

AN ALGORITHMIC LOOK AT
PHASE-CONTROLLED BRANCHING
PROCESSES

SOPHIE HAUTPHENNE

Thèse présentée en vue de l'obtention
du grade de docteur en sciences

Octobre 2009

Université Libre de Bruxelles

Faculté des sciences

Sophie Hautphenne
Université Libre de Bruxelles
Département d'Informatique
Blvd du Triomphe - CP 212
1050 Bruxelles
Belgique
Email: shautphe@ulb.ac.be

Thèse de doctorat présentée en séance publique le 15 octobre 2009 à l'Université
Libre de Bruxelles.

Jury: Nigel Bean, University of Adelaide, Australia
Gianluca Bontempi, Secrétaire du jury, ULB
Thomas Bruss, ULB
Jean Cardinal, ULB
Udo Krieger, Universität Bamberg, Deutschland
Guy Latouche, Promoteur, ULB
Claude Lefèvre, Président du jury, ULB
Marie-Ange Remiche, Co-promoteur, ULB

Contents

Acknowledgments	v
Introduction	vii
1 Markovian trees	1
1.1 Multitype branching processes	1
1.2 Extinction probability	3
1.3 Transient Markovian arrival processes	5
1.4 Application in demography	7
1.5 Markovian trees	19
1.6 Extinction probability of a Markovian tree	23
2 Linear functional algorithms	25
2.1 The Depth and the Order algorithms	25
2.2 The Thicknesses algorithm	27
2.3 Convergence rates	30
2.4 Numerical examples	35
2.5 General Markovian Trees	37
3 Quadratic algorithms	47
3.1 The Newton algorithm	47
3.2 Probabilistic interpretation	51
3.3 Numerical examples	53
3.4 Application in demography	54
3.5 Alternate Newton sequences	57

4	Reducible branching processes	63
4.1	Definitions and notations	64
4.2	Extinction criteria	65
4.3	Partial extinction	72
4.4	Algorithms	74
4.5	Numerical examples	78
5	Transient measures	81
5.1	Matrix derivatives	82
5.2	Population size	83
5.3	Time until extinction	91
5.4	Total progeny size	94
5.5	Application in demography	96
6	Structured Markov chain approach	103
6.1	Structured Markov chains	103
6.2	Extinction probability	105
6.3	Maximum population size	107
6.4	Time until extinction	109
6.5	Time to reach k individuals	112
7	Random environments	117
7.1	Definition	118
7.2	Transient features	119
7.3	Extinction criteria	126
7.4	Numerical partial differential equations	130
7.5	Integral equations approach	136
7.6	Structured Markov chain approach	140
7.7	Comparison of the methods	144
8	Catastrophes	147
8.1	Definition	147
8.2	Transient features	148
8.3	Extinction criteria	154
8.4	Numerical partial differential equations	158
8.5	Integral equations approach	160
8.6	Structured Markov chain approach	164
	Conclusion and perspectives	173
	Bibliography	175

Acknowledgments

I would like to warmly thank my supervisor, Guy Latouche. After my *mémoire de licence* made under his direction, it did not take a long time for me to decide to start a doctoral thesis, something that I had never really thought of before; it promised four exciting years, and I have never been disappointed. Thank you, Guy, for your high availability, for your help, patience, and precious advices, for having made me discover the world of matrix analytic methods and for having shared your knowledge; I wish to thank you also for reassuring me in moments of doubt, and for the chocolate breaks.

Of course, I also thank my co-supervisor, Marie-Ange Rémiche, for her many useful tips, for our collaborations and our various discussions, and for her constant support.

I would like to express my gratitude to the other persons with whom I had the opportunity to work during these four years. Thanks to Kenji Leibnitz of the University of Osaka for our successful collaborations, for inviting me to the symposium in Kobe, and for his great helpfulness. Thanks to Benny van Houdt of the University of Antwerp for our very effective collaboration. Thanks also to Pauline Lafitte of the University of Lille 1 for her interest in my problems of partial differential equations, these have become *our* problems, on which we have always enjoyed working together; thanks for the invitations to Lille, and for having commented upon my last two chapters.

A big thank also goes to Peter Taylor who welcomed me twice at the University of Melbourne, and whose department helped me financially. I learned a lot from these stays in Australia.

These trips would not have been possible without financial help: I would like to thank the F.N.R.S. for the grants it offered me and for the financial support which has permitted me to pursue my PhD under good conditions.

My love for mathematics was born in large part thanks to my mathematics teacher in secondary school, Didier Pauwels. I am grateful for his way of teaching, and for his encouragements during the years at the university.

I thank my colleagues from the Computer Science Department for their hospitality, their sympathy, their support and the interest they took in my work. The good atmosphere allowed me to work in a very pleasant environment. I am of course very grateful to the members of the Mathematics Department too, for having contributed in many ways to my years at the university. Finally, I wish to thank Ana and Denis for their helping hands.

I take the opportunity to thank my friends and relatives too; special thanks go to Catherine for our longstanding friendship, to Mélanie for all the good times shared since the first year at the university, and to Céline and Maude for being there in good as in less good times.

I thank my family, in particular my parents who offered me an exemplary life frame, and who always supported and encouraged me in all my enterprises. And thank you, little sister, for being there, simply.

Finally, I would like to thank Gaétan for his help, patience and encouragements, and above all, for the love and happiness he brings to my everyday life.

Brussels, October 2009.

Introduction

Around 1870, when studying the problem of family names extinction in British peerages, Galton and Watson showed for the first time how the computation of probabilities could explain the effects of randomness in the development of families or populations. They proposed a mathematical model that went unnoticed for many years, and that reappeared in isolated papers in the 1920's and 1930's.

Galton and Watson's model, and its many extensions, became widely studied in the 1940's, both from a strictly theoretical and from a more practical point of view. Applications ranged from the evolution of genes populations to chain reaction of neutrons, and cosmic rays. This body of work was brought under the name of *branching processes*, which nowadays still form a lively field of research.

Branching processes can be seen as stochastic processes describing the evolution of a population of individuals which reproduce and die independently, according to some specific probability distributions. These processes may be classified into several categories. We briefly review some of them in the next paragraphs, so as to give an idea of how wide the field has grown, and we provide some references for the interested reader.

The individuals in a population may be all identical, or they may belong to several types differing by their reproduction and mortality rates, and one then writes about *multitype* branching processes. These individuals evolve in discrete or continuous time, with exponential or general lifetime distributions, respectively corresponding to what we call the *Markovian* branching process, and the *age-dependent* branching process. Galton and Watson studied the discrete, one-type case, which is the simplest form of branching process. Some general reference books are Harris [26] and Athreya and Ney [6]; Mode [54] is specifically dedicated to the multitype case.

The reproduction rules of an individual may depend on the actual size of the population, and one then refers to *population-size-dependent branching processes* (Klebaner [42], Gonzalez, Martinez and Mota [23]). In *bisexual branching processes*, female

and male individuals are considered separately, and a mating function has to be taken into account in the reproduction rules (Bruss [12], Hull [34]).

Finally, external processes may influence in different manners the growth of a population. First, new individuals may immigrate in the initial system according to some point process (Pakes [60]). So far, the individuals are supposed to behave independently of each others, but things may be different; for instance, a branching process may undergo *catastrophic* events, killing a random number of living individuals (Bartoszynski *et al.* [7], Thilaka, Kumar and Vijayakumar [68, 44]). The branching process may also evolve in a *random environment* controlling the lifetime and the reproduction laws of individuals over time (Athreya and Karlin [5], Tanny [67]). In the last two cases, the assumption of independence between individuals does not hold anymore, which notably complicates the analysis.

When immigration is not allowed, branching processes satisfy a dichotomy property: either the population eventually explodes, or it becomes extinct; there is no stationary behaviour. An important part of the literature on branching processes deals with questions such as finding criteria for almost sure extinction of the population, or determining the population size distribution at a given time, and the distribution of the time until extinction. Some authors also examine asymptotic behaviours of a branching process such as its asymptotic growth. If immigration is taken into account, then one may study the stationary distribution of the population size.

When individuals behave independently, it is well-known that the conditional extinction probability of a multitype branching process, given the type of the initial individual, is the minimal nonnegative solution of the fixed point equation

$$\mathbf{x} = \mathbf{P}(\mathbf{x}), \tag{1}$$

where \mathbf{x} is a vector and $\mathbf{P}(\cdot)$ is the probability generating function of the individuals' reproduction law (see for instance Harris [26] or Athreya and Ney [6, Section V.3]). Harris pointed out that the extinction probability could be computed by functional iteration, using this fixed point equation [26, Theorem 7.2]. This seems to be the first evocation of the practical question of the computation of the extinction probability. Up to now, few authors investigated other numerical techniques to assess the extinction probability of a population. From this question stems our interest in developing algorithms in the field of branching processes.

Algorithmic techniques have already proved themselves in a field of applied probabilities called the *matrix analytic methods*. These methods have been developed first in the context of queueing models and have given rise to the theory of quasi-birth-and-death (QBD) processes and to that of skip-free Markov chains (Neuts [56, 57], Latouche and Ramaswami [47], Bini, Latouche and Meini [10]), both belonging to the family of *structured Markov chains*.

Matrix analytic methods focus on algorithmic approaches to compute, for instance, stationary distributions and first passage times in structured Markov chains; they give much importance to the probabilistic interpretation of the proposed numerical procedures. Our idea is thus to draw our inspiration from these techniques and to

develop new tools to answer questions related to branching processes.

Recently, Bean, Kontoleon and Taylor [8, 9, 43] worked on a special class of multi-type branching processes, called *general Markovian trees* (GMT) (or simply *Markovian trees*), in which the lifetime of an individual has a phase-type distribution (defined as the distribution of the time until absorption of a Markovian process [47, Chapter 2]), and a random number of offsprings are born at epochs which are determined by a Markovian arrival process. With these assumptions, the GMTs form a very rich and varied class of branching processes. The authors also consider the special case where individuals can give birth to one child at a time only, and use the name *Markovian binary tree* (MBT) for these processes.

