

In the case when the Malthusian parameter exists asymptotic properties of process $\mathbf{X}(t)$ can be derived using results from the theory of multi type processes. However in subcritical processes, which is the case in most epidemic models, the Malthusian parameter may not exist. In this case the study of the process requires more delicate analysis and needs additional restrictions on the life time distributions. These restrictions define a class of so called sub-exponential distributions, which have tails that decay at a slower rate than exponential. The family of sub-exponential distributions was first introduced by Chistyakov[17], who studied asymptotic properties of the single type age-dependent process with sub-exponential life-time distributions. In Ref [18] a class of distributions which is larger than sub-exponential is described. Some of distributions from this class may have tails which do not decay at a slower rate than exponential. We note that the sub-exponential class includes distributions, such as, Weibull, with decreasing hazard function, Log-normal, Log-logistic, Pareto and some of other heavy tailed distributions. These distributions are very important in applications. Possibilities of using the heavy tailed distributions in modelling of the incubation period of infectious diseases, including HIV or AIDS, discussed in Chapter 2 of Ref[14].

This situation, in particular, explains the interest in the study of the family of sub-exponential distributions by a number of authors, who have investigated various aspects of the family. However an important problem on closure of the family under convolutions was open until the 90's. In Ref [19] an example, demonstrating that the sub-exponential family is not closed under convolution, is constructed.

In the monograph[20], p. 201, Ch. J. Mode mentions that the extension of the results of Chistyakov [17] to multitype branching processes, in which the life-span distributions are not the same, is an important research problem. We address this problem in a case of two-type process of a special form. For this purpose we first extend some properties of sub-exponential distributions related to the finite number of convolutions. In particular we define a subclass of the sub-exponential family, which is closed with respect to the convolution. This extension allows us to study the limiting behavior of the process $\mathbf{X}(t)$ as $t \to \infty$ and obtain results extending known limit theorems in the case when the Malthusian parameter does not exist. We note that consideration of the problems related to sub-exponential distributions and to the asymptotic behavior of the process, when the Malthusian parameter does not exist, was not initially planned in the project.

The report is organized as follows. In Part 3 we provide main results and discussion. In Section 3.1 we demonstrate that integral equations for the generating functions of the process with incubation and existence of solutions can be derived using similar equations for a multi type age-dependent process and also define a threshold parameter of the process. In Section 3.2 an equation, which allows to derive the extinction probability is obtained. In Section 3.3 exact formulas for the mean extinction time are derived. Section 3.4 is devoted to the distribution of the number of generations before extinction in the linear fractional case. Interesting applications in SIR epidemic models are provided in Section 3.5. Section 3.6 contains a theorem providing asymptotic formulas for the mean of the process, when the Malthusian parameter exists, in all cases of criticality. In Section 3.7 we provide results related to sub-exponential distributions. In Sections 3.8 and 3.9 asymptotic behavior of the first and second moments of the process and the limit theorems in the non-malthusian case are discussed. In Section 4 we provide conclusions and recommendations. Sections 5 and 6 contain activities related to the project and a list of publications respectively.

3. RESULTS AND DISCUSSION

3.1 EQUATIONS FOR GENERATING FUNCTIONS AND EXISTENCE OF SOLUTIONS

The process that has been described can be given by the distributions of pairs (L, ν) and (τ, ξ). If the offspring number does not depend on the life span of the parent and also the fate of the egg is independent of the incubation period, then the marginal distributions

$$G_1(t) = P\{L \le t\},\ G_2(t) = P\{\tau \le t\},\ t \ge 0$$

with support on $[0, \infty)$ and distributions

$$p_k = P\{\nu = k\},\ k \ge 0,\ p = P\{\xi = 1\} = 1 - P\{\xi = 0\}$$

define the process completely.

Realizations of the process are given by the vector $\mathbf{X}(t) = (X_1(t), X_2(t))$, where $X_1(t)$ is the number of individuals and $X_2(t)$ is the number of eggs. The process $\mathbf{X}(t)$ can be considered as a multi-type age-dependent process with types of individuals K_1 and K_2. Individuals of type K_1 generate only individuals of type K_2 and vice versa i.e. evolution of the process has the form of transformations $K_1 \to K_2$ and $K_2 \to K_1$. The components of the vector $\mathbf{X}(t)$ are, naturally, the numbers of individuals of types K_1 and K_2 at time t. Let $\mathbf{s}^{\mathbf{x}} = s_1^{x_1} s_2^{x_2}$ for any two vectors $\mathbf{s} = (s_1, s_2),\ \mathbf{x} = (x_1, x_2)$ and

$$F^i(t, \mathbf{s}) = E[\mathbf{s}^{\mathbf{x}(t)} | \mathbf{X}(0) = \varepsilon_i], i = 1, 2,$$

where $|\mathbf{s}| \le 1,\ \varepsilon_i = (\delta_{1i}, \delta_{2i})$ and δ_{ij} is the Kronecker delta ($\delta_{ii} = 1, \delta_{ij} = 0, i \ne j$). We also denote by $\Phi(s)$ and $\varphi(s)$ the generating functions of ν and ξ respectively:

$$\Phi(s) = \sum_{k=0}^{\infty} p_k s^k,\ \ \varphi(s) = q + ps,$$

and $m = E\nu = \Phi'(1),\ \sigma^2 = E\nu(\nu - 1) = \Phi''(1),\ p_k = P\{\nu = k\}$.

