A simple finite delayed multi-type branching process for infectious disease modeling

Andrew Hart*    Servet Martínez†

Center for Mathematical Modeling, IRL 2807 CNRS-UCHILE, Facultad de Ciencias Físicas y Matemáticas, Universidad de Chile, Santiago, Chile.

25 January, 2023

Abstract

We study a model for the spread of an infectious disease which incorporates spatial and temporal effects. The model is a delayed multi-type branching process in which types represent geographic regions while infected individuals reproduce offspring during a finite time interval and have convalescence times and random death/recovery outcomes. We give simple expressions for the limit of the geometrically weighted mean evolution of the process.

Keywords: delayed multi-type branching process; Perron-Frobenius theory; Malthusian parameter; infectious disease modeling.

2020 MSC: 60J80; 60J85, 92D30.

1 Introduction

Inspired by agent-based simulation studies of the spread of SARS-CoV2 such as that reported in [7], our aim is to study a model for the epidemic spread of an infectious agent which possesses levels of infectiousness that vary both spatially and according to the time elapsed since infection within a fixed finite time window and has a finite, but not necessarily bounded, convalescence time.

Our model is based on discrete-time branching processes (we shall write $bp$ for branching process in future), which find a natural application in describing disease spread, for instance, see [1, 11]. More precisely, the model is a cross between a multi-type $bp$ and a delayed $bp$ sporting the following characteristics. Individuals who contract an infectious disease are only contagious for a short time immediately following their infection, say, $D$ days. Thus, an individual born (infected) at time $s$ has the opportunity to reproduce offspring (cause infections) at times $\{s + d : 1 \leq d \leq D\}$, and the number of offspring born at time $s + d$ follows a law that depends on the time offset $d$. Individuals may continue suffering the effects of the disease long after they have ceased to be infectious and the model assigns each individual in the population a random lifetime (convalescence time). This time, which is not necessarily bounded, may be zero, signifying that the individual is asymptomatic. Symptomatic Individuals either die or recover according to a Bernoulli random variable at the end of their lifetimes. If they die before $D$ days have lapsed, they cease to be infectious. Asymptomatic individuals (with zero lifetimes) do not die, but remain contagious for $D$ days following infection. Spatial disparity is captured by including a multi-type component in which types represent regions and the numbers of offspring of all types produced by individuals of distinct types can have different distributions. The model plays host to three closely related processes that evolve in time: the offspring process $X$, the asymptomatic population size process $Y$ and the symptomatic population size process $U$. In epidemiological terms, $X$ captures disease incidence while $Y + U$ models the prevalence.

*E-mail: ahart@dim.uchile.cl
†E-mail: smartine@dim.uchile.cl
The class of models we study here is much more restrictive than the C-M-J bp’s in which individuals reproduce according to a random point process and are alive during random time intervals. These are described and comprehensively studied in a large body of work (see [2, 3, 4, 5, 6, 8]) that encompasses more general frameworks than that considered here and they mostly deal with the continuous-time setting. This literature examines the limiting behavior of processes weighted by an exponential function of the Malthusian parameter in great detail and has the establishment of long-term mean behavior, convergence in distribution (see [2, Theorem 2]) and conditions for a.s. convergence (see [2, Theorem 2] and [5, Proposition 1.1]) as notable achievements. In particular, concerning the mean limits of processes, there are analytical procedures for obtaining these (see [2, Lemma 2 and Proposition 2] and [4, Theorem 4.1]) which are general, but difficult to employ in practical modeling applications in epidemiology where explicit estimates are desirable.

The paper is arranged as follows. Section 2 defines delayed multi-type bp’s and describes the offspring distribution specific to the model studied here. It also derives the evolution equations for the mean population sizes of the X, Y and U processes, which are governed by a family of mean matrices at different delay times. The (i, j) element of the $d^{th}$ mean matrix indicates the average number of $j$-type individuals an $i$-type individual infects a time $d$ after contracting the disease. Section 3 then presents the main result, Proposition [1] which gives simple-to-compute analytical expressions for the limits of the mean population sizes of the three processes weighted according to an exponential of the Malthusian parameter. These are analogous to results for classical multi-type bp’s.

2 Delayed multi-type branching processes

In this model, each individual is born at some time $s \in \mathbb{N}_0 = \{0, 1, 2, \ldots\}$ and generates offspring independently of all other individuals. The offspring can be of any type $i \in I$ and each is born within a finite set of times $D \subset \mathbb{N} = \{1, 2, \ldots\}$ following the birth of the parent. Thus, an individual born at $s$ generates offspring at times in $s + D$. The number of offspring of each type in $I$ produced by the same parent at different ages in $D$ are independent. If min$D > 1$ there is a latency period during which an individual is not yet contagious. One can assume that g.c.d. $D = 1$ and we write $D = \max D$ for the maximum delay. Our interest is in the case $|D| > 1$.