For MBTs, the probability generating function $\mathbf{P}(\cdot)$ is a second order polynomial matrix function, and the fixed point equation (1) is quadratic in the unknown vector \mathbf{x} . Using matrix analytic methods, the authors analyze two algorithmic procedures to solve the fixed point equation, they determine their probabilistic interpretations, and use it to compare the efficiency of the numerical schemes. Their results are the starting point of our work.

The main objective we have pursued all along is to further develop algorithmic methods to compute the extinction probability of an MBT, emphasizing the probabilistic interpretation of these methods in terms of the branching process itself. The idea is to compute at successive iterations the probability that the MBT eventually becomes extinct *with some constraints*. At each step, the constraints are relaxed, so that the sequence of probabilities converges to the ultimate extinction probability of the branching process. These constraints characterize each algorithm, and inform us about its speed of convergence.

We investigate in depth the extinction probability in the case where individuals behave independently of each others. This gives rise to efficient linear and quadratic algorithms. In this work, we generally only consider the MBT case for the sake of clarity. Usually, the results can be naturally generalized to the GMT case; we give more details whenever the difference in the computation or in the probabilistic interpretation is notable.

In order to prove some of our results, we need to make some irreducibility assumptions on the multitype branching process, that is, it is common to assume that any type of individual is able to generate any other type of individual. In that case, the extinction probability is either equal to one for *all* initial types or strictly less than one for *all* initial types. A natural question then arises: what happens if we remove this assumption? How does a multitype branching process behave in case some types of individuals are not able to produce other types of individuals? Such multitype branching processes are called *reducible*. It turns out that in that case, some groups of individuals may eventually become extinct without the whole process doing so, and we investigate several extinction criteria. We elucidate the exact importance of the irreducibility assumption, and we discuss algorithms to compute total and partial extinction probabilities.

Our second objective is to analyze the transient features of an MBT. We use the forward and the backward Kolmogorov equations approach and obtain the population size distribution of an MBT at any given time. Its probability generating function is the solution of two differential systems of equations. These equations may not be solved explicitly in the general case, but we derive recursive expressions for all the factorial moments. We also investigate other transient measures such as the distribution of the time until extinction, and the distribution of the total progeny size until some given time, or until extinction, conditionally given that extinction occurs.

Markovian trees may be seen as particular level-dependent structured Markov chains. Let us give a little more details here: structured Markov chains are two-dimensional Markovian processes of which the two components are discrete and are called the *level* and the *phase*. Suppose the process is in level k . In the particular case of a QBD, the only possible transitions are to levels $k - 1$, k , or $k + 1$, while in the case of a skip-free Markov chain, it is allowed to move either to levels $k - 1$, k and any higher level (like in the M/G/1-type Markov chain), or to levels $k + 1$, k , and any lower level (like in the G/M/1-type Markov chain).

One can associate a level-dependent QBD process to the MBT, and a level-dependent M/G/1-type Markov chain to the GMT. This correspondence allows one to use numerical tools from matrix analytic methods to compute the extinction probability. This is particularly useful when the fixed point equation (1) does not hold anymore. For instance, the extinction probability of a population-size dependent MBT may be computed by adapting to the level-dependent case some linear and quadratic algorithms developed for level-independent QBDs [47].

Various transient characteristics of MBTs may also be computed thanks to their parallelism with QBDs: the time until extinction and the time until the population reaches k individuals may be obtained by adapting numerical procedures for first passage times to lower and to upper levels in structured Markov chains (Gaver, Jacobs and Latouche [22]). The distribution of the maximum population size before extinction may be computed with a linear algorithm developed for QBDs in [47, Chapter 8]. The drawback of the structured Markov chain approach is that it must be confined to Markovian trees with a small number of phases in order to be numerically efficient.

In the final part of the thesis, we study the MBT under two types of external influences: first, we introduce a Markovian random environment controlling the evolution and reproduction parameters of individuals, and second, we define a catastrophe process affecting the population. In both cases, independence between individuals is lost and the fixed point equation (1) characterizing the extinction probability does not hold anymore. The forward Kolmogorov approach, leading to a partial differential system, is the only tool which may be exploited to characterize the population size distribution at any given time. The analysis of the extinction probability is then tackled through the numerical computation of this distribution.

We first adapt to our purpose numerical techniques for general partial differential equations, like the finite difference methods or the semi-Lagrangian method. Such techniques are efficient but do not have any physical interpretation in terms of the

branching process.

We also analyze the probability generating function of the population size under specific constraints related to the external process, leading to recursive integral equations.

Both approaches provide us with the distribution of the time until extinction of the MBT under external influence and, in the limit, give us the extinction probability.

Finally, the extinction probability of an MBT under external influence may also be analyzed with the structured Markov chain approach, since an MBT under Markovian random environment may be associated to a level-dependent QBD, and an MBT undergoing catastrophes to a level-dependent G/M/1-type Markov chain.

The theory of branching processes has applications in a large number of fields such as molecular biology, evolution, ecology, medicine, epidemiology, and biology of populations, one example being the propagation of human and animal species and genes. We refer to the books of Jagers [35], Kimmel and Axelrod [40], and Haccou, Jagers and Vatutin [25]. Kontoleon [43] shows that several of the current models of the macroevolutionary process are subsumed by the MBT. Branching processes also find applications in physics, for instance to model nuclear chain reaction, and in telecommunication systems (Yang and de Veciana [75]).

Here, we extensively study one application of MBTs in human demography. This example is used throughout the thesis as illustration of our results. Using real data, we analyze and compare *female* populations in several countries. The reason is twofold: the MBT is an asexual process and, in addition, the available fertility rates are those of women. First, we structure the lifetime of a woman in five years age classes, allowing us to make direct use of the available fertility and mortality rates data. In a second step, we aim at making the model more accurate by interpolating these data to one year age classes. We show that the same mathematical model not only enables us to determine features about individual women, such as the distribution of her lifetime, the time until her first and her last daughter, and the number of daughters, but also to analyze properties of the whole population, such as the extinction probability a female family, or the distributions of the time until its extinction, of the family size at any given time, and of the total progeny.

Another application of MBTs is worth mentioning. It falls in the field of telecommunications, and is developed in collaboration with Kenji Leibnitz from the University of Osaka. It is the object of two publications [30, 31], but it is not presented in details in this thesis. In short, the MBT is used to model the spread of a single file in a peer-to-peer network. We compute the probability that the sharing process of the file eventually ends, which corresponds to the extinction probability of the MBT. We first suppose that the parameters in the MBT are constant over time, which allows us to use the numerical techniques stemming from the fixed point equation (1). Then, we investigate the non-homogeneous case where the parameters of the MBT are population-size dependent, and we solve it using a structured Markov chain approach.

The thesis is organized as follows. In the first chapter we recall the definition of

the multitype branching process and the main results about its extinction probability. Then, we introduce the Markovian arrival process (MAP), which is a general model for the lifetime and birth epochs of individuals. We illustrate the main features of the MAP on the demography application. We use real data for a few selected countries and derive the survival expectancy of a woman, the mean time until the first and the last daughter, and the mean number of daughters. Finally, with these lifetime processes, we define the Markovian tree and we show the correspondence with multitype branching processes. We then specify the matrix extinction equation for MBTs and GMTs, which may not be solved analytically in general. We give the explicit solutions in the particular cases of exponential and phase-type MBTs.

The second chapter is devoted to linear algorithms based on functional iterations for computing the extinction probability of Markovian trees. We begin with the MBT case, and we first recall the Depth and the Order algorithms from Bean, Kontoleon and Taylor [9]. Then, we construct another linear algorithm, called the Thicknesses algorithm, and we prove its convergence through its physical interpretation. We analyze the convergence rates of all linear algorithms, and we show that both the Order and the Thicknesses algorithms surpass the Depth algorithm. However, no comparison may be done in general between the Order and the Thicknesses algorithm, and we illustrate on some numerical examples that their performances actually depend on the MBT under consideration. Finally, we generalize to the GMT case the Thicknesses algorithm and its probabilistic interpretation.

In the third chapter, we apply the Newton iteration method to the extinction equation and we show that the resulting algorithm has a global quadratic convergence. We give it a probabilistic interpretation, which is more involved than for the linear algorithms. We then compare the efficiency of the linear and the Newton algorithms on the same examples as in Chapter 2, as well as on the demographic application; for each country studied, we compute the extinction probability of a female family generated by a single woman. We conclude the chapter by showing that other quadratic algorithms may be constructed by applying the Newton method to other formulations of the extinction equation, and we study the convergence properties of one of them.

In Chapter 4, we investigate the reducible multitype branching process. We give necessary and sufficient conditions under which the total extinction of the process is equal to one. We also analyze different questions; for instance, is it possible to observe the partial extinction of some groups of individuals and not of others? Under which conditions is it possible to infer the extinction of a group of individuals from the extinction of another group? We show that the extinction equation (1) still plays a major role in the characterization of total and partial extinction probabilities, and we clarify the need of the irreducibility assumption made in the preceding chapters. We conclude with some numerical illustrations.

In the next chapter, we focus on transient measures for MBTs. We use the Kolmogorov approach to characterize the MBT size distribution at any given time, and we obtain recursive matrix differential equations for the factorial moments. We next turn our attention to the time until extinction of an MBT: we determine an ordinary system of differential equations for its distribution function and we show how it may be

used to compute the conditional mean time until extinction, given extinction occurs. Next, we study the total progeny size in an MBT, and we conclude the chapter by illustrating the various transient measures on the demographic application.

In Chapter 6, we discuss how numerical tools from the matrix analytic methods may be used to solve questions about Markovian trees. We start by showing the link between Markovian trees and structured Markov chains. Then, we show how to numerically calculate the extinction probability with the Markov chain approach when (1) does not hold anymore because the independence between individuals is lost. Next, we adapt algorithms for structured Markov chains and compute the distribution of the maximum population size in an MBT, the mean time until its extinction, and the mean time until the population reaches a given size.

Finally, Chapters 7 and 8 are devoted to MBTs evolving under the influence of two external processes, a Markovian random environment and a catastrophe process respectively, which affect the lifetime of the individuals in the branching process. The same approaches are used to analyze both types of influences. The structure of the two chapters is thus exactly the same, but details are sufficiently different to justify separate treatments. We provide criteria for the almost sure extinction of the MBT under external influence. Then, we investigate the extinction probability through the analysis of transient features, and we describe three numerical methods to evaluate this probability: the first one is a general method to numerically solve partial differential equations, the second one is based on recursive integral equations obtained by imposing constraints on the external process, and the last one follows the structured Markov chain approach. In Chapter 7, we also compare limitations and complexities of the various numerical methods.