Proposition 1. *The probability generating functions $F^i(t, \mathbf{s})$ for $|\mathbf{s}| \le 1, i = 1, 2$, satisfy the following non linear integral equations*

$$F^1(t, \mathbf{s}) = s_1(1 - G_1(t)) + \int_0^t \Phi(F^2(t - u, \mathbf{s}))dG_1(u), \tag{3.1}$$

$$F^2(t,\mathbf{s}) = s_2(1-G_2(t)) + qG_2(t) + p\int_0^t F^1(t-u,\mathbf{s})dG_2(u). \tag{3.2}$$

with initial conditions $F^i(0,\mathbf{s}) = s_i, i = 1,2.$

Denote $\mathbf{X}_n = (X_n^1, X_n^2),\ n \geq 0$, where $X_n^i, i = 1,2$, is the number of individuals of type K_i in the n th generation. It is well known that $\mathbf{X}_n, n \geq 0$, is a simple two type Galton-Watson process with offspring generating functions $F^i(\mathbf{s}) = E[\mathbf{s}^{\mathbf{X_1}}|\mathbf{X}_0 = \varepsilon_i], i = 1,2$. It follows from the definition of the process that

$$F^1(\mathbf{s}) = \Phi(s_2),\ \ F^2(\mathbf{s}) = \varphi(s_1). \tag{3.3}$$

By substitution we obtain from equations (2.1) and (2.2) that

$$F^2(t,\mathbf{s}) = (1-G_2(t))s_2 + qG_2(t) + ps_1(G_2 - G_1 * G_2(t)) + pC(t), \tag{3.4}$$

where

$$C(t) = \int_0^t \int_0^{t-u} \Phi(F^2(t-u-x,\mathbf{s}))dG_1(x)G_2(u),$$

and * stands for the convolution. The last equation says, if there is an egg at time zero, then at time t with probability $1-G_2(t)$ it still exists, with probability $qG_2(t)$ the incubation period ends but no individual is born and with probability $p(G_2(t) - G_1 * G_2(t))$ after the incubation period an individual is born and still alive. The last term in (3.4) takes care of the case, when the individual dies after laying a random number of eggs.

If $G_2(0+) = 1$, i.e. no incubation period, we obtain from (3.2) that $F^2(t,\mathbf{s}) = \varphi(F^1(t,\mathbf{s}))$. Consequently, the equation (3.1) will take the form

$$F^1(t,\mathbf{s}) = s_1(1-G_1(t)) + \int_0^t \Phi(\varphi(F^1(t-u,\mathbf{s})))dG_1(u).$$

In this case process $X_1(t)$ is the following modification of single-type age-dependent process. The reproduction of individuals is according to the usual branching process, however, after reproduction, each of the new born individuals may emigrate (or may be killed) with probability q. Note that this model is close to the branching process with disasters, considered by Kaplan

et al.[11], where individuals participating in the process, may disappear at renewal moments of a renewal process. If $G_2(0+) = 1$ and $p = 1$, we obtain the single type Bellman-Harris process.

We denote by $\mathbf{M} = (M_{ij},\ i,j = 1,2)$ the matrix of expected offspring of a single individual, where i and j denote types of the parent and of the offspring respectively. It is clear that

$$M_{ij} = \frac{\partial F^i(\mathbf{s})}{\partial s_j}|_{\mathbf{s}=\mathbf{1}},$$

where $\mathbf{1}^T = (1,1)$. Therefore we have due to (3.3) that

$$\mathbf{M} = \begin{pmatrix} 0 & m \\ p & 0 \end{pmatrix}$$

where $m = E\nu$. It is easy to see that $\mathbf{M}$ has eigenvalues $\pm\sqrt{pm}$. Thus $\rho = \sqrt{pm}$ is the Perron eigenvalue and corresponding positive right and left eigenvectors $\mathbf{U} = (u^1, u^2)^T, \mathbf{V} = (v_1, v_2)$ are

$$\mathbf{U} = \left(\frac{\sqrt{pm}}{p+\sqrt{pm}},\ \frac{p}{p+\sqrt{pm}}\right)^T,\ \ \mathbf{V} = \left(\frac{p+\sqrt{pm}}{2\sqrt{pm}},\ \frac{p+\sqrt{pm}}{2p}\right).$$

The eigenvectors are normalized such that $\mathbf{U}^T\mathbf{1} = 1, \mathbf{V}\ \mathbf{U} = 1$.
We have $\sum_{j=1}^2 EX_j^i u^j = \rho u^i$ and $\sum_{i=1}^2 EX_j^i v_i = \rho v_j$. Concerning the second factorial moments $b_{jk}^i = E[X_j^i X_k^i],\ j \neq k$ and $b_{jj}^i = E[X_j^i(X_j^i - 1)]$, we find due to (2.3) that $b_{22}^1 = \sigma^2$ and $b_{jk}^i = 0$ for all other possible values of i, j and k. Therefore

$$b = \sum_{i=1}^2\sum_{j=1}^2\sum_{k=1}^2 v_i b_{jk}^i u^j u^k = \sigma^2 v_1 (u^2)^2 = \frac{\sigma^2 p\sqrt{p/m}}{2(p+\sqrt{pm})}.$$

Following the general theory, we call process $\mathbf{X}(t)$ subcritical, critical and supercritical, if $mp < 1, mp = 1, \sigma^2 > 0$ and $mp > 1$ respectively.

Since $\mathbf{X}(t)$ is two type age-dependent branching process with the offspring distribution of a special form, **existence of solutions** for equations (3.1), (3.2) and (3.4) follows from corresponding existence theorems in the general theory. For example, it follows from Theorem 8.2.1 (see Ref.[16], p. 234)

that, if $G_i(0+) = 0, i = 1, 2$, and $E\nu < \infty$, then the system of equations (3.1) and (3.2) has a unique solution $(F^1(t, \mathbf{s}),\ F^2(t, \mathbf{s}))$ in the class of probability generating functions. The condition $G_i(0+) = 0, i = 1, 2$, excludes the situation of instantaneous death of the individuals and the case of zero incubation period. From now on we assume that $G_i(t), i = 1, 2$, have no atoms at point zero.

3.2 THE EXTINCTION PROBABILITY

First we discuss the probability of ultimate extinction of the process $\mathbf{X}(t)$. Since the state $\mathbf{0}$ is absorbing, it can be defined as

$$Q_i = P\{\mathbf{X}(t) = \mathbf{0},\ for\ some\ t > 0 | \mathbf{X}(0) = \varepsilon_i\}$$

for the process starting with one individual of type K_i. Since, when $G_i(0+) = 0, i = 1, 2$,

$$\{\mathbf{X}(t) = \mathbf{0},\ for\ some\ t > 0\} = \{\mathbf{X}_n = \mathbf{0},\ for\ some\ n > 0\},$$

we just need to find the extinction probability of the Galton-Watson process $\mathbf{X}_n, n \geq 0$, constituted by generation sizes of $\mathbf{X}(t)$.