2.1 The random structure

The set of nodes $\mathcal{I}$ represents all the potential individuals involved in the process. A node $b \in \mathcal{I}$ is identified by $b = (a; i, t, l)$ where $a$ is its parent node, $i \in I$ is its type, $t$ is its time of birth and $l$ enumerates the nodes born to parent $a$ of type $i$ at time $t$. When $t = 0$, $b$ is a root and we set $a = \emptyset$. Each node $b$ gives rise to a set of nodes $(b; j, s, h)$ for $j \in I$, $s = t + d$ for $d \in D$ and $h \in \mathbb{N}$. Let $\mathcal{I}^t$ denote the set of all type $i$ nodes.

Next, we associate with $b \in \mathcal{I}$ independent random elements $\xi(b)$ and $\zeta(b)$ which are also mutually independent. Variables $\xi(b)$ of the same type $i$ are identically distributed for $b \in \mathcal{I}^t$. For each $b = (a; i, t, l)$, $\xi(b) = (\xi_{a,i,t,l,d}^j : d \in D, j \in I)$ is a vector of random variables where $\xi_{a,i,t,l,d}^j$ is the number of potential offspring of type $j$ born to $b$ at time $t + d$ and its distribution only depends on $d$ and $(i, j)$. We shall let $\xi_{a,i,t,l,d}^j$ denote a random variable having this distribution. The variables $(\zeta, \xi)(b)$ are identically distributed for all $b \in \mathcal{I}$. Variable $\zeta(b)$ takes values in $\mathbb{N}_0$ and indicates the lifetime of $b$ while $\xi(b)$ may depend on $\zeta(b)$, taking the value 1 or 0 according as $b$ recovers or dies respectively after time $\zeta(b)$ has elapsed. If $\zeta(b) = 0$, $b$ is asymptomatic and cannot die, so we set $\xi(b) = 1$. In contrast, if $\zeta(b) > 0$, then $b$ is symptomatic and able to produce offspring at times in $D$ up to $D$, except if it dies before $D$. Here, we use ‘die’ to mean a shift to a non-reproductive state like actual death or isolation, as in [11]. Note that symptomatic individuals that recover before time $D$ remain contagious and able to produce offspring at all times in $D$ up to $D$. Let $(\zeta, \xi)$ denote a random element with the same law as $(\zeta, \xi)(b)$. To avoid the possibility of having trivial dynamics, we assume $\mathbb{P}(\zeta < \infty) = 1$ and $\mathbb{P}(\zeta > 0) > 0$, and when modelling asymptomatic individuals we assume $\mathbb{P}(\zeta = 0) > 0$.

We now fix a random realization on $\mathcal{T}_{\mathbb{N}_0}$. In order for an individual $b = (a; t, l, d)$ to produce offspring as described above, one requires that it has not yet died. So, the total number of offspring of type $j$ born at
time \( t + d \) will be

\[
\xi_{i,j}^{s,t,l,d} = \frac{\gamma_{i,j}^{s,t,l,d}}{1 - \gamma_{i,j}^{s,t,l,d}} \left( 1 - 1 \left( \mathcal{L}(a; i, t, l) \leq d, \epsilon(a; i, t, l) = 0 \right) \right).
\]

This ensures no offspring are produced after the death of the parent and fixes a dependence on the pair \((\mathcal{L}, \epsilon)\) specific to the individual. The distribution of \(\xi_{i,j}^{s,t,l,d}\) only depends on \(d\) and \((i, j)\), and we will use \(\xi_{i,j}^{s,t,l,d}\) to denote a random variable having this distribution. The individuals so generated, also denoted by \(b \in \mathcal{I}\) in what follows, are identified by a triplet \((i, s, l)\) where \(i\) is the type, \(s\) the time of birth and \(l\) enumerates all the individuals of type \(i\) born at time \(s\) and, from now on, we dispense with the parent and simply write \(\xi_{i,j}^{s,t,l,d}\) and \(\xi_{i,j}^{s,t,l,d}\). When an individual \(b = (i, s, l)\) is generated by the process, then it is ill and manifests symptoms in the time interval \([s, s + \mathcal{L} - 1]\) when \(\mathcal{L} > 0\). In contrast, if \(\mathcal{L} = 0\), then once infected the individual is asymptomatic during the time interval \([s, s + D]\) but is not counted as being ill. This means that asymptomatic individuals are able to infect others and produce offspring during the interval \([s, s + D]\) while symptomatic individuals can only do so during \([s, s + \min(\mathcal{L} - 1, D)]\).