The following standard notations are used throughout the text.

- Matrices are denoted by capital letters; I stands for the identity matrix, its dimension being generally made clear by the context. When there is a risk of ambiguity, we use I_n to indicate that the dimension is n .
- Vectors are denoted by boldface letters. They are generally columns, except initial and stationary probability vectors. We write $\mathbf{0}$, and $\mathbf{1}$ for vectors of zeros and ones, respectively, and \mathbf{e}_i for a vector whose only nonnull entry is the i th one, equal to one. Again, unless specified, the vector dimensions are set by the context.
- The superscript T indicates the transposition operation.
- We use $\text{sp}(A)$ to denote the spectral radius of a square matrix A , and $\mu(A)$ to denote its eigenvalue of maximal real part. In our case, $\mu(A)$ will be real. If A is nonnegative, then $\text{sp}(A) = \mu(A)$.
- We use the natural partial order for matrices and vectors where $A \leq B$ if $A_{ij} \leq B_{ij}$ for all i, j , and $\mathbf{x} \leq \mathbf{y}$ if $x_i \leq y_i$ for all i .

CHAPTER 1

Markovian trees

How to study the evolution over time of a population of individuals, or more particularly of a human family? Which mathematical model might suitably fit with the lifetime of an individual and its reproduction epochs?

To answer these questions, we analyze a class of continuous-time branching processes with general lifetime distributions and reproduction rules, called the Markovian trees. The extinction probability of such processes is a major question addressed in this work.

We start the chapter by defining the continuous-time multitype branching process. Then, we recall the criterion for its almost-sure extinction and the equation which characterizes the extinction probability.

Next, we introduce the transient Markovian arrival process, which is a tool to represent general birth processes and lifetime distributions. We illustrate the main features of this Markovian process with an example in human demography, that we repeatedly use throughout the thesis.

We then go on to define the Markovian tree, in which the lifetime and the reproduction times of the individuals are governed by a transient Markovian arrival process. A particular case of these Markovian trees is the Markovian binary tree, which we analyze in depth in the next chapters.

1.1 Multitype branching processes

A continuous-time multitype branching process describes the evolution of a finite number of individuals, classified in one of n possible types corresponding to different probabilistic behaviours, which evolve independently of each others. In the Markovian case,

the lifespan of an individual is exponentially distributed with a parameter depending on its type, but the lifespan distribution may be more general, in which case we refer to the multitype age-dependent branching process (see Harris [26]).

At the end of its life, an individual of type i reproduces by giving birth to a random number of new individuals of various types, according to the progeny distribution $\{p_{ij} : \mathbf{j} \in \mathbb{N}^n\}$. If $\mathbf{j} = [j_1, \dots, j_n]$, then p_{ij} denotes the probability that the parent of type i gives birth to j_1 children of type 1, j_2 of type 2, \dots , j_n of type n . One usually assumes that this probability distribution does not change over time. The progeny generating function of an individual of type i is

$$P_i(\mathbf{s}) = \sum_{\mathbf{j}} p_{ij} \mathbf{s}^{\mathbf{j}} = \sum_{j_1, \dots, j_n} p_{ij} s_1^{j_1} \cdots s_n^{j_n} \quad i = 1, \dots, n, \quad (1.1)$$

where $\mathbf{s} = [s_1, \dots, s_n]^T$ with $|s_i| \leq 1$.

The mean progeny matrix M is defined by

$$M_{ij} = \left. \frac{\partial P_i(\mathbf{s})}{\partial s_j} \right|_{\mathbf{s}=\mathbf{1}}, \quad i, j = 1, \dots, n. \quad (1.2)$$

The entry M_{ij} is interpreted as the mean number of direct offsprings of type j born from a parent of type i .

A multitype branching process is said *irreducible* (we also say *indecomposable*) when any type of individual may have individuals of all types among its (direct or indirect) descendance. This is stated more formally as follows

Definition 1.1.1. *A multitype branching process is irreducible if the mean progeny matrix M is irreducible, that is if for each $1 \leq i, j \leq n$, there exists an integer $k \geq 0$ such that $(M^k)_{ij} \neq 0$.*

If in addition there exists one positive integer N such that M^N has all its components strictly positive, then we say that the branching process is positive regular.

Suppose we start with one individual of a given type at time 0. Define the random variable $Z_i(t)$ as the total number of individuals of type i alive at time t . The random vector $\mathbf{Z}(t) = [Z_1(t), \dots, Z_n(t)]^T$ is an n -dimensional Markovian process with states space \mathbb{N}^n , and one absorbing state $\mathbf{0} = [0, 0, \dots, 0]^T$.

We say that the branching process *eventually becomes extinct* if the process $\mathbf{Z}(t)$ enters the absorbing state at some time; this corresponds to a situation where all the individuals in the system have died.

We discuss the extinction probability of a multitype branching process in the next section. For a detailed analysis of multitype branching processes, we refer to Mode [54], Harris [26], and Athreya and Ney [6].

1.2 Extinction probability

We denote by q_i the extinction probability of the multitype branching process $\{\mathbf{Z}(t) : t \in \mathbb{R}^+\}$, given that it starts with one individual of type i , that is,

$$q_i = \mathbb{P}[\exists T < \infty : \mathbf{Z}(T) = \mathbf{0} \mid \mathbf{Z}(0) = \mathbf{e}_i],$$

where \mathbf{e}_i is a vector with all components equal to zero, except for the i th one equal to 1. We bring these probabilities together in the vector $\mathbf{q} = [q_1, q_2, \dots, q_n]^T$.

Denote by $\mu(M)$ the eigenvalue with maximal real part of the mean progeny matrix M defined in (1.2). By the Perron-Frobenius Theorem for nonnegative matrices, this eigenvalue is real positive, and is algebraic simple in the irreducible case (Gantmacher [21, Chapter 13]); it corresponds to the spectral radius of M , that is, $\mu(M) = \text{sp}(M)$. In this section, we use the notation $\rho = \text{sp}(M)$.

The following theorem is a fundamental result in the theory of branching processes. A nice proof may be found for instance in Mode [54, Chapter 1, Theorem 7.1].

Theorem 1.2.1. *If $\rho < 1$, then $\mathbf{q} = \mathbf{1}$, and we say that the branching process is subcritical.*

If $\rho = 1$, then $\mathbf{q} = \mathbf{1}$, and we say that the branching process is critical.

If $\rho > 1$, then we say that the branching process is supercritical, and $\mathbf{q} < \mathbf{1}$ in the positive regular case, $\mathbf{q} \leq \mathbf{1}$, $\mathbf{q} \neq \mathbf{1}$ otherwise.

In all cases, \mathbf{q} is the minimal nonnegative solution of the vector equation

$$\mathbf{P}(\mathbf{s}) = \mathbf{s}, \tag{1.3}$$

where $\mathbf{P}(\mathbf{s}) = [P_1(\mathbf{s}), P_2(\mathbf{s}), \dots, P_n(\mathbf{s})]^T$ is the progeny generating vector of which the components are defined in (1.1). \square

To better understand the extinction criterion in the multitype case, let us have a look at the one-type case. The mean progeny is a scalar $m = P'(1)$ which represents the mean size of the first generation, if we assume that there is one individual at time 0. The mean size of the second generation is easily shown to be m^2 , and in general, the mean size of the n th generation is m^n . We thus observe that if $m < 1$, then the mean generation size tends to zero as n tends to infinity, if $m = 1$, then it is constantly equal to one, and if $m > 1$, then the mean generation size explodes. These three cases respectively correspond to the subcritical, critical, and supercritical cases.

The extinction probability q is the minimal nonnegative solution of the fixed point equation $s = P(s)$. We see on Figure 1.1 that when $P'(1) \leq 1$, the solution of the equation is unique in the interval $[0, 1]$ and is equal to 1, while when $P'(1) > 1$, the minimal nonnegative solution is strictly less than 1.

In the multitype case, it is natural that the spectral radius ρ of the mean progeny matrix M should play the same role as the scalar m . Indeed, M^n tends to zero as n tends to infinity if $\rho < 1$, it diverges to infinity if $\rho > 1$, and it remains nonzero and finite if $\rho = 1$. As we shall see in Section 5.2, there is another matrix which plays a similar role in the criticality of a branching process.

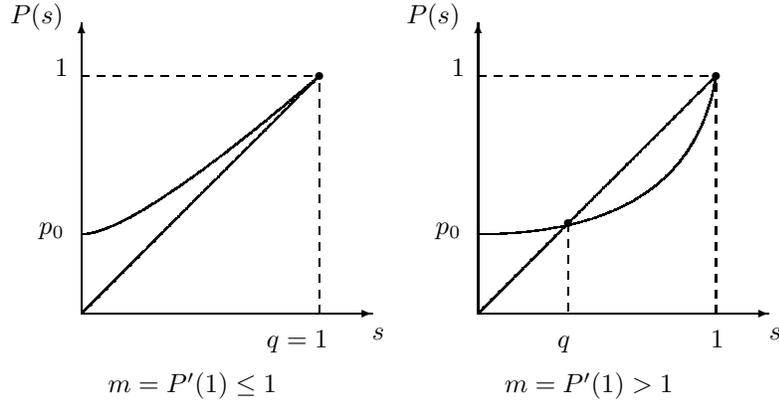


Figure 1.1: The solutions of the fixed point equation $s = P(s)$ in the cases $m \leq 1$ and $m > 1$.

A branching process is called *singular* if each individual generates exactly one and only one direct descendant. We always assume that the branching process $\mathbf{Z}(t)$ is nonsingular. In addition, we suppose that extinction is actually always possible, that is, we assume that there is a path to extinction from each type of individual. We express this as follows.

Assumption 1.2.2. For all $1 \leq i \leq n$, $q_i > 0$.

As a consequence, each state $\mathbf{z} \neq \mathbf{0}$ of the branching process is *transient*, that is, the total number of visits of such states is finite, and we have the following important dichotomy (Harris, [26, Chapter 2, Theorem 6.1]).