Proposition 2. *The extinction probability Q_2 is the smallest non-negative root of the equation*

$$\Phi(x) = \frac{x - q}{p} \tag{3.5}$$

and $Q_1 = (Q_2 - q)/p$.

Remark. It is obvious that the equation (3.5) always has at least one root $x = 1$. Since $\Phi(x)$ is convex and increasing, it may have another root which is less than one. If $p = 1$, we have a situation, when an individual who had a contact will surely be infected. In this case the extinction probability of the process is the smallest non-negative root of $\Phi(x) = x$ and coincides with the extinction probability of the contact process. Figure 1 shows that, generally speaking, the extinction probability of the process with vaccination is greater than the extinction probability of the contact process. If the vaccination rate is large enough, we may have a situation, where the epidemic becomes extinct while the process of contacts explodes (for example, when $m > 1$ but

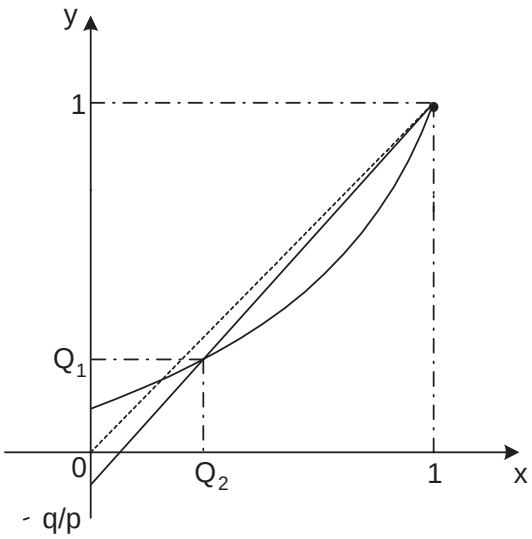

Figure 1

$mp < 1$).

It follows from Proposition 2 that, if $mp \leq 1$, then $\mathbf{X}(t)$ become extinct with probability 1 and, if $mp > 1$, then there are positive probabilities $1 - Q_i, i = 1, 2$, that the process explodes.

3.3 THE TIME TO EXTINCTION

Now we consider an important variable related to survival of the process, namely the time to extinction. It is defined as

$$T_0^i = \min\{t : \mathbf{X}(t) = \mathbf{0} | \mathbf{X}(0) = \varepsilon_i\}, i = 1, 2.$$

The time to the extinction measured by the number of generations can similarly be defined as

$$N_0^i = \min\{n : \mathbf{X}_n = \mathbf{0} | \mathbf{X}_0 = \varepsilon_i\}, i = 1, 2.$$

Now we use a traditional notation for the individuals participating in our process. We label the individuals by elements of the set $I = \cup_{k=0}^{\infty} N^k,\ N = \{1, 2, ...\},\ N^k = N^{k-1} \times N,\ N^0 = \{0\}$. The initial ancestor will have the label 0. The direct offsprings of the initial ancestor we label by $(0, 1), (0, 2), ...,$

and so on. Similarly we denote by $\gamma' = (\gamma, j) = (0, i_1, ..., i_k, j)$ the jth direct offspring of the individual $\gamma = (0, i_1, ..., i_k)$. For given two vectors $\gamma = (0, i_1, ..., i_k)$ and $\lambda = (j_1, ..., j_m)$ the ordered pair $(\gamma,\ \lambda)$ we understand as $k+m+1$ dimensional vector $(0, i_1, ..., i_k, j_1, ..., j_m)$. Note, for example, that, if the initial ancestor is an egg, then the population of the first generation contains only individual $(0, 1)$ and the individuals of the second generation are $(0, 1, 1),\ (0, 1, 2)$ and so on.

If $N_0^i = n$, then there is at least one individual $\gamma = (0, i_1, i_2, ..., i_{n-1})$ in $(n-1)$th generation. Therefore the survival time T_0^i of the process is equal to the sum of the life time of γ and the life times of all parents of γ. Thus we obtain the following relationship between T_0^i and N_0^i:

$$T_0^1 = \begin{cases} \sum_{i=1}^{N_0^1/2}(L_i + \tau_i), & \text{if n is even,} \\ \\ \sum_{i=1}^{(N_0^1-1)/2}(L_i + \tau_i) + L_0, & \text{if n is odd,} \end{cases}$$

where $L_i, \tau_i, i \geq 0$ are independent random variables such that $L_i \stackrel{d}{=} L, \tau_i \stackrel{d}{=} \tau$ and "d" means equality of distributions. Similarly we find

$$T_0^2 = \begin{cases} \sum_{i=1}^{N_0^2/2}(L_i + \tau_i), & \text{if n is even,} \\ \\ \sum_{i=1}^{(N_0^2-1)/2}(L_i + \tau_i) + \tau_0, & \text{if n is odd.} \end{cases}$$

Since the life times and offspring numbers of the individuals are independent, we conclude that in the above random sums summands and the number of summands are independent. Therefore, when $EN_0^i,\ EL$ and $E\tau$ are finite, by simple total probability arguments we obtain:

$$\begin{cases} ET_0^1 = \frac{EL+E\tau}{2} EN_0^1 + \frac{EL-E\tau}{2} P\{N_0^1\ is\ odd\}, \\ \\ ET_0^2 = \frac{EL+E\tau}{2} EN_0^2 + \frac{E\tau-EL}{2} P\{N_0^2\ is\ odd\}. \end{cases} \tag{3.6}$$

It is not surprising that the expected time to extinction essentially depends on the means of the infectious and incubation periods.