We should mention that having offspring born at a fixed set of delays covers the case where the birth times of an individual’s offspring are random and bounded. In fact, delays in a bounded random time span \(\mathcal{A}\) can be viewed within the deterministic framework as follows: replace the number of \(j\)-type offspring produced by an \(i\)-type individual at delay \(d\) by \(\xi_{i,j}^{s,t,l,d}(\mathcal{A} \geq d)\).

### 2.2 The processes

The offspring process \(\mathcal{X}(s) = (\mathcal{X}_j(s) : j \in \mathcal{I})\) is defined by \(\mathcal{X}(s) = 0\) for \(s < 0\) and

\[
\mathcal{X}_j(s) = \mathbf{1}(j = i_0, s = 0) + \sum_{i \in \mathcal{I}} \sum_{d \in \mathcal{D}} \sum_{l = 1} \xi_{i,j}^{s-t,l,d} \text{ for } s \in \mathbb{N}_0.
\]

The initial condition is a single type \(i_0\) individual (which can be written as \(\mathcal{X}(0) = \mathcal{X}_{i_0}\)) and \(\mathcal{X}_j(s)\) is the number of type \(j\) offspring born at time \(s\) for \(s > 0\). Since \(\mathcal{X} = (\mathcal{X}(s) : s \geq 0)\) only counts offspring, there is the implicit assumption that individuals live for a single unit of time.

Each individual \(b = (i, t, l)\) has a lifetime \(\mathcal{L}(i, t, l)\) distributed as \(\mathcal{L}\) during which it is considered to be ill. Define \(\mathcal{U}(s) = (\mathcal{U}_j(s) : j \in \mathcal{I})\) to be the number of ill (symptomatic) individuals of each type at time \(s\). Now, recall that the set \(\{(j, s, l) : l = 1, \ldots, \mathcal{X}_j(s)\}\) enumerates the type \(j\) offspring born at time \(s \geq 1\). For \(s = 0\), \((i_0, 0, 1)\) denotes the initial individual. We set \(\mathcal{U}(s) = 0\) for \(s < 0\). Since an individual with \(\mathcal{L}(i, t, l) = 0\) is never ill one has

\[
\mathcal{U}_j(s) = \sum_{c = 0}^{s} \mathcal{X}_j(s-c) \mathbf{1}(\mathcal{L}(j, s-c, l) > c), \ s \in \mathbb{N}_0.
\]

We shall call \(\mathcal{U} = (\mathcal{U}(s) : s \in \mathbb{N}_0)\) a delayed multi-type \(bp\).

Individuals for whom \(\mathcal{L} = 0\) are not counted as ill by the model. They are asymptomatic for \(D\) time units and are able to infect others during that time. The process of asymptomatic cases present at each time is \(\mathcal{Y}(s) = (\mathcal{Y}_j(s) : j \in \mathcal{I})\) where \(\mathcal{Y}(s) = 0\) for \(s < 0\) and

\[
\mathcal{Y}_j(s) = \sum_{c = 0}^{D} \mathcal{X}_j(s-c) \mathbf{1}(\mathcal{L}(j, s-c, l) = 0), \ s \in \mathbb{N}_0.
\]

In the epidemiological setting, \(\mathcal{X}\) models disease incidence while \(\mathcal{Y} + \mathcal{U}\) gives the prevalence.

The three processes \(\mathcal{U}, \mathcal{X}\) and \(\mathcal{Y}\) become extinct together almost surely or they all have some positive probability of not dying out. In other words, the extinction time of \(\mathcal{X}\), \(T^\mathcal{X} = \inf\{t \geq 0 : \sum_{j \in \mathcal{I}} \mathcal{X}_j(t + s) = 0 \text{ for all } s \geq 0\}\), and the analogously defined \(T^\mathcal{U}\) and \(T^\mathcal{Y}\) satisfy:

\[
P(T^\mathcal{U} < \infty) = 1 \iff P(T^\mathcal{X} < \infty) = 1 \iff P(T^\mathcal{Y} < \infty) = 1.
\]

The first equivalence is a direct consequence of the fact that all individuals \(b\) generated during this process have an almost surely finite lifetime \(\mathcal{L}(b)\). For the second equivalence, the implication \((\Rightarrow)\) follows
from \( T^Y \leq T^X + D < \infty \) a.s. and conversely, if \( Y \) becomes extinct and \( X \) is not extinct, one gets \( \mathbb{P}(T^Y < \infty, \exists t_n \to \infty, \exists b_n = (i_n, t_n, 1)) > 0 \). Since lifetimes are identical and independent of all other variables, imposing the condition that \( L(b_n) = 0 \) merely thins the set of individuals born after time \( T^Y \), so \( X \) must become extinct.