Theorem 1.2.3. Under Assumption 1.2.2, a nonsingular branching process $\mathbf{Z}(t)$ either grows to infinity, or goes to $\mathbf{0}$, that is,

$$P\left[\lim_{t \rightarrow \infty} |\mathbf{Z}(t)| = +\infty\right] + P\left[\lim_{t \rightarrow \infty} |\mathbf{Z}(t)| = 0\right] = 1.$$

It does not remain positive and bounded. □

Remark 1.2.4. The dichotomy $\mathbf{q} = \mathbf{1}$ or $\mathbf{q} < \mathbf{1}$ in Theorem 1.2.1 does not require the process to be positive regular; actually, it holds for any irreducible branching process.

Indeed, suppose that the process is irreducible and that there is one type j such that $q_j < 1$. By Theorem 1.2.3, it means that $1 - q_j = P[\lim_{t \rightarrow \infty} |\mathbf{Z}(t)| = +\infty \mid \mathbf{Z}(0) = \mathbf{e}_j] > 0$. Let T_j denote the first instant such that $Z_j(t) \geq 1$. For any $i \neq j$, we have

$$\begin{aligned} 1 - q_i &= P\left[\lim_{t \rightarrow \infty} |\mathbf{Z}(t)| = +\infty \mid \mathbf{Z}(0) = \mathbf{e}_i\right] \\ &\geq P[T_j < \infty \text{ and } \lim_{t \rightarrow \infty} |\mathbf{Z}(t)| = +\infty \mid \mathbf{Z}(0) = \mathbf{e}_i] \\ &= P[T_j < \infty \mid \mathbf{Z}(0) = \mathbf{e}_i] P\left[\lim_{t \rightarrow \infty} |\mathbf{Z}(t)| = +\infty \mid \mathbf{Z}(0) = \mathbf{e}_j\right], \end{aligned}$$

by the strong Markov property. Since the process is irreducible, $P[T_j < \infty | \mathbf{Z}(0) = \mathbf{e}_i] > 0$, thus $1 - q_i > 0$ and $q_i < 1$.

By contrast, in the supercritical *reducible* case, some (but not all) components of the extinction probability vector may be equal to one. This is discussed in Chapter 4.

We end the section with the following result which asserts that the extinction probability vector \mathbf{q} may be obtained by applying the functional iteration on the extinction equation (1.3) (Harris [26, Chapter 2, Theorem 7.2]). Let $\mathbf{P}^{(1)}(\mathbf{s}) = \mathbf{P}(\mathbf{s})$, and $\mathbf{P}^{(k)}(\mathbf{s}) = \mathbf{P}(\mathbf{P}^{(k-1)}(\mathbf{s}))$, for $k \geq 2$.

Theorem 1.2.5. *If $\mathbf{0} \leq \mathbf{a} < \mathbf{1}$, then $\lim_{k \rightarrow \infty} \mathbf{P}^{(k)}(\mathbf{a}) = \mathbf{q}$. This still holds if $\mathbf{a} \leq \mathbf{1}$, $\mathbf{a} \neq \mathbf{1}$ in the irreducible case. \square*

This property is exploited in depth in Chapter 2 from a probabilistic point of view.

1.3 Transient Markovian arrival processes

A transient Markovian arrival process (MAP) is a two-dimensional continuous-time Markovian process $\{(M(t), \phi(t)) : t \in \mathbb{R}^+\}$ on the states space $\mathbb{N} \times \{0, 1, \dots, n\}$, where $n \in \mathbb{N}_0$ is finite. The process $\phi(t)$ is called the *phase* process; transitions between phases may be *hidden* or *observable*, and $M(t)$ counts the number of observable transitions up to time t . The phase 0 is absorbing so that, if $\phi(t) = 0$ for some t , then there are no more transitions of any kind; the phases 1 to n are all transient, so that the MAP eventually stops by getting absorbed after a finite number of transitions.

A MAP with n transient phases is characterized by two $n \times n$ transition rates matrices D_0 and D_1 , respectively for hidden and for observable phase transitions among the transient phases, and an $n \times 1$ vector \mathbf{d} of transition rates to the absorbing phase 0. The matrix D_1 and the vector \mathbf{d} are nonnegative, D_0 has strictly negative elements on the diagonal and nonnegative off-diagonal elements, and they are such that $D_0 \mathbf{1} + D_1 \mathbf{1} + \mathbf{d} = \mathbf{0}$. One also needs an $1 \times n$ initial probability vector $\boldsymbol{\alpha} = [\alpha_1, \dots, \alpha_n]$, and we assume that $\phi(0) \neq 0$, or equivalently that $\boldsymbol{\alpha} \mathbf{1} = 1$, which implies that the time until absorption of a transient MAP is strictly positive. See Figure 1.2 for an example of a MAP path.

Let us assume that the current state is (k, i) , $k \geq 0$, $1 \leq i \leq n$. The process remains in this state during an exponentially distributed time interval with parameter $(-D_0)_{ii}$. At the next transition, independently of k ,

- with probability $(D_0)_{ij} / (-D_0)_{ii}$, $i \neq j$, there is a hidden transition and the new state becomes (k, j) ,
- with probability $(D_1)_{ij} / (-D_0)_{ii}$, an observable transition takes place and the new state of the system becomes $(k + 1, j)$, and finally,
- with probability $d_i / (-D_0)_{ii}$, the process terminates by getting absorbed in the final state $(k, 0)$.

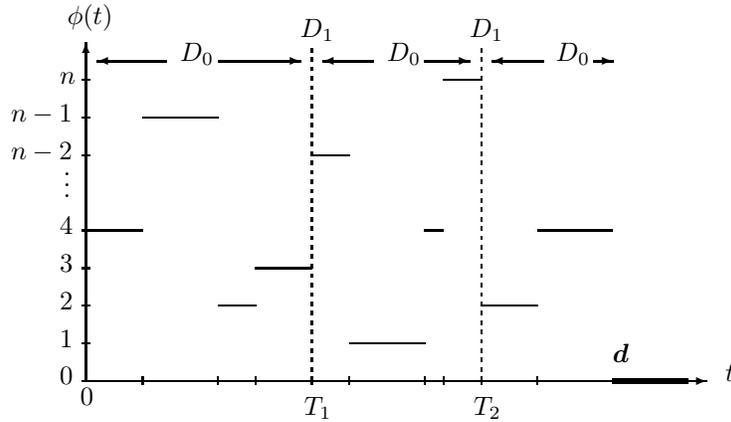


Figure 1.2: An example of evolution of a transient MAP. There are seven hidden transitions and two observable transitions (at T_1 and T_2) before the MAP enters its absorbing phase.

We shall need later the probability that the MAP gets absorbed before the occurrence of a first observable event. Given the process starts in phase i , this probability is given by

$$\theta_i = \sum_j (-D_0^{-1})_{ij} d_j.$$

We gather the probabilities θ_i in a vector $\boldsymbol{\theta} = (-D_0)^{-1} \mathbf{d}$. Note that $(-D_0^{-1})_{ij}$ may be interpreted as the mean sojourn time in phase j , starting in phase i , before the first observable event or the absorption of the MAP.

Special cases

The simplest case of transient MAP is the transient *Poisson process*, in which there is only one transient phase. Consequently, only observable transitions may occur, at rate λ , and the process may eventually stop at rate μ . We thus have $D_0 = -\lambda - \mu$, $D_1 = \lambda$, and $d = \mu$.

Before discussing another special case of transient MAP, let us introduce the *phase-type* distribution (Latouche and Ramaswami [47, Chapter 2]).

Definition 1.3.1. Consider a Markovian process on n transient states and one absorbing state 0^* , with initial probability vector $[\tau_0, \boldsymbol{\tau}]$ and infinitesimal generator

$$Q = \begin{bmatrix} 0 & 0 \\ \boldsymbol{t} & T \end{bmatrix},$$

where $\boldsymbol{\tau}$ is $1 \times n$, T is $n \times n$ and \boldsymbol{t} is $n \times 1$.

The distribution of the time X until absorption into the absorbing state 0^* is called a phase-type distribution with representation $(\boldsymbol{\tau}, T)$. We write that X is $\text{PH}(\boldsymbol{\tau}, T)$.

The class of phase-type distributions is dense in the class of positive-valued distributions [47, Chapter 2].

A second special case of transient MAP is the transient *phase-type renewal process*. In such a process, there is one additional absorbing phase 0^* , and the time intervals between the observable events are phase-type $\text{PH}(\boldsymbol{\tau}, T)$ distributed.

The process starts at time 0 with the initial distribution $\boldsymbol{\alpha}$, and evolves among the transient phases with transition rates given by the matrix T . At the time of a renewal, which corresponds to an observable transition, the process attempts to enter the phase 0^* , with the rates given by the vector $\boldsymbol{t} = -T\mathbf{1}$. Then, it instantaneously enters a new phase given by the initial probability vector $\boldsymbol{\tau}$, and evolves until its next transition to 0^* , which corresponds to the next renewal. The process ends when it enters the absorbing phase 0, at the rates given by the vector \boldsymbol{d} .

The phase-type renewal process is thus a particular MAP where $D_0 = T$, $D_1 = \boldsymbol{t} \cdot \boldsymbol{\tau}$, and where the time intervals between observable events are independent.

A MAP can be used to approximate any counting process, in the same way as a phase-type distribution can be used to approximate any positive valued distribution (Asmussen and Koole [4]). That makes the MAP a very versatile modeling tool. We refer the reader to Latouche, Remiche and Taylor [48] for further details on the features of a transient MAP.

In this thesis, the transient MAP is a tool to represent the lifetime of an individual. In the next section, we illustrate the theory related to transient MAPs on an example in human demography, and in Section 1.5, we define the Markovian tree with the help of the transient MAP. Finally, in Chapter 8, an irreducible MAP also allows us to describe an external process of catastrophes.

1.4 Application in demography

We use the transient MAP to model the lifetime of a woman and her reproduction epochs. The transient phases of the MAP then correspond to the successive age classes of the woman, and the observable events correspond to the times she gives birth to a daughter.