3.4 DISTRIBUTION OF THE NUMBER OF GENERATIONS BEFORE EXTINCTION

Now we focus our attention on the distribution of N_0^i. The distribution of the number of generations before the extinction in branching processes has received little attention in the literature. Harris[9] considered the special case when the number of offspring is at most 2. In Karlin and Taylor[12] (page 318) certain results for the distribution of the number of generations before extinction are presented, when the offspring distribution is geometric. In Farrington and Grant[5] the generation distribution is derived for Bernoulli, geometric and Poisson offspring distributions. In the recent book by Haccou *et al.* (see Ref[8], p. 115) lower and upper bounds for the distribution in the general case are obtained. All these results are related to simple Galton-Watson branching processes.

We obtain exact formulas for the distribution of the number of generations before the extinction $N_0^i, i = 1, 2$, for the process with incubation, in the case, when the offspring generating function has the form of a linear fractional transformation. Namely, we assume that

$$\Phi(s) = \frac{\alpha + \beta s}{1 - \delta s}, \tag{3.7}$$

where $0 \leq \delta < 1$. Since $\Phi(s)$ is the probability generating function, coefficients in Taylor expansion must be positive. Therefore (3.7) includes the general case of the ratio of two arbitrary linear functions. Note that probability generating functions of some known distributions, such as Bernoulli, first success, geometric or modified geometric distributions have a form of (3.7). Probability generating distributions of this form are the only known non-trivial generating functions whose iterates can explicitly be computed.

We denote $F_n^i(\mathbf{s}) = E[\mathbf{s}^{\mathbf{X}_n} | \mathbf{X}_0 = \varepsilon_i],\ i = 1, 2$, where $\mathbf{X}_n$ is the embedded Galton-Watson process, defined in the proof of Proposition 1. Then $F_1^i(\mathbf{s}) = F^i(\mathbf{s})$ and

$$F_{n+1}^i(\mathbf{s}) = F_n^i(F^1(\mathbf{s}),\ F^2(\mathbf{s})),\ i = 1, 2. \tag{3.8}$$

Since $\{N_0^i \leq k\} = \{\mathbf{X}_k = \mathbf{0} | \mathbf{X}_0 = \varepsilon_i\}$, we obtain that for any $k \geq 1$

$$P\{N_0^i \leq k\} = F_k^i(\mathbf{0}),\ i = 1, 2. \tag{3.9}$$

Let $\pi_1(s) = \Phi(\varphi(s)),\ \pi_2(s) = \varphi(\Phi(s))$ and $\pi_i(k, s),\ i = 1, 2$, be kth functional iteration of $\pi_i(s)$. Using relations (3.3) and (3.8) we obtain

$$F_{2k}^i(\mathbf{s}) = \pi_i(k, s_i) \tag{3.10}$$

for $i = 1, 2$ and for the odd iterations we have

$$F^1_{2k+1}(\mathbf{s}) = \pi_1(k, \Phi(s_2)),\ F^2_{2k+1}(\mathbf{s}) = \pi_2(k, \varphi(s_1)). \tag{3.11}$$

Proposition 3. *If $\Phi(s)$ has the form of (3.7) and $mp = 1$, then*

a) $P\{N^1_0 \le 2k\} = 1 - (1 + \Delta pk)^{-1}$;

b) $P\{N^1_0 \le 2k + 1\} = 1 - (1 - p_0)(1 + \Delta p(1 - p_0)k)^{-1}$;

c) $P\{N^2_0 \le 2k\} = 1 - (1 + \Delta k)^{-1}$;

d) $P\{N^2_0 \le 2k + 1\} = 1 - p(1 + \Delta pk)^{-1}$;

where $\Delta = \delta(1 - \delta)^{-1},\ p_0 = \Phi(0)$ and $k = 0, 1, 2, ...$

The next proposition is devoted to the noncritical case.

Proposition 4. *If $\Phi(s)$ has the form of (3.7) and $mp \ne 1$, then*

a) $P\{N^1_0 \le 2k\} = 1 - (p\delta - \alpha - q\beta)(p\delta - (\alpha + q\beta)\Delta^k_0)^{-1}$;

b) $P\{N^1_0 \le 2k + 1\} = 1 - (p\delta - \alpha - q\beta)(p\delta + \Delta_1\Delta^k_0)^{-1}$;

c) $P\{N^2_0 \le 2k\} = 1 - (\delta - q - p\alpha)(\delta - (q + p\alpha)\Delta^k_0)^{-1}$;

d) $P\{N^2_0 \le 2k + 1\} = 1 - (\delta - q - p\alpha)(\delta + \Delta_2\Delta^k_0)^{-1}$,

where $\Delta_0 = p^{-1}(\alpha + \beta)/(1 - \alpha),\ \Delta_1 = (1 - p_0)^{-1}(pp_0\delta - \alpha - q\beta),\ \Delta_2 = p^{-1}(q\delta - q - p\alpha)$ and $k = 0, 1, 2, ...$

Now we consider some particular cases of the offspring distribution.

Example 1. Let us consider the Bernoulli offspring distribution, i.e. $\Phi(s) = p_0 + p_1 s$. Then from Proposition 4 we obtain that $P\{N^i_0 > 2k\} = (pp_1)^k,\ P\{N^1_0 > 2k + 1\} = p_1(pp_1)^k$ and $P\{N^2_0 > 2k + 1\} = p(pp_1)^k$. Therefore we find, when

$pp_1 < 1$,

$$EN_0^1 = \sum_{n=0}^{\infty} P\{N_0^1 > n\} = \frac{1+p_1}{1-pp_1}. \tag{3.12}$$

Since $P\{N_0^1 = 2k+1\} = p_0(pp_1)^k$, we get $P\{N_0^1 \; is \; odd\} = p_0(1-pp_1)^{-1}$. Hence we conclude from this and relation (3.6) that

$$ET_0^1 = \frac{(EL+E\tau)(1+p_1)}{2(1-pp_1)} + \frac{p_0(EL-E\tau)}{2(1-pp_1)}$$

By similar arguments we obtain from (3.6)

$$ET_0^2 = \frac{(EL+E\tau)(1+p)}{2(1-pp_1)} + \frac{q(E\tau-EL)}{2(1-pp_1)}.$$

Example 2. Let now the offspring distribution be geometric i.e. $p_k = d^k(1-d),\ 0<d<1,\ k=0,1,2,...$ Then

$$\Phi(s) = \frac{1-d}{1-ds},\ \ m = \frac{d}{1-d}.$$

In this case we obtain from Proposition 4 that, if $mp \neq 1$, then

$$P\{N_0^1 \leq 2k\} = 1 - \frac{1-(mp)^{-1}}{1-(mp)^{-k-1}}, \tag{3.13}$$

$$P\{N_0^1 \leq 2k+1\} = 1 - \frac{1-(mp)^{-1}}{1+m^{-1}(1-(pd)^{-1})(mp)^{-k}}, \tag{3.14}$$

We can derive similar formulas for N_0^2 from parts (c) and (d) of Proposition 4.