When averaging the processes \( \mathcal{U} \) and \( \mathcal{X} \) with respect to \( (\varepsilon(b) : b \in \mathcal{I}) \), one obtains particular classes of the processes considered in [6] and [8]. The individuals of \( \mathcal{X} \) have unit lifetimes, reproduce at time offsets in \( \mathcal{D} \) and \( i \)-type individuals produce \( j \)-type offspring using a copy of \( \xi_{i,j}^{l} \). Similarly, individuals of \( \mathcal{U} \) have lifetimes given by \( \mathcal{L} > 0 \), reproduce at times in \( \{d \in \mathcal{D} : d < \mathcal{L}\} \) and \( i \)-type individuals reproduce \( j \)-type offspring using a copy of \( \xi_{i,j}^{l} \).

Let us average the law of \( \xi_{i,j}^{l} \) over \((\mathcal{L}, \varepsilon)\). This gives us the offspring law of a contagious individual when there is no information available about lifetime or recovery \((\mathcal{L}, \varepsilon)\). The law \( (p_{i,j}^{l}(n) : n \in \mathbb{N}_0) \) only depends on \( i, j \) and \( d \). Due to the independence between \( j(b) \) and \( (\mathcal{L}, \varepsilon)(b) \), \( p_{i,j}^{l}(n) = \mathbb{E}_{(\mathcal{L}, \varepsilon)}(\mathbb{P}(\xi_{i,j}^{l} = n)) \), \( n \geq 0 \), takes the form

\[
p_{i,j}^{l}(n) = \begin{cases} \mathbb{P}(\xi_{i,j}^{l} = n)(1 - \mathbb{P}(\mathcal{L} \leq d, \varepsilon = 0)), & \text{if } n > 0, \\ \mathbb{P}(\xi_{i,j}^{l} = 0)(1 - \mathbb{P}(\mathcal{L} \leq d, \varepsilon = 0)) + \mathbb{P}(\mathcal{L} \leq d, \varepsilon = 0), & \text{if } n = 0. \end{cases}
\]

Naturally, \( \sum_{n \geq 0} p_{i,j}^{l}(n) = 1 \). The mean number of offspring of type \( j \) produced by an individual of type \( i \) and age \( d \) is then given by

\[
M_d(i, j) = \mathbb{E}(\xi_{i,j}^{l}) = \sum_{n \geq 0} n p_{i,j}^{l}(n), \text{ for } i, j \in I, d \in \mathcal{D}.
\]

Let \( M_d = (M_d(i, j) : i, j \in I) \). We assume \( M_d \) is irreducible for all \( d \in \mathcal{D} \). By convention, set \( M_d = 0 \) and \( p_{i,j}^{l}(n) = 1(n = 0) \) for any \( d \notin \mathcal{D} \).

We will denote the expected value when starting with a single individual of type \( i_0 \) by \( \mathbb{E}_{i_0} \), but if there is no confusion we shall simply write \( \mathbb{E} \). Set \( \mathbb{E}(\mathcal{X}(s)) = 0 \) for \( s < 0 \). Since \( \mathcal{X}(s - d) \) is independent of the sequence of variables \((\xi_{s-d,i,j}^{l})\) by Wald’s equation [10], taking expectations on both sides of \[14\] gives

\[
\mathbb{E}_{i_0}(\mathcal{X}(s))' = \xi_{i_0}' \mathbf{1}(s = 0) + \sum_{d \in \mathcal{D}} \mathbb{E}_{i_0}(\mathcal{X}(s - d))'M_d, \ s \in \mathbb{N}_0.
\]

To evaluate the expected number of individuals of each type ill at time \( s \), \( \mathbb{E}_{i_0}(\mathcal{U}_j(s)) \), we can use \( M_d = 0 \) for \( d \notin \mathcal{D} \) together with relation \[12\] and Wald’s Equation [10] once again to obtain

\[
\mathbb{E}_{i_0}(\mathcal{U}_j(s)) = \sum_{c = 0}^{s} \mathbb{E}_{i_0} \left( \sum_{l = 1}^{\mathcal{Y}_j(s - c)} \mathbf{1}(\mathcal{L}(j, s - c, l) > c) \right) = \sum_{c = 0}^{s} \mathbb{E}_{i_0}(\mathcal{Y}_j(s - c)) \mathbb{P}(\mathcal{L} > c).
\]