We consider the births of daughters only, at the exclusion of boys. Indeed, our final objective is to model female families with Markovian binary trees, which are asexual processes. We chose women since available fertility rates are those of women.

We studied female populations of about twenty countries¹, but we decide to present here the nine countries which were the most representative of the features we observed. The data have been obtained from two United Nations websites [71, 74]. They consist in *age-specific* fertility and mortality rates, and the *sex-ratio* at birth, denoted by S_r , for the nine countries in Table 1.1. We give later the exact definitions of these quantities, taken from the United Nation Glossary [71].

¹The twenty countries are Afghanistan, Australia, Belgium, Brazil, Canada, China, Democratic Republic of Congo, Denmark, France, Germany, Greece, India, Italy, Japan, Morocco, New-Zealand, Poland, South Africa, Sweden, Turkey, United Kingdom, and USA.

Country	V_1	Country	V_1	Country	V_1
Congo	45.8	Brazil	71.6	USA	78.8
South Africa	51.5	Morocco	73.3	Belgium	80.5
China	71.5	Turkey	74.1	Japan	84.8

Table 1.2: Life expectancies at birth

used the values given in Table 1.1, coming from the United Nations website [71].

We used in the following way the data from [71, 74]:

- the age-specific fertility rates are defined as the number of living births during the calendar year, per 1000 women in the same age-class at mid-year. We divide these numbers by 1000, and by $S_r + 1$, to obtain the vector γ of fertility rate per woman, as a function of her age class, taking daughters into account only.
- the age-specific mortality rates are given as the ratio of the number of deaths during the year of persons in the i th age class to the population in the same age class at mid-year. This ratio corresponds to the death rate d_i ($1 \leq i \leq 22$).

We now use the features of the MAP to answer some relevant questions about the lifetime of a woman and her direct female progeny. Afterwards, we propose two ways to improve the accuracy of the model by increasing the number of phases.

Life expectancy

The life expectancy \mathbf{V} of a woman, given her age class, is the conditional mean time until absorption of the associated transient MAP. It is equally the mean of a phase-type distribution $\text{PH}(\boldsymbol{\alpha}, D)$, where $D = D_0 + D_1$ [48], and is given by

$$\mathbf{V} = (-D)^{-1} \mathbf{1}.$$

The first component V_1 is the life expectancy of a woman at birth, and is given in Table 1.2 for the nine countries under study.

The whole vector \mathbf{V} is plotted on Figure 1.3 for six countries (the other three countries show a behaviour similar to one of the six countries, and are thus not represented). The curves must be read as follows: we perform a linear interpolation between the points (x_i, V_i) , where x_i is the middle of the interval corresponding to the i th age class; for instance, V_3 is the survival expectancy in the age class 5 – 9, its value is plotted just above the abscissa 7.

We clearly see the infant mortality effect, especially for Congo for which the life expectancy at birth is lower than in the age class 1 – 4 and is still growing five years later. We also remark that most of the curves decrease quite linearly, while it is less the case for Congo, due to the high mortality.

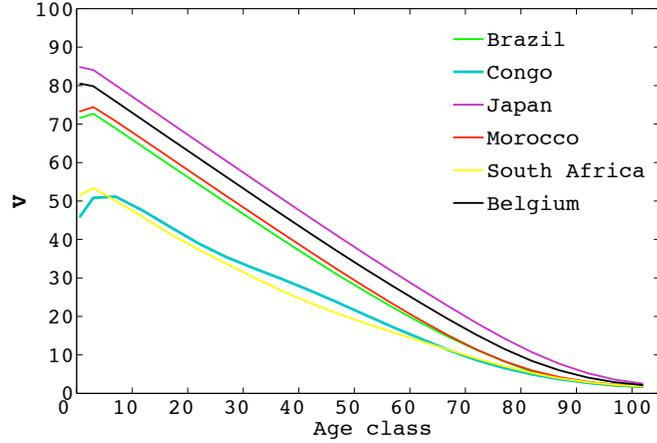


Figure 1.3: Life expectancy of a woman as a function of her age class

Time until the first daughter

Let F denote the time until the birth of a first daughter, this time being almost surely infinite if the mother does not have any daughter.

Let φ_0 be the age class index of the woman at time 0. The conditional expectation $E[F|\varphi_0 = i]$ is the mean time until the *next* daughter, since a woman in the i th age class at time 0 might already have had daughters before time 0. As this conditional expectation is infinite, we shall rather compute $E[F \cdot \mathbf{1}_{\{F < \infty\}} | \varphi_0 = i]$. This corresponds to the mean time until the first observable event in the transient MAP, given it started in phase i .

Recall that $\mathbf{1} - \boldsymbol{\theta} = (-D_0)^{-1} D_1 \mathbf{1}$ is the conditional probability that a first observable event occurs in the MAP before it gets absorbed, given its initial phase. We have

$$\begin{aligned}
 E[F \cdot \mathbf{1}_{\{F < \infty\}} | \varphi_0 = i] &= \int_0^\infty x [e^{D_0 x} D_1 \mathbf{1}]_i dx \\
 &= \int_0^\infty [e^{D_0 x} (\mathbf{1} - \boldsymbol{\theta})]_i dx \\
 &= [(-D_0)^{-1} (\mathbf{1} - \boldsymbol{\theta})]_i.
 \end{aligned} \tag{1.4}$$

To obtain the expectation of F , *given* there is at least one daughter, we have to divide the right-hand side of (1.4) by the probability $1 - \theta_i$ that a woman taken in the i th age class will have at least one daughter

$$\mathcal{F}_i = E[F | F < \infty, \varphi_0 = i] = \frac{[(-D_0)^{-1} (\mathbf{1} - \boldsymbol{\theta})]_i}{1 - \theta_i}.$$

We give in Table 1.3 the conditional mean time until the first daughter of a newborn woman, that is \mathcal{F}_1 , and the probability $1 - \theta_1$ that this woman has at least one daughter, for the nine countries.

Country	\mathcal{F}_1	$1 - \theta_1$	Country	\mathcal{F}_1	$1 - \theta_1$	Country	\mathcal{F}_1	$1 - \theta_1$
Congo	20.7	0.69	Turkey	25.9	0.59	Morocco	28.2	0.62
Brazil	24.5	0.61	China	26.4	0.48	Belgium	28.6	0.51
South Africa	25	0.58	USA	26.4	0.59	Japan	30.2	0.43

Table 1.3: Conditional mean time until the first daughter of a new-born woman, and the probability that there is a first daughter.

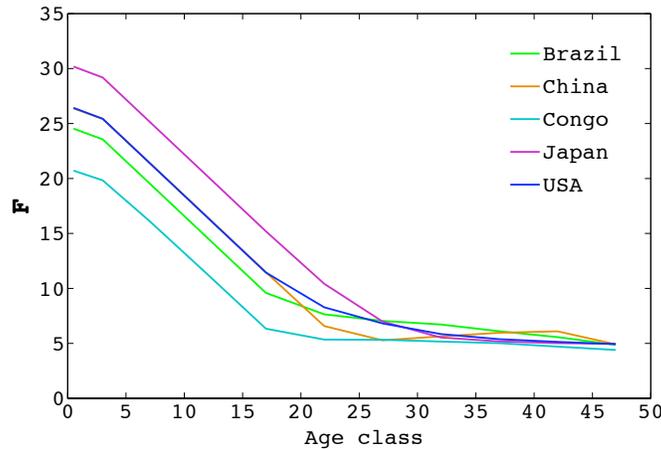


Figure 1.4: Mean time until the first daughter of a woman as a function of her age class, given there is one.

We depict on Figure 1.4 the \mathcal{F}_i 's for $1 \leq i \leq 11$, which shows the evolution of the conditional mean time until the first daughter as a function of the age class of the mother. Generally, we see that until the age class 15 – 19, the curves are decreasing linearly, after what the behaviour of each country becomes more specific. We also notice an atypical increase in the curve for China after the age class 25 – 29.

We cannot compute \mathcal{F}_i for $i \geq 12$, since the corresponding fertility rate γ_i is zero, that is, women do not have daughters beyond the age class 50 – 54.

Remark 1.4.1. On Figure 1.4, \mathcal{F}_i does not tend to zero as i increases, as we might have expected, but seems to tend to five, which is the length of the age intervals. This is due to the memorylessness property of the exponential distribution.

Indeed, assume that a woman is in the last fertile age class (45 – 50), and consider the time until her next daughter, *given that there is one*; this birth must happen *in* this age class and *before* her death. We are thus led to compute the mean of the minimum of three exponential random variables corresponding respectively to the time before moving to the following age class, before giving birth, and before dying, given that birth is the first event to occur. A property of the exponential distribution is that the

mean of the minimum is independent of which of the events occurs first, and is thus equal to the inverse of the sum of the three parameters of the exponential distributions. Here, the three parameters are the fertility rate in the last fertile age class, the death rate in this class, and the transition rate to the next age class which is 0.2. The two first rates being almost negligible with respect to 0.2, the mean time until the first event in the last fertile age class approximatively equals 5.

We will see later how we may improve the model with this respect.

Time until the last daughter

The lifetime L of a transient MAP is defined as the time until the last observable event [48]. If the MAP gets absorbed before a first observable event, then $L = 0$.

In our demographic application, L then represents the time until the last daughter. Assume the woman is in phase i at initial time. If she dies before giving birth, which occurs with probability θ_i , then $L = 0$. For $x > 0$, the event $[L > x]$ occurs if at time x the woman is in one of the transient phases, with distribution given by e^{Dx} , and a birth event occurs in the future with probability $\mathbf{1} - \boldsymbol{\theta}$. We thus get

$$\mathbb{P}[L > x \mid \varphi_0 = i] = [e^{Dx} (\mathbf{1} - \boldsymbol{\theta})]_i,$$

and the mean $\mathbb{E}[L \mid \varphi_0 = i]$ is given by

$$\mathbb{E}[L \mid \varphi_0 = i] = [(-D)^{-1} (\mathbf{1} - \boldsymbol{\theta})]_i.$$

The vector $(-D)^{-1} (\mathbf{1} - \boldsymbol{\theta})$ is thus the mean time until the last daughter of a woman, as a function of her age class.