3.5 APPLICATIONS IN SIR EPIDEMIC MODELS

Example 3. The rate of vaccination (proportion of vaccinated individuals in the population) is an important parameter in the preventive medicine. The formulas (3.13) and (3.14) allow to compute desired rate of vaccination to have the epidemic ceased before a given generation with a given probability for a given mean number of contacts. For a numerical example, if the mean

number of contacts is 4, what should be the vaccination rate for the epidemic to cease before the third generation with probability say 0.95? We denote by N the extinction generation number of the population of infective individuals. Since in our model the infective individuals correspond to generations labelled by even numbers, we obtain from equation

$$P\{N \leq 2\} = P\{N_0^1 \leq 4\} = 0.95$$

and formula (3.20) the following:

$$\frac{1-(4p)^{-1}}{1-(4p)^{-3}} = 0.05,$$

which is equivalent to $((4p)^{-1}+0.5)^2 = 19.25$. From this we find $p = 0.0643$. Consequently we conclude that the vaccination rate should be $q = 0.9357$, i.e. almost 93.5 per cent of individuals must be vaccinated. For illustration we provide the values of the vaccination rate for different mean numbers of the contacts in Table 1.

m	2	3	4	5	6	7	8	9
q	0.8714	0.9143	0.9357	0.9486	0.9571	0.9633	0.9679	0.9714

Table 1. Vaccination rate for different mean numbers of the contacts.

As it was mentioned before, the contact process is the simple Galton-Watson process with the offspring generating function $\Phi(s)$. Therefore the mean number of contacts can always be estimated using known statistical estimators (see Ref[10], p. 47, for example).

Example 4. Now we consider an example of spread of infections such as measles and mumps in vaccinated school populations presented in Nkowane *et al.*[15] and Gustafson *et al.*[7]. In these papers the authors identified *four* generations of spread, for highly vaccinated populations. Using our results, we can determine the probability that a single infective generates an outbreak of *more than four* generations, depending on the rate of vaccination. Let the mean number of contacts during the infectious period be 4. Let again N be

the extinction generation number of the population of infective individuals. In this case we have

$$P\{N > 4\} = P\{N_0^1 > 8\} = \frac{1 - (4(1-q))^{-1}}{1 - (4(1-q))^{-5}}.$$

Table 2 gives some numerical examples.

q	0.2	0.4	0.6	0.8	0.9
P{N > 4}	0.6896	0.5907	0.4145	0.1218	0.0155

Table 2. Change of the probability with the vaccination rate.

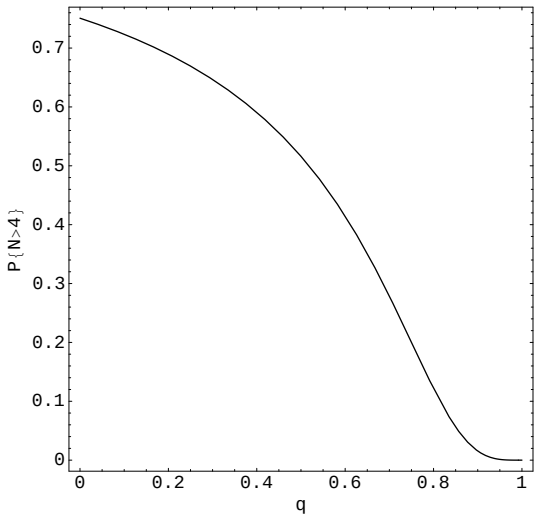

Figure 2.

Figure 2 shows, if the vaccination rate is less than 0.6 outbreaks of more than four generations are more likely. Around 12 percent of infections will lead to such outbreaks, if the vaccination rate is 0.8.

In some applications modified geometric distribution, in which zero has not necessarily the probability $1 - d$, may be appropriate. It can be given as

$$P_k = b(1-d)d^{k-1}, k = 1, 2, ...$$

and $P_0 = 1 - b$. Note that its generating function has also form of (3.7) and the propositions 3 and 4 are applicable for this distribution as well.

3.6 THE EXPECTED VALUE

If an epidemic is initiated by a single infective at time zero, what is the expected number of infective individuals and individuals who had a contact with an infective at time t? This is a standard problem in the theory of branching processes and the long run behavior of the expectations is not surprising. However, obtaining an explicit dependence of constants on initial parameters in asymptotic formulas is important for applications. In this section we derive asymptotic formulas for the expectation with explicit constants. Hence we consider expected values

$$A_j^i(t) = E[X_j(t)|\mathbf{X}(0) = \varepsilon_i],\ i = 1, 2.$$

The matrix $\mathbf{M}^\theta = (a_{ij},\ i, j = 1, 2)$, where $a_{ii} = 0,\ i = 1, 2$ and

$$a_{12} = m\int_0^\infty e^{-\theta x} dG_1(x),\ \ a_{21} = p\int_0^\infty e^{-\theta x} dG_2(x),$$

plays an important role in the study of asymptotic behavior of the expected values. The Malthusian parameter θ of the process is defined from condition $\rho_\theta = 1$, where ρ_θ is the Perron eigenvalue of $\mathbf{M}^\theta$. Since $\rho_\theta = (a_{12}a_{21})^{1/2}$ and the random variables L and τ are independent, the Malthusian parameter is the root of equation

$$mpEe^{-\theta(L+\tau)} = 1. \tag{3.15}$$

Note that, if $mp = 1$, then $\theta = 0$ and, if $mp > 1$, then $\theta > 0$. When $mp < 1$, then θ may not exist. But, if it does exist, then $\theta < 0$.