Now, from \[3\] and the independence properties of \( \mathcal{L} \) and \( \mathcal{X} \), the expected number of asymptomatic cases is given by

\[
\mathbb{E}_{i_0}(\mathcal{Y}(s))' = \mathbb{P}(\mathcal{L} = 0) \sum_{d = 0}^{\mathcal{D}} \mathbb{E}_{i_0}(\mathcal{X}(s - d))', \ s \in \mathbb{N}_0.
\]

3 The encoding and the main result

Following Definition 2 in [6] where the Malthusian parameter is given for general delayed multi-type processes, we have that the exponential of the Malthusian parameter of \( \mathcal{X} \), say \( \lambda \), is uniquely defined by

\[
\lambda \text{ is the unique value for which the Perron-Frobenius eigenvalue of } \sum_{d \in \mathcal{D}} \lambda^{-d} M_d \text{ is } 1.
\]
We are interested in \( \lim_{s \to \infty} \lambda^{-s} \mathbb{E}((X(s))) \). First, notice that \( X \) is equally distributed as a delayed \( \text{bp} \) \( \hat{X} \) whose definition includes no concept of lifetime and where each individual \((i, t, l)\) generates \( \zeta^i_{t,l} \) offspring of type \( j \) at time \( t + d \) according to law \( \rho^j \). So, \( \hat{X} \) satisfies \( \hat{X}(s) = 0 \) for \( s < 0 \) and \( \hat{X}_1(s) = 1(j = i_0, s = 0) + \sum_{i \in I} \sum_{d \in D} \sum_{l=1}^{s-d} \zeta^i_{s-d,l} \) for \( s \in \mathbb{N}_0 \). The mean number of offspring in \( \hat{X} \) and \( X \) is given by \( M^j_d = \sum_{n \geq 0} n \rho^j(n) \), and \( \mathbb{E}(\hat{X}(s)) = \mathbb{E}(\hat{X}(s)) \), \( s \in \mathbb{N}_0 \). Now we will encode \( \hat{X} \) by a multi-type \( \text{bp} \).

Set \( [D] = \{1, \ldots, D\} \) and consider the new set of types \( \hat{I} = [D] \times I \). Then, \( \hat{X} \) may be viewed as the following multi-type \( \text{bp} \) \( \hat{Z} \) on the set of types \( \hat{I} \) defined by:

\[
\hat{Z}(s) = (\hat{Z}_{d,j}(s) : (d, j) \in \hat{I}), \quad s \geq 0, \text{ with } \hat{Z}_{d,j}(s) = \hat{X}_j(s + 1 - d).
\]

So, \( \hat{Z}_{d,j}(0) = 1(d = 1)1(j = i_0) \). For \( 1 < d \leq D \) one has \( \hat{Z}_{d,j}(s + 1) = \hat{Z}_{d-1,j}(s) \) while for \( d = 1 \) one obtains from (1) that

\[
\hat{Z}_{1,j}(s + 1) = \hat{X}_j(s + 1) = \sum_{e \in D} \sum_{l \in I} \hat{X}_e(s + 1 - e) \sum_{l=1}^\nu \zeta^i_{s+1-\nu,l} = \sum_{e \in D} \sum_{l \in I} \sum_{l=1}^\nu \hat{Z}_e(s) \zeta^i_{s+1-\nu,l}.
\]

The mean matrix of \( \hat{Z} \) is given by \( \hat{M}((t, e), (d, j)) = 1(i = j)1(e = d - 1) \) if \( d > 1 \). When \( d = 1 \), one has \( \hat{M}((t, e), (1, j)) = 0 \) if \( e \notin D \) and \( \hat{M}((t, e), (1, j)) = M_e(i, j) \) otherwise. One can check that the matrix \( \hat{M} \) is irreducible. Let \( \hat{\nu} = (\hat{\nu}(e, i) : (e, i) \in \hat{I}) \) be a left eigenvector of \( \hat{M} \) corresponding to its Perron-Frobenius eigenvalue \( \rho \) and let \( \hat{\lambda} = (\hat{\lambda}(e, i) : i \in I) \) for \( e \in [D] \). For \( d > 1 \), one has \( \rho \hat{\nu}_d = \hat{\nu}_{d-1} \) and so

\[
\hat{\nu}_d = \rho^{-(d-1)} \hat{\nu}_1, \quad d \in [D].
\]