In order to make comparisons with the conditional mean time until the first daughter, given there is one, we compute

$$\mathcal{L}_i = \mathbb{E}[L \mid L > 0, \varphi_0 = i] = \frac{\mathbb{E}[L \mid \varphi_0 = i]}{\mathbb{P}[L > 0, \mid \varphi_0 = i]} = \frac{[(-D)^{-1} (\mathbf{1} - \boldsymbol{\theta})]_i}{1 - \theta_i},$$

for $1 \leq i \leq 11$.

We provide in Table 1.4 the conditional mean time until the last daughter of a new-born woman, that is \mathcal{L}_1 . Note the large gap $\mathcal{F}_1 - \mathcal{L}_1$ between the conditional mean time until the first and the last daughters in Congo, compared to other countries.

Country	\mathcal{L}_1	Country	\mathcal{L}_1	Country	\mathcal{L}_1
China	29.8	Turkey	31.2	Japan	33.3
Brazil	30.7	USA	31.7	Congo	33.4
South Africa	31.2	Belgium	32.5	Morocco	34.5

Table 1.4: Conditional mean time until the last daughter of a new-born woman, given there is one

Let us now look at the distribution of the time T between the first and the last births, given there is at least one birth. By conditioning on the time at which the first daughter is born, we get

$$\begin{aligned} \mathbb{P}[T \leq x, L > 0 \mid \varphi_0 = i] &= \int_0^\infty \sum_j (\exp(D_0 u) D_1)_{ij} \mathbb{P}[L \leq x \mid \varphi_0 = j] du \\ &= \sum_j [(-D_0)^{-1} D_1]_{ij} [\mathbf{1} - \exp(Dx)(\mathbf{1} - \boldsymbol{\theta})]_j, \end{aligned}$$

and

$$\mathcal{G}_i(x) = \mathbb{P}[T \leq x \mid L > 0, \varphi_0 = i] = 1 - \frac{[(-D_0)^{-1} D_1 \exp(Dx)(\mathbf{1} - \boldsymbol{\theta})]_i}{1 - \theta_i},$$

for $1 \leq i \leq 11$. This distribution is shown on Figure 1.5 for $i = 1$.

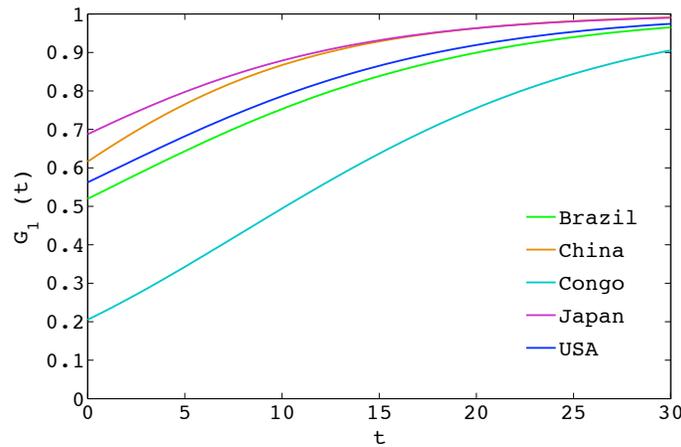


Figure 1.5: Distribution of the time between the first and the last daughters of a new-born woman, given she has at least one daughter

Remark 1.4.2. $\mathcal{G}_1(0)$ is the probability for a woman to have only one daughter, given that she has at least one; observe that this probability is lower than one might expect, especially in countries where the parental control is high. One reason is that the fertility rates we use are *global rates*, and do not take previous births into account. However, for most of the countries, there is a dependence between the fertility rate of a woman and the fact that she already had a daughter or not in the past.

The appropriate fertility rates data, taking previous births into account, are available for some countries like Belgium (Belgian National institute of Statistics [65]). We would be able to adapt our model for these by adding some phases to keep track of the number of previous births.

In like manner, if a parental control limits the number of children to one for instance, then we might also adapt our model by adding new phases in which the mother would

enter just after the birth of her first daughter, and for which the fertility rate would be close to zero, and the death rate would be kept the same.

Number of daughters

The number of future daughters of a woman corresponds to the total number of observable events of a transient MAP, which has the discrete phase-type distribution $\text{PH}(\alpha F, F)$ with $F = (-D_0)^{-1} D_1$ [48]. Thus, the vector \mathbf{K} of conditional mean, given the initial phase, is given by

$$\mathbf{K} = F(I - F)^{-1} \mathbf{1}.$$

We give in Table 1.5 the mean number K_1 of daughters to a new-born woman, and we plot the other nonzero entries of \mathbf{K} on Figure 1.6 for five countries. We see that until age 15, the mean number of future daughters is almost constant, except in Congo where we see the dramatic effect of the youth mortality again. The curves begin to decrease at the ages at which women start having children. That age varies from country to country, as we see when comparing the curves for Brazil and Japan.

Country	K_1	Country	K_1	Country	K_1
Japan	0.61	USA	0.98	Brazil	1.09
China	0.75	Turkey	1.00	Morocco	1.10
Belgium	0.79	South Africa	1.05	Congo	2.28

Table 1.5: Mean number of future daughters of a new-born woman

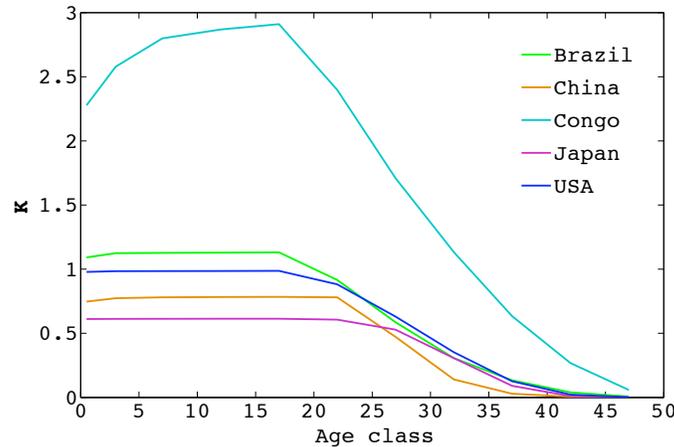


Figure 1.6: Mean number of future daughters of a woman as a function of her age class

Smoothing the data

We might improve the precision of the results by reducing the length of the age classes from five to one year. This would lead to 101 age classes instead of 22. However, as said previously, the United Nations websites [71, 74] do not provide sufficiently detailed age-specific fertility and mortality rates. A solution would be to interpolate the available data, and we have compared three different approaches.

The first idea consists in keeping the fertility and death rates constant over five years age intervals. But this can sometimes lead to quite big gaps between the rates of two consecutive ages. Anyway, it would be a quite gross interpolation of the data.

Our second idea is to make a continuous piecewise-linear interpolation which preserves the average rate over five years intervals. But we quickly get confronted to meaningless negative rates.

Finally, we decided to make a *non-continuous* piecewise-linear interpolation of the rates which preserves the average rate over five years intervals, while minimizing the discontinuities at the interval boundaries.

We denote by a_i and b_i , $i = 1, 2, \dots, 21$, the left and right fertility rates values at the boundaries of an age class interval, as represented on Figure 1.7 for the age class 20 – 25 (corresponding to the mean fertility rate γ_6).

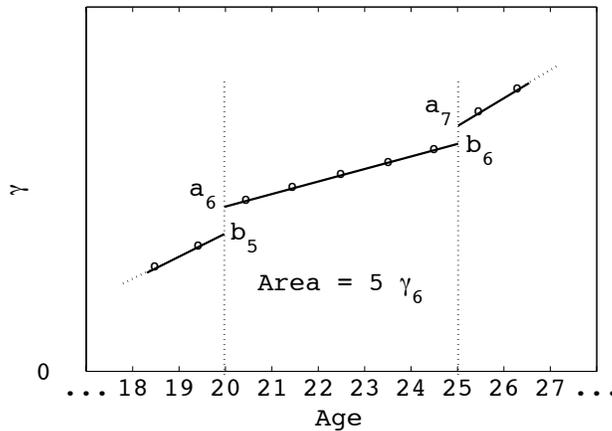


Figure 1.7: Non-continuous piecewise-linear interpolation used to obtain the fertility (and death) rates at each age

These parameters must satisfy the constraints

$$\frac{a_i + b_i}{2} = \gamma_i \quad a_i, b_i \geq 0 \quad i = 1, 2, \dots, 21.$$

In order to minimize the global discontinuity of the interpolation, we chose to look for

values a_i and b_i which minimize the function $\sum_{i=2}^{21}(a_i - b_{i-1})^2$. It is easy to numerically solve this constrained linear problem, using for instance the solver `fmincon` in MATLAB.

With the optimal values a_i and b_i , we linearly interpolate the fertility rates for each one year age interval. We proceed similarly for the death rates. We will call this second model the *smooth* model, in contrast with the previous model with $n = 22$ age classes which can be qualified as the *raw* model.

We show on the two graphs on the top of Figure 1.8 the discontinuity points a_i and b_i obtained for fertility (left) and death (right) rates in Belgium, and on the bottom, the non-continuous piecewise-constant and piecewise-linear interpolations of the data.

As mentioned above, for Belgium, it is actually possible to find data for age-specific fertility rates at one year intervals in 1997, and death rates in 2006 [65], so that we have been able to validate our interpolation by comparing it to the real values; the comparison is shown on Figure 1.9. The L^∞ -norm of the difference between the interpolation curve and the real curve, divided by the L^∞ -norm of the real curve, is equal to 0.1158 for the fertility rates and 0.0719 for the death rates.