The right and left eigenvectors of $\mathbf{M}^\theta$ corresponding to the Perron eigenvalue are

$$\mathbf{U}_\theta = \left(\frac{\rho_\theta}{a_{21} + \rho_\theta},\ \frac{a_{21}}{a_{21} + \rho_\theta}\right)^T,\ \ \mathbf{V}_\theta = \left(\frac{a_{21} + \rho_\theta}{2\rho_\theta},\ \frac{a_{21} + \rho_\theta}{2a_{21}}\right).$$

When the Malthusian parameter exists, they will take the form

$$\mathbf{U}_\theta^T = \frac{1}{1 + a_{21}}(1,\ a_{21}),\ \mathbf{V}_\theta = \frac{1 + a_{21}}{2}(1,\ a_{12}).$$

Note also that $\mathbf{U}_\theta^T\mathbf{1} = 1,\ \mathbf{V}_\theta\mathbf{U}_\theta = 1$, where $\mathbf{1}^T = (1, 1)$.

We define constants $A_j^i, C_j^i,\ i, j = 1, 2$, as following

$$A_i^i = \frac{\delta_{1i}EL + \delta_{2i}E\tau}{EL + E\tau},\ A_j^i = \frac{\delta_{1i}mE\tau + \delta_{2i}pEL}{EL + E\tau}, i \neq j,$$

$$C_j^i = \frac{\delta_{ij} D_i + (1 - \delta_{ij}) D_j}{2D},$$

where δ_{ij} is the Kroneker delta and

$$D = \frac{a_{21} m}{2} \int_0^\infty u e^{-\theta u} dG_1(u) + \frac{a_{12} p}{2} \int_0^\infty u e^{-\theta u} dG_2(u), \tag{3.16}$$

$$D_i = \int_0^\infty e^{-\theta u} (1 - G_i(u)) du.$$

We also need the following condition in subcritical case, when $\theta < 0$:

$$\int_0^\infty u^2 e^{-\theta u} dG_i(u) < \infty, i = 1, 2. \tag{3.17}$$

Note that similar condition is also required in the case of Bellman-Harris process (see Ref.[16], p. 312).

Theorem 1. *Let $m < \infty$ and the Malthusian parameter exists and $i, j = 1, 2$.*

a) If $mp = 1$, then $\lim_{t\to\infty} A_j^i(t) = A_j^i$;

b) If $mp > 1$, then $\lim_{t\to\infty} e^{-\theta t} A_j^i(t) = C_j^i$;

c) If $mp < 1$ and (3.17) is satisfied, then again $\lim_{t\to\infty} e^{-\theta t} A_j^i(t) = C_j^i$.

Thus Theorem 1 provides asymptotic formulas for the expected values of the process in the case, where the Malthusian parameter exists. When it does not exist, as it was mentioned before, we need additional restrictions, which define the class of sub-exponential distributions.

3.7 SUB-EXPONENTIAL DISTRIBUTIONS

We consider cumulative distribution functions of positive random variables. Following Chistyakov [17] define three classes of distributions.

Definition. *Let $A(t), t \in [0, \infty)$ be cumulative distribution of a positive random variable.*

a) We say $A(t) \in \Re_0$, *if for any* $\varepsilon > 0$

$$\int_0^\infty e^{\varepsilon t} dA(t) = \infty. \tag{3.18}$$

b) Function $A(t) \in \Re_1$, *if for any fixed* $u > 0$

$$\lim_{t\to\infty} \frac{1 - A(t-u)}{1 - A(t)} = 1. \tag{3.19}$$

c) Function $A(t) \in \Re_n, n \geq 2$, *if*

$$\lim_{t\to\infty} \frac{1 - A^{*n}(t)}{1 - A(t)} = n. \tag{3.20}$$

We note that, as it was proved in Ref [17], $\Re_2 \subset \Re_n$ for any $n \geq 2$ and also $\Re_2 \subset \Re_1 \subset \Re_0$. Distributions belonging to the class $\Re_2$ are called sub-exponential, describing the property of their tail which decay at a rate slower than exponential (see Ref [2], p.147, for example). We obtain certain properties of sub-exponential distributions. Let τ_1 and τ_2 be independent nonnegative random variables and $A_i(t) = P\{\tau_i \leq t\}, i = 1, 2$.

We denote $C(t) := (1 - A_1(t))/(1 - A_2(t))$. Let $A_i(t), i = 1, 2$ be such that there exists the limit

$$\lim_{t\to\infty} C(t) = C \in [0, \infty]. \tag{3.21}$$

The following lemma gives a new property of the sub-exponential family related to convolutions.

Lemma 1. *If* $A_i(t) \in \Re_2, i = 1, 2$ *and (3.21) is satisfied, then*

$$\lim_{t\to\infty} \frac{1 - (A_1 * A_2)(t)}{1 - A_2(t)} = 1 + C. \tag{3.22}$$

We denote $A(t) = (A_1 * A_2)(t)$ and by $\Re_2^*$ the subclass of $\Re_2$ such that for each pair $A_i(t) \in \Re_2^*, i = 1, 2$ the condition (3.21) is satisfied. The following result is important in the proof of main theorems.

Lemma 2.
a) If $A_i(t) \in \Re_2, i = 1, 2$ *and (3.21) is satisfied, then* $A(t) \in \Re_2$.
b) The subclass of sub-exponential distributions $\Re_2^*$ *is closed with respect to the convolution.*

Applying lemmas 1 and 2 we obtain the following result, which has direct application in proofs of our theorems.

Lemma 3. *If* $A_i(t) \in \Re_2, i = 1, 2$ *and condition (3.21) is satisfied, then for each* $i \geq 1$

$$\lim_{t\to\infty} \frac{1 - (A_2 * A^{*i})(t)}{1 - A(t)} = \frac{1}{1 + C} + i. \tag{3.23}$$

3.8 ASYMPTOTIC BEHAVIOR OF MOMENTS

If an epidemic is initiated by a single infective at time zero, what is the expected number of infective individuals and individuals who had a contact with an infective at time t? This is a standard problem in the theory of branching processes when the Malthusian parameter does exist. However, when the parameter does not exist, the problem requires more refined analysis and additional restrictions on the distributions of the incubation and infectious periods.