Hence,

\[
\rho \hat{\nu}_1(j) = \sum_{e \in D} \sum_{i \in I} \rho^{-(e-1)} \hat{\nu}_1(i) M_e(i, j) = \sum_{i \in I} \hat{\nu}_1(i) \left( \sum_{e \in D} \rho^{-(e-1)} M_e(i, j) \right),
\]

from which it follows that \( \hat{\nu}_1 \) satisfies \( \lambda^\nu M_\rho = \hat{\nu}_1 \), where

\[
M_\rho = \sum_{e \in D} \rho^{-e} M_e.
\]

Therefore \( \hat{\nu}_1 \) is the Perron-Frobenius eigenvalue of \( M_\rho \) and it follows that \( \lambda \) defined in (7) is also the Perron-Frobenius eigenvalue of \( \hat{M} \). Similarly take \( \hat{h} = (\hat{h}(e, i) : (e, i) \in \hat{I}) \) to be a right Perron-Frobenius eigenvector of \( \hat{M} \) so that \( \hat{M} \hat{h} = \lambda \hat{h} \). Write \( \hat{h}_e = (\hat{h}(e, j) : j \in I) \) for \( e \in [D] \). Then \( M_e \hat{h} = \lambda \hat{h}_e - \hat{h}_{e+1}1(e < D) \) and hence \( \lambda^{-e} M_e \hat{h} = \lambda^{-e} \hat{h}_e - \lambda^{-e} \hat{h}_{e+1}1(e < D) \). By summing over \( e = 1, \ldots, D \), we obtain \( M_\rho \hat{h} = \hat{h}_1 \), so that \( \hat{h}_1 \) is the eigenvector corresponding to eigenvalue 1 of the matrix \( M_\lambda \). Also we can iterate equality \( M_e \hat{h} = \hat{h}_e - \hat{h}_{e+1}1(e < D) \) to get

\[
\hat{h}_d = \sum_{e=d}^D \lambda^{-e-d+1} M_e \hat{h}_1 \quad \text{for } d \in [D].
\]

(Recall that \( M_d = 0 \) when \( d \notin D \)).

Since \( (\hat{Z}(s) : s \geq 0) \) is a multi-type \( \text{bp} \) with mean matrix \( \hat{M} \), we have

\[
\mathbb{E}(\hat{Z}(s)) = \mathbb{E}(\hat{Z}(0)) \hat{M}^s.
\]

Also \( \hat{Z}_{d,0}(0) = 1(d = 1)1(j = i_0) \) which means \( \mathbb{E}(\hat{Z}(0)) = \mathbf{1}_{i_0} \).

It is well known that if \( A \) is an irreducible non-negative matrix with Perron-Frobenius eigenvalue \( \rho_A \) and corresponding left and right eigenvectors normalized so that \( \nu' h = 1 \), Then, for any norm \( \| \cdot \| \), there exists
$C < \infty$ and $\delta \in (0, 1)$ such that $\|\rho^{-s}A^s - \mu'\| \leq C\delta^s$ for all $s \geq 0$ and $\lim_{s \to \infty} \rho^{-s}A^s = \mu'$ componentwise (see Chapter 1 of [9]).

So, when we normalize $\hat{\nu}$ and $\hat{h}$ such that $\hat{\nu}^T \hat{h} = 1$ we have $\lim_{s \to \infty} \lambda^{-s}\hat{M}^s = \hat{h}\mu$ componentwise. Therefore,

$$\lim_{s \to \infty} \lambda^{-s}E((\hat{Z}(s)) = \epsilon_{1,0} \hat{h} \mu'.
$$

Using $E(\hat{X}(s)) = E(\hat{X}(s)) = E(\hat{Z}_1(s))$, we get

$$\lim_{s \to \infty} \lambda^{-s}E((\hat{X}(s)) = \epsilon_{1,0} \hat{h} \mu'.
$$

Next we compute the condition $\hat{\nu}^T \hat{h} = 1$ in terms of $\hat{\nu}$ and $\hat{h}$. We have

$$1 = \hat{\nu}^T \hat{h} = \sum_{d=1}^{D} \lambda^{-(d-1)} \hat{\nu}_d^T \left( \sum_{e=d}^{D} \lambda^{-(1+e-d)} M_e \right) \hat{h}_1 = \hat{\nu}_d^T \left( \sum_{d=1}^{D} \lambda^{d} M_d \right) \hat{h}_1.$$