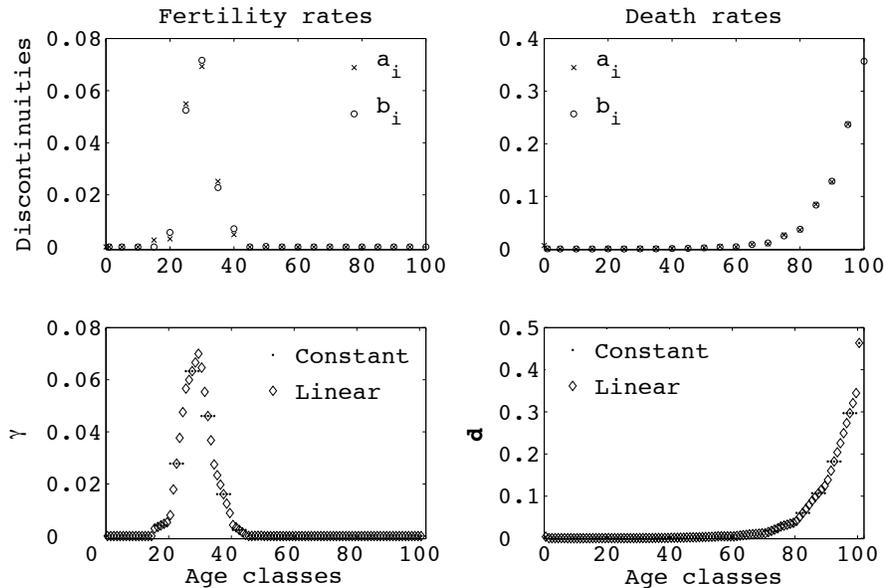


Figure 1.8: Top: the left and right discontinuity points a_i and b_i for the interpolation of fertility and death rates in Belgium. Bottom: piecewise-constant and piecewise-linear interpolations.

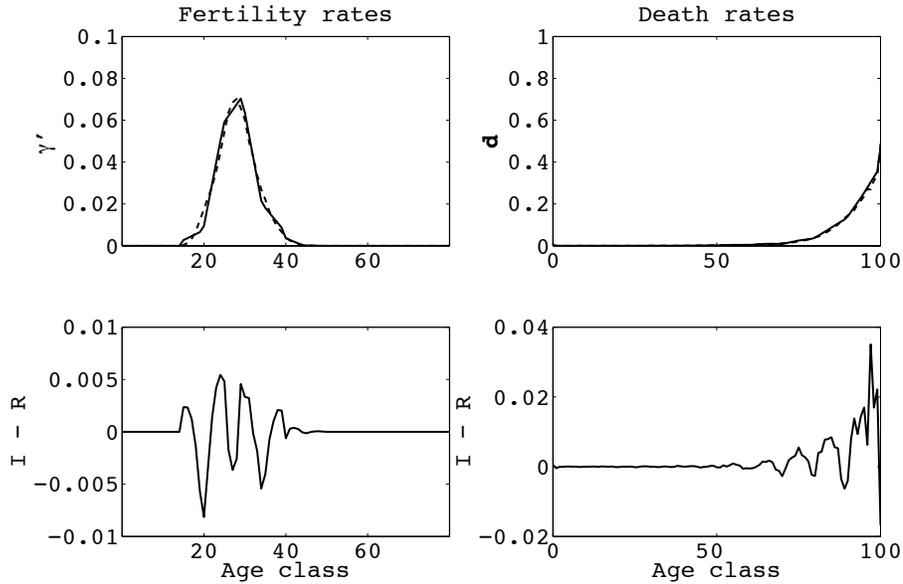


Figure 1.9: Top: comparison between de interpolation curve (plain line) and the real curve (dashed line) of the fertility and death rates in Belgium. Bottom: the difference $I - R$ between the values obtained by interpolation (I) and the real data (R).

After-birth gap periods

We can further improve the accuracy of the model by adding some new phases corresponding to a gap period of about one year after the birth of a child, during which a mother does not have any new child. This gap period corresponds, for instance, to the breast-feeding period.

We define new phases so that if a mother has a daughter when she is in phase i , then she moves to an intermediate phase i' in which the fertility rate is equal to zero and the death rate is the same as in phase i . We may also take births of sons into account: if a mother has a son when she is in phase i , which happens at the rate $\gamma_i \cdot S_r$, then, we do not consider it as a real birth event, but rather as a phase change toward the intermediate phase i' .

In the previous model with 101 phases there are 35 phases with a nonzero fertility rate (phases 16 to 50). Therefore, we need 35 intermediate phases, and the total number of phases becomes 136. The whole set of phases is now

$$\mathcal{S} = \{1, 2, \dots, 15, 16, 16', 17, 17', \dots, 50, 50', 51, 52, \dots, 101\}.$$

The matrix D_0 becomes such that

$$\begin{aligned} D_0(i, i+1) &= 1 & \text{for } i &= 1, 2, \dots, 101, \\ D_0(i, i') &= \gamma_i \cdot S_r & \text{for } i &= 16, 17, \dots, 50, \\ D_0(i', i+1) &= 1 & \text{for } i &= 16, 17, \dots, 50, \end{aligned}$$

and the other non-diagonal entries remain zero. The matrix D_1 is now such that $D_1(i, i') = \gamma_i$, the other entries being zero. Finally, the vector \mathbf{d} is such that $d_{i'} = d_i$ for each intermediate phase i' . This model will be called the *gap* model.

In comparing the raw and the smooth models, we observe that the improvement is sometimes not really noticeable. For instance, we compare on Figure 1.10 the survival expectancy \mathbf{V} of a Belgian woman, as a function of her age class, and we do not see any significant difference.

We also compare the conditional mean time until the first daughter \mathcal{F} . The curve of the smooth model now converges to 1, instead of 5 for the raw model, which is an improvement, as discussed in Remark 1.4.1. We plot the curve corresponding to *real data* for one year age classes taken from [65]. We see that the curve of the smooth model is close to the real one, except from the age 44; this is due to the fact that some small inaccuracies in the computation of the piecewise-linear interpolation are amplified when dividing by the very small probability of having a daughter after that age.

Finally, we compare in Table 1.6 the mean total number of daughters of a Belgian woman for the three models. We observe that with the smooth model, the total fertility of a woman is a bit higher than with the raw model, while it remarkably decreases when taking gap periods into account.

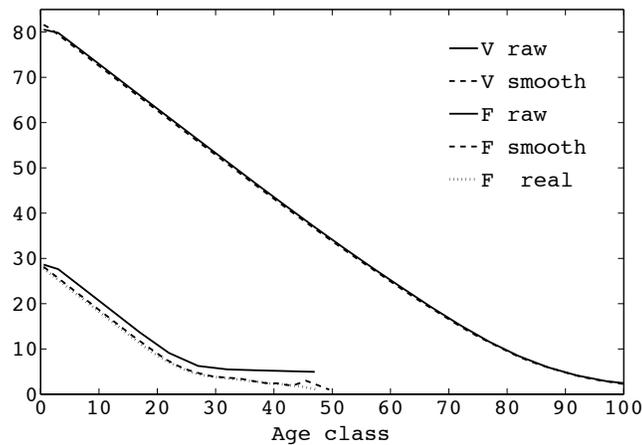


Figure 1.10: Comparison of the survival expectancy \mathbf{V} with the raw and the smooth models (upper curves), and of the mean time until the first daughter, given there is one \mathcal{F} , with these two models and with the real data (lower curves), for Belgium.

Model	n	K_1
Raw	22	0.789
Smooth	101	0.79
Gap	136	0.721

Table 1.6: Mean total number of daughters of a new-born woman in Belgium

Concluding remarks

Remark 1.4.3. Our interpolation method is not satisfactory when the changes in birth or death rates from one five years class to the next one are too big, as in the example of Congo, which leads to jagged curves for the interpolated rates. This is a reason why, in the rest of the thesis, we mostly use the raw model. We will however discuss the differences between the various models when it is notable.

Remark 1.4.4. The values we obtained for the survival expectancy and the mean number of daughters of a woman are roughly the same as those provided by [71, 74], our results being in general slightly smaller than the reality.

Despite the shortcomings of our model, the MAP representation allows us to emphasize general tendencies about the lifetime of a woman and her feminine progeny, and to make interesting comparisons between different countries.

1.5 Markovian trees

A general Markovian tree (GMT) describes the evolution over time of a random collection of independent individuals with the same characteristics. We start at time 0 with one individual whose lifetime is controlled by a transient MAP with characteristics α , D_0 , D_1 , and d . To each observable transition corresponds the birth of a random number of children. After the birth of the children, the parent MAP continues to evolve, possibly giving birth again, until it eventually dies when it makes a transition to its absorbing phase. Upon a birth, each child's lifetime is controlled by an independent replica of the parental MAP. The hidden transitions correspond to state changes in the lifetime of the individual, associated with birth and death rates changes.

In the particular case where birth events are restricted to exactly one child, we use the name Markovian *binary* tree (MBT) to describe the process. In this thesis, most of the results are developed in the particular case of the MBT only, for the sake of clarity. Usually, these results may be naturally generalized to the GMT case, and we provide details whenever the difference is notable enough.

When the MAP controlling the lifetime of the individuals is a Poisson process, we talk about *exponential GMT* or *MBT*, and in the case it is a phase-type renewal process, we talk about *phase-type GMT* or *MBT*.

Figure 1.11 depicts an example of an MBT path. The thick line represents the lifetime of the first individual. Births are represented by the *branching points* of the tree. Deaths are represented by the *leaves* of the tree. In addition, we use the following

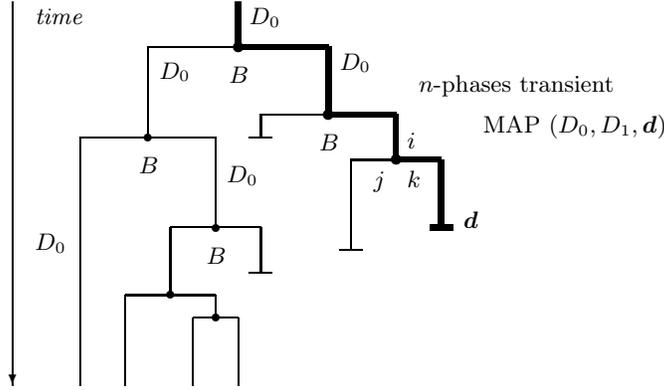


Figure 1.11: An example of evolution of a MBT

terminology: an *arc* of the tree is an edge connecting two branching points, or a branching point and a leaf; by convention, after a branching point, the left arc is the *child arc* and the right arc is the *parental arc*. Hidden transitions are not shown.