First we consider the following moments of the process

$$A_j^i(t) = E[X_j(t)|\mathbf{X}(0) = \varepsilon_i], B_{jk}^i(t) = E[X_j(t)(X_k(t) - \delta_{jk})|\mathbf{X}(0) = \varepsilon_i], \tag{3.24}$$

where $i, j, k = 1, 2$. We also denote $\mathbf{A}(t) = (A_j^i(t), i, j = 1, 2)$ the matrix of expected values of the process.

Assume that there exists $c \in [0, \infty]$ such that

$$\lim_{t\to\infty} \frac{1 - G_2(t)}{1 - G_1(t)} = c. \tag{3.25}$$

We also denote $G = G_1 * G_2$, $a_i = \delta_{1i} + \delta_{2i}c$ and $b_i = \delta_{1i}cm + \delta_{2i}p$. We put by definition $c(1 + c)^{-1} = 1$, when $c = \infty$.

We now formulate results which are devoted to the asymptotic behavior of the first and second moments of the process. We prove a theorem in more

general case when each type of individuals may generate a random number of individuals of another type. This would relate to a situation, when an egg may generate more than one new individuals.

Let $F^i(s_1, s_2) = F^i(s_j),\ i = 1, 2$ be the offspring generating functions of types T_1 and T_2 and

$$m_i = \frac{dF^i(s_j)}{ds_j}|_{s_j=1}, \quad B_i = \frac{d^2F^i(s_j)}{ds_j^2}|_{s_j=1}, \quad i, j = 1, 2$$

be the offspring mean and the second moments.

Theorem 2. *Let $m_1m_2 < 1,\ G_i(t) \in \Re_2, i = 1, 2$ and (3.25) is satisfied. Then*

a)

$$\lim_{t\to\infty} \frac{\mathbf{A}(t)}{1 - G(t)} = \frac{1}{(1 + c)(1 - m_1m_2)} \begin{pmatrix} 1 & cm_1 \\ m_2 & c \end{pmatrix}$$

b) If in addition $B_i \in (0, \infty)$, then for $i, j, k = 1, 2$

$$\lim_{t\to\infty} \frac{B^i_{jk}(t)}{1 - G(t)} = 0.$$

It is easy to see that, if $G(0+) = 1$ and $m_2 = 1$, from Theorem 1 we obtain the asymptotic formula for the first moment of the single-type age dependent process (Theorem 3B(ii) in Ref [2], p. 152). In particular, for the process with incubation we obtain the following result.

Corollary. *Let $mp < 1,\ G_i(t) \in \Re_2, i = 1, 2$ and (3.25) is satisfied. Then for $i, j, k = 1, 2$ and expected values of the process defined in (3.24)*

a)

$$\lim_{t\to\infty} \frac{A^i_j(t)}{1 - G(t)} = \frac{\delta_{ij}a_i + (1 - \delta_{ij})b_i}{(1 + c)(1 - mp)}.$$

b) If in addition $\sigma^2 \in (0, \infty)$, then for $i, j, k = 1, 2$

$$\lim_{t\to\infty} \frac{B^i_{jk}(t)}{1 - G(t)} = 0.$$

The proof of Theorem 2, which is based on the renewal theory, uses the above lemmas.

3.9 THE LIMIT THEOREM

Now we prove the limit theorem which gives asymptotic behavior of the non-extinction probability $Q^i(t) = P\{\mathbf{X}(t) \neq \mathbf{0} | \mathbf{X}(0) = \varepsilon_i\}$ and the limiting distribution of the process conditioned on non-extinction. For vectors $\mathbf{s} = (s_1, s_2)$ and $\mathbf{x} = (x_1, x_2)$ denote $\mathbf{s}^{\mathbf{x}} = s_1^{x_1} s_2^{x_2}$.

Theorem 3. *If* $mp < 1, \sigma^2 \in (0, \infty)$, $G_i(t) \in \Re_2$, $i = 1, 2$ *and (3.25) is satisfied, then*

a)

$$\lim_{t\to\infty} \frac{Q^i(t)}{1 - G(t)} = \frac{a_i + b_i}{(1 + c)(1 - mp)};$$

b)

$$\lim_{t\to\infty} E[\mathbf{s}^{\mathbf{X}(t)} | \mathbf{X}(t) \neq 0, \mathbf{X}(0) = \varepsilon_i] = \frac{a_i s_i + b_i s_j}{a_i + b_i}.$$

Remarks. 1. It follows from Theorem 3 that, if the process does not become extinct, in the long run with probability one a single individual is alive. It is the individual of the initial type with probability $a_i(a_i + b_i)^{-1}$ and of the opposite type with probability $b_i(a_i + b_i)^{-1}$. Recall that $a_i = \delta_{1i} + \delta_{2i} c$, $b_i = \delta_{1i} cm + \delta_{2i} p$. In terminology of epidemics the results illustrate the following situation. By preventive measures, such as isolating of infective individuals or increasing of the immunization rate one can ensure that $mp < 1$, which leads to extinction of the epidemic with probability one. However, if an epidemic initiated by a single infective does not cease, then in the long run one infective may exist with probability $(1 + cm)^{-1}$. With probability $cm(1 + cm)^{-1}$ an individual who had a contact with an infective may exist in the long run.

2. If in particular $G_2(0+) = 1$ and $p = 1$ from Part (b) of Theorem 2 we obtain the result for subcritical single-type process (Theorem 2 in Ref [2], p. 171).

4. CONCLUSIONS AND RECOMMENDATIONS

In the project we achieved all the objectives. The following results were obtained.

1. The age-dependent branching process which takes into account the incubation period of the life of individuals is defined.

2. It is discovered that the process with incubation can be considered as a two type Bellman-Harris process with a periodic mean matrix.