Let $\nu$ and $h$ be the left and right eigenvectors $\hat{\nu}_1$ and $\hat{h}_1$ of $M_\lambda$ but normalized so that $\nu^T h = 1$. Define

$$\mu = \nu^T \left( \sum_{d=1}^{D} d \lambda^{-d} M_d \right) h.$$

**Proposition 1.** The limit mean for the offspring process is

$$\lim_{s \to \infty} \lambda^{-s}E((\hat{X}(s)) = \mu^{-1} \epsilon_{1,0} \mu'.
$$

while the limit mean for the asymptomatic individuals is

$$\lim_{s \to \infty} \lambda^{-s}E(\hat{U}_1(s)) = \mu^{-1} \left( \sum_{d=0}^{D} \lambda^d \right) \epsilon_{1,0} \mu'.$$

Some additional assumptions are required to handle process $\hat{U}_1$: If the processes are subcritical ($\lambda < 1$), assume that $E(\lambda^{-\mathcal{L}}) < \infty$, while if they are critical ($\lambda = 1$), assume that $E(\mathcal{L}) < \infty$. Then, the long-term behavior of the mean number of symptomatic individuals is given by

$$\lim_{s \to \infty} \lambda^{-s}E(\hat{U}_1(s)) = \mu^{-1} \left( \sum_{c=0}^{\infty} \lambda^{-c} \mathbb{P}(\mathcal{L} > c) \right) \epsilon_{1,0} \mu'.$$

**Proof.** Equation (10) follows directly from (8) and (9). This equality together with (6) then leads to (11). Next consider the case for symptomatic individuals. From (5), we have

$$E_{\epsilon_{1,0}}(\hat{U}_1(s)) = \sum_{c=0}^{s} E_{\epsilon_{1,0}}(\hat{X}_j(s-c)) \mathbb{P}(\mathcal{L} > c).$$

Multiplying both sides of this by $\lambda^{-s}$ and taking limits as $s \to \infty$ yields

$$\lim_{s \to \infty} \lambda^{-s}E_{\epsilon_{1,0}}(\hat{U}_1(s)) = \lim_{s \to \infty} \lambda^{-s} \sum_{c=0}^{s} E_{\epsilon_{1,0}}(\hat{X}_j(s-c)) \mathbb{P}(\mathcal{L} > c)

= \lim_{s \to \infty} \sum_{c=0}^{s} \left( \lambda^{-s-c} E_{\epsilon_{1,0}}(\hat{X}_j(s-c)) \right) \lambda^{-c} \mathbb{P}(\mathcal{L} > c)

= \lim_{s \to \infty} \sum_{c=0}^{\infty} \left( \lambda^{-s-c} E_{\epsilon_{1,0}}(\hat{X}_j(s-c)) 1(s \geq c) \right) \lambda^{-c} \mathbb{P}(\mathcal{L} > c).$$
Next,
\[
\lambda^{-(s-c)}E_{i_0}(X_j(s-c))I(s \geq c) = \lambda^{-(s-c)}E_{i_0}(X_j(s-c))
\]
because \(X_j(s) = 0\) for \(s < 0\). We have already seen that
\[
\lim_{s \to \infty} \lambda^{-(s-c)}E_{i_0}(X_j(s-c)) = \mu^{-1}\epsilon_{i_0} \nu',
\]
for \(c \geq 0\). Since \(\lim_{s \to \infty} \lambda^{-(s-c)}E_{i_0}(X_j(s-c))\) is finite, we have
\[
\sup \{\lambda^{-(s-c)}E_{i_0}(X_j(s)) : s \geq 0\} < \infty,
\]
so there is some \(K > 0\) that bounds \(\lambda^{-(s-c)}E_{i_0}(X_j(s-c))\) for all \(s \geq 0, 0 \leq c \leq s\). If \(\mathcal{U}\) is supercritical, then \(\lambda > 1\) and
\[
\sum_{c=0}^{\infty} \left(\lambda^{-(s-c)}E_{i_0}(X_j(s-c))\right) \lambda^{-c}P(\mathcal{L} > c) \leq K \sum_{c=0}^{\infty} \lambda^{-c}P(\mathcal{L} > c) < \infty.
\]
However, this also holds under the additional assumptions made for the critical and subcritical cases. Consequently, the dominated convergence theorem can be used to justify exchanging the limit with the summation and we obtain
\[
\lim_{s \to \infty} \lambda^{-s}E_{i_0}(|U_j(s)|) = \lim_{s \to \infty} \sum_{c=0}^{s} \left(\lambda^{-(s-c)}E_{i_0}(X_j(s-c))\right) \lambda^{-c}P(\mathcal{L} > c)
\]
\[
= \sum_{c=0}^{\infty} \left(\lim_{s \to \infty} \lambda^{-(s-c)}E_{i_0}(X_j(s-c))\right) \lambda^{-c}P(\mathcal{L} > c)
\]
\[
= \mu^{-1} \left(\sum_{c=0}^{\infty} \left[\lambda^{-c}P(\mathcal{L} > c)\right] \epsilon_{i_0} \nu'\right).
\]