3. When the Malthusian parameter exists, it is demonstrated that the asymptotic properties of the process with incubation can be obtained from those of multi-type Bellman-Harris processes.

4. Exact formulas for the expected extinction time and for the distribution of the number of generations to extinction are obtained. Applications in determining of the optimal vaccination rate in SIR epidemics are demonstrated.

5. In the project we obtained certain new properties of sub-exponential distributions, in particular, a subclass, which is closed with respect to convolutions is described.

6. Using these new properties of sub-exponential distributions we derived asymptotic behavior of the first and second moments and of the probability of non-extinction, in the case when the Malthusian parameter does not exist. A limit theorem for the process conditioned on non-extinction is also proved.

We recommend for a future research work the following:

1. Developing an estimation theory of parameters (such as the main reproduction number m and the vaccination rate q) of the process with incubation.

2. Adopting the model to more general (such as SIS, SIRS and Household) epidemic models. Applying the results of the project in these models.

3. Generalization of the model in frameworks of more general age-dependent and Crump-Mode-Jagers processes.

5. ACTIVITIES RELATED TO THE PROJECT

1. Seminars:

a) "Branching Processes with Incubation" , seminar in the Department of Mathematical Sciences, KFUPM, December 04, 2006.

b) "Closure of the Sub-Exponential class under the convolution" , seminar in the Department of Mathematical Sciences, KFUPM, March 27, 2007.

c) "Incubation and delay in a stochastic model of population dynamics", presentation in Applied Mathematics Day, April 17, 2007, KFUPM.

2. Conferences: The problems related to the project were discussed in the following conference:

a) Rahimov, I. "Age-dependent branching processes with incubation", Workshop on Stochastic Modelling in Population Dynamics , 10-13 April 2007 Luminy- Marseille, France.
$http://www.cirm.univ-mrs.fr/videos/2007/resumes/10a_abs.pdf$

6. LIST OF PUBLICATIONS

1. Rahimov, I. and Chanane, B. "Branching processes with incubation", STOCHASTIC MODELS, (ISI journal, accepted).

2. Rahimov, I. "Two type branching processes with sub-exponential lifespans and SIR epidemic models", JOURNAL OF STOCHASTIC ANALYSIS AND APPLICATIONS, (ISI journal, accepted).

3. Rahimov, I. and Chanane, B. "Branching processes with incubation", Technical Report No 375, KFUPM, May, 2007.

REFERENCES

1. Andersson H., Britton T. *Stochastic Epidemic Models and their Statistical Analysis*, Springer, Ser. LN in Statistics 151, New York, 2000.
2. Athreya K. B., Ney P. E. *Branching Processes*, Springer-Verlag, New York, 1972.
3. Ball F., Donelly P. Strong approximation for epidemic models. *Stoch. Proc. Appl.*, **1995** 55, 1-21.
4.Bartlett M. S. *An introduction to stochastic processes*, Cambridge University Press, Cambridge, 1955.
5. Farrington C. P., Grant A. D. The distribution of the time to extinction in subcritical branching processes: application to outbreaks of infectious disease, *Journal of Applied Probability*, **1999**, 36, 771-779.
6. Farrington C. P, Kanaan M. N. and Gay N. J. Branching process models for surveillance of infectious diseases controlled by mass vaccination, Biostatistics, **2003**, 4, 279-295.
7. Gustafson, T. L., Lieverns, A. W., Bunell P. A., Moellenberg, R. G.,Buttery, C., M., G. and Senulster, L. M. Measles outbreak in a fully immunized secondary-school population, *N. Engl.J. Med.*, **1987**, 316, 771-774.
8. Haccou P., Jagers, P., Vatutin V. A. *Branching processes: Variation, Growth and Extinction of populations*. Cambridge University Press, 2005.
9. Harris T. E. Branching processes, Ann. Math. Stat. 19, **1948**, 19, 474-494.
10. Jagers, P. *Branching Processes with Biological Applications*, London, Wiley Sons XIII, 1975.
11. Kaplan, N., Subdury A. and Nilsen T. S. A branching process with disasters, *J. Appl. Probab.*,**1975**, 12, No 1, 47-59.
12. Karlin, S., Taylor, H.M. *A First Cource in Stochastic Process*, 2nd edn. Academic Press, New York, 1985.
13. Kendall D. Deterministic and stochastic epidemics in closed populations, in *Proc. 3rd Berkeley Symp. Math. Stat. Prob.*, **1956**, 4, 149-165.
14. Mode Ch., J. Sleeman C., K. *Stochastic Processes in Epidemiology*, World Scientific , Singapore-New Jersey-London-Hong Kong, 2000.
15. Nkowane, B., M., Bart, S. W. Orenstein, W., A. and Balter, M. Measles outbreak in a vaccinated school population: epidemiology, chains of transmission and the role of vaccine failures. *Am. J. Publ. Health*, **1987**, 77, 437-438.
16. Sevastyanov, B. A. *Branching Processes*, Moscow, "Nauka", 1971.

17. Chistyakov V.P. 1964. "A theorem on sums of independent positive random variables and its applications to branching random processes." *Theory of Probab. Appl.* V.9, 640-648.
18. Chover J., Ney P. and Wainger S. 1973. "Degeneracy properties of subcritical branching processes." *Ann. Prob.* V. 1, 663-673.
19. Leslie J. R. 1989. "On the non-closure under convolution of the subexponential family." *J. Appl. Probab.* 26, 58-66.
20. Mode Ch. J. 1971. *Multitype Branching Processes*, American Elsevier, New York.

ACKNOWLEDGMENTS:

This project has been funded by King Fahd University of Petroleum and Minerals under project No FT-2006/03. We are indebted to KFUPM for the excellent research facilities. We thank Ch. Jacob and E. Vergu, from INRA-Jouy en Josas, for useful discussions during the Workshop on Stochastic Modelling in Population Dynamics, April, 2007, CIRM, France. We are also grateful to referees and the editors of both journals, "STOCHASTIC MODELS" and "STOCHASTIC ANALYSIS AND APPLICATIONS" for their valuable comments on the first versions of our articles.