**Corollary 2.** The normalized left eigenvector \(\nu'\) is the limit of types for the processes \(\mathcal{X}, \mathcal{Y}\) and \(\mathcal{U}\), that is,
\[
\lim_{s \to \infty} \frac{E(|\mathcal{X}(s)|')}{E(\mathcal{X}(s))1} = \lim_{s \to \infty} \frac{E(|\mathcal{Y}(s)|')}{E(\mathcal{Y}(s))1} = \lim_{s \to \infty} \frac{E(|\mathcal{U}(s)|')}{E(\mathcal{U}(s))1} = \nu'.
\]

**Proof.** This follows straightforwardly from Proposition 1 since \(\nu'1 = 1\). As the calculation of the limits is the same for all three processes, we will only present those for \(\mathcal{U}\).
\[
\lim_{s \to \infty} \frac{E(|\mathcal{U}(s)|')}{E(\mathcal{U}(s))1} = \frac{\mu^{-1}(E(|\mathcal{U}(0)|')h)}{\mu^{-1}(E(|\mathcal{U}(0)|')h)} \left(\sum_{c \geq 0} P(\mathcal{L} > c) \lambda^{-c}\right) \nu' = \nu'.
\]

**Remark 3.** Analogous to what happens in the case of a multi-type bp, \(\nu'\) is a stationary distribution for the mean evolution of types for the process \(\mathcal{X}\). In fact, \(\nu'\) is the left eigenvector corresponding to the eigenvalue 1 of \(M_{\lambda} = \sum_{d \in D} \lambda^{-d}M_d\) normalized to sum to unity. So when it is taken as the initial distribution one gets
\[
E(\mathcal{X}(s))' = \nu' \lambda^s \text{ for } s = 0, 1, \ldots, D - 1 \text{ and yields } E(\mathcal{X}(s))' = \sum_{d \in D} \nu'M_d \lambda^{-d} = \lambda^s \nu' \sum_{d \in D} \lambda^{-d}M_d = \nu' \lambda^s. \text{ Therefore, } E(\mathcal{X}(s))' / E(\mathcal{X}(s))1 = \nu' \text{ for all } s \geq 0.
\]

**Acknowledgments**

This work was supported by the Center for Mathematical Modeling ANID Basal Projects ACE210010 and FB210005.
References

[1] N. Becker. Estimation for discrete time branching processes with application to epidemics. *Biometrics*, 33(3):515–522, 1977.

[2] Kenny S. Crump and Charles J. Mode. A general age-dependent branching process. i. *Journal of Mathematical Analysis and Applications*, 24(3):494–508, 1968.

[3] Kenny S. Crump and Charles J. Mode. A general age-dependent branching process. ii. *Journal of Mathematical Analysis and Applications*, 25(1):8–17, 1969.

[4] K.S. Crump. On systems of renewal equations. *J. Math. Anal. Appl.*, 30:425–434, 1970.

[5] R.A. Doney. A limit theorem for a class of supercritical branching processes. *J. Appl. Probab.*, 9(4):707–724, 1972.

[6] R.A. Doney. On single- and multi-type general age-dependent branching processes. *J. Appl. Probab.*, 13(2):239–246, 1976.

[7] N.M. Ferguson, D. Laydon, G. Nedjati-Gilani, N. Imai, K. Ainslie, M. Baguelin, S. Bhatia, A. Boonyasiri, Z. Cucunubá, G. Cuomo-Dannenburg, and A. Diage. Report 9: Impact of non-pharmaceutical interventions (npis) to reduce covid-19 mortality and health-care demand. Imperial College COVID-19 Response Team, London, 16 March 2020. [https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College-COVID19-NPI-modelling-16-03-2020.pdf](https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College-COVID19-NPI-modelling-16-03-2020.pdf), 2020.

[8] O. Nerman. On the convergence of supercritical general (C-M-J) branching processes. *Z. Wahrscheinlichkeitstheorie verw. Gebiete*, 57:365–395, 1981.

[9] E. Seneta. *Nonnegative Matrices and Markov Chains*. Springer Series in Statistics. Springer-Verlag, New York, 2nd edition, 1981.

[10] Abraham Wald. On cumulative sums of random variables. *Ann. Math. Statist.*, 15(3):283–296, 1944.

[11] N.M. Yanev, V.K. Stoimenova, and D.V. Atanasov. Stochastic modeling and estimation of covid-19 population dynamics. *C. R. Acad. Bulg. Sci.*, 73(4):451–460, 2020.