At the time of a birth of $m \geq 1$ new individuals, the parental individual in phase i may make a transition to phase k , and initial phases j_1, j_2, \dots, j_m are chosen for the children MAPs ($1 \leq i, j_1, j_2, \dots, j_m, k \leq n$). This occurs at the rate

$$(B_m)_{i, j_1 j_2 \dots j_m k} = (D_1)_{ik} P_{j_1 j_2 \dots j_m | ik},$$

where $P_{j_1 j_2 \dots j_m | ik}$ is the conditional probability that the m children start their life in phases j_1, j_2, \dots, j_m respectively, given that their parent made a transition from phase i to phase k at the birth time.

In the particular case of an MBT, we use the notation B instead of B_1 , and $B_{i,jk} = (D_1)_{ik} P_{j|ik}$ is the rate at which an individual in phase i gives birth to a child in phase j , and makes a transition to phase k after the birth.

The $n \times n^{m+1}$ matrices B_m ($m \geq 1$) are called the *birth rates* matrices. We use the lexicographic order to enumerate their column entries. So, for instance in the case of an MBT with $n = 3$ phases, the birth rates matrix has the following structure

$$B = \left[\begin{array}{ccc|ccc|ccc} B_{1,11} & B_{1,12} & B_{1,13} & B_{1,21} & B_{1,22} & B_{1,23} & B_{1,31} & B_{1,32} & B_{1,33} \\ B_{2,11} & B_{2,12} & B_{2,13} & B_{2,21} & B_{2,22} & B_{2,23} & B_{2,31} & B_{2,32} & B_{2,33} \\ B_{3,11} & B_{3,12} & B_{3,13} & B_{3,21} & B_{3,22} & B_{3,23} & B_{3,31} & B_{3,32} & B_{3,33} \end{array} \right].$$

Examples of birth rates matrices

At this stage, we need to define the *Kronecker product* between two matrices.

Definition 1.5.1. *If A is an $m \times n$ matrix and B is a $p \times q$ matrix, then the Kronecker*

product $A \otimes B$ is the $mp \times nq$ block matrix defined by

$$A \otimes B = \begin{bmatrix} A_{11} B & \cdots & A_{1n} B \\ \vdots & \ddots & \vdots \\ A_{m1} B & \cdots & A_{mn} B \end{bmatrix}.$$

One property of the Kronecker product that we will routinely use is

$$(AC \otimes BD) = (A \otimes B)(C \otimes D). \quad (1.5)$$

If all the children independently start with the same initial distribution α , then

$$P_{j_1 j_2 \dots j_m | ik} = \alpha_{j_1} \alpha_{j_2} \cdots \alpha_{j_m},$$

independently of i and k , and the birth rates matrices take the special form $B_m = \alpha^{(m)} \otimes D_1$, where $\alpha^{(m)}$ is the m th-fold Kronecker product of α with itself: $\alpha^{(0)} = 1$, and $\alpha^{(m)} = \alpha^{(m-1)} \otimes \alpha$, for $m \geq 1$.

If in addition we deal with a phase-type GMT, then recall that $D_1 = \mathbf{t} \cdot \boldsymbol{\tau}$, where the vector \mathbf{t} gives the rates of a renewal (birth), and $\boldsymbol{\tau}$ is the initial probability vector of the parent after a birth. We thus have $B_m = \mathbf{t} \cdot (\alpha^{(m)} \otimes \boldsymbol{\tau})$.

Example 1.5.2 (Women populations). This particular structure of birth rates matrix appears in the demographic application described in Section 1.4. Recall that we represent the lifetime of a woman with a transient MAP of which the observable events correspond to births of daughters.

We suppose that a woman gives birth to *one* daughter at a time, which is a fair assumption since multiple human births represent three percent of the total births only [13]. Each daughter starts her life in the first age class, that is, in phase 1. The initial probability vector α is then given by $\alpha = [1, \mathbf{0}]$.

Therefore, we model the whole female family generated by a woman by an MBT with birth rates matrix $B = \alpha \otimes \text{diag}(\boldsymbol{\gamma})$, where $\boldsymbol{\gamma}$ is the fertility rates vector.

We assume that the fertility and mortality rates are constant and identical for all the family members, that the population is not subject to migration phenomena, and that there is no dependence between the individuals who form the families. Throughout the thesis, we illustrate various results on this particular example of MBT.

Sometimes, the initial phase of the children depends on the phase of the parent at the time of birth, so that

$$P_{j_1 j_2 \dots j_m | ik} = (P_1)_{ij_1} \cdots (P_m)_{ij_m}$$

where the matrices P_ℓ ($1 \leq \ell \leq m$) are stochastic matrices giving the conditional probabilities for each child phase. An example will be given in Section 2.4.

In a Markovian tree, recall from the previous section that the lifetime of an individual is phase-type distributed $\text{PH}(\alpha, D)$, where $D = D_0 + D_1$. We may thus approach any age-dependent branching process by suitably choosing the controlling MAP. Moreover, the progeny distribution of an individual may depend on the age of the parent at the birth time, through the birth rates matrices.

One can interpret Markovian trees as multitype branching processes in several ways. We present two interpretations herebelow.

In a first interpretation, we associate the phases 1 to n of the MAP to the n *types* of the branching process. In this view, a GMT corresponds to a Markovian multitype branching process in which an individual of type i lives for an exponentially distributed interval of time, with parameter $\nu_i = (-D_0)_{ii}$. At the end of this interval, it may die without offspring with the probability d_i/ν_i (this corresponds to the MAP entering its absorbing phase), or it may give birth to one individual of type $j \neq i$, with the probability $(D_0)_{ij}/\nu_i$ (this corresponds to a hidden phase change), or it may give birth to $m + 1$ individuals of types j_1, j_2, \dots, j_m , and k , with the probability $(B_m)_{i, j_1 j_2 \dots j_m k}/\nu_i$ (this corresponds to an observable event).

The progeny generating function then takes the matrix form

$$\mathbf{P}^*(\mathbf{s}) = (-\Delta)^{-1} \mathbf{d} + (-\Delta)^{-1} (D_0 - \Delta) \mathbf{s} + (-\Delta)^{-1} \sum_{m \geq 1} B_m \mathbf{s}^{(m+1)}, \quad (1.6)$$

where $\Delta = \text{diag}(D_0)$. The mean progeny matrix, defined by (1.2), is

$$M^* = I + (-\Delta)^{-1} \left[D_0 + \sum_{m \geq 1} B_m \sum_{i=0}^m (\mathbf{1}^{(i)} \otimes I \otimes \mathbf{1}^{(m-i)}) \right]. \quad (1.7)$$

In the MBT case, this simplifies to

$$\mathbf{P}^*(\mathbf{s}) = (-\Delta)^{-1} \mathbf{d} + (-\Delta)^{-1} (D_0 - \Delta) \mathbf{s} + (-\Delta)^{-1} B (\mathbf{s} \otimes \mathbf{s}), \quad (1.8)$$

and

$$M^* = I + (-\Delta)^{-1} [D_0 + B (\mathbf{1} \oplus \mathbf{1})], \quad (1.9)$$

where the symbol \oplus must be understood as $\mathbf{a} \oplus \mathbf{b} = \mathbf{a} \otimes I_n + I_n \otimes \mathbf{b}$ if \mathbf{a} and \mathbf{b} are two $n \times 1$ vectors, and similarly as $A \oplus B = A \otimes I_n + I_n \otimes B$ if A and B are two $n \times n$ matrices.

In a second interpretation, we consider the process embedded at the epochs where an observable transition of the MAP gives rise to a branching point in the tree, or where the MAP ends and leads to a leaf in the tree. An individual of type i may eventually die without offspring, possibly after having undergone various hidden transitions, with probability θ_i , where $\boldsymbol{\theta} = (-D_0)^{-1} \mathbf{d}$ (see Section 1.3). It may eventually give birth to $m + 1$ children of types j_1, j_2, \dots, j_m , and k , with the probability $(\Psi_m)_{i, j_1 j_2 \dots j_m k}$, where $\Psi_m = (-D_0)^{-1} B_m$.

In that view, a GMT corresponds to an age-dependent multitype branching process. The progeny generating function is given by

$$\mathbf{P}(\mathbf{s}) = \boldsymbol{\theta} + \sum_{m \geq 1} \Psi_m \mathbf{s}^{(m+1)}, \quad (1.10)$$

and the mean progeny matrix by

$$M = \sum_{m \geq 1} \Psi_m \sum_{i=0}^m (\mathbf{1}^{(i)} \otimes I \otimes \mathbf{1}^{(m-i)}). \quad (1.11)$$

In the MBT case, $\Psi = \Psi_1$, and we get

$$\mathbf{P}(\mathbf{s}) = \boldsymbol{\theta} + \Psi(\mathbf{s} \otimes \mathbf{s}), \quad (1.12)$$

and

$$\mathbf{M} = \Psi(\mathbf{1} \oplus \mathbf{1}). \quad (1.13)$$

In terms of MBT, the (i, j) th entry of \mathbf{M} gives the mean number of arcs starting in phase j , following an observable event, if we start with a first arc in phase i .

We will say that a GMT (respectively an MBT) is *irreducible* if the mean matrix (1.7) (respectively (1.9)) is irreducible. Notice that this does not necessarily imply that the matrix (1.11) (respectively (1.13)) is irreducible; for instance, suppose that for an MBT, $(D_0)_{ij} > 0$ for all $i \neq j$, and the only nonzero entries of B are $B_{i,11}$. In that case, the mean progeny matrix (1.9) is irreducible while (1.13) is not.

The material of Chapters 2 and 3 is based on the assumption of irreducibility. In Chapter 4 we specifically investigate the reducible case.

1.6 Extinction probability of a Markovian tree

Recall from Section 1.2 that \mathbf{q} denotes the extinction probability of a multitype branching process, given the type of the initial individual. We use the same notation to refer to the extinction probability of a GMT, given the initial phase of the first individual.

Using the interpretations of a GMT as multitype branching processes given in the previous section, together with Theorem 1.2.1, we can check the criticality of a GMT by looking at the spectral radius of one of the mean progeny matrices (1.7) and (1.11).

As a result, in the subcritical and critical cases, the extinction probability of the GMT is $\mathbf{q} = \mathbf{1}$. In the supercritical case, $\mathbf{q} \leq \mathbf{1}$, $\mathbf{q} \neq \mathbf{1}$, and we need to find the minimal nonnegative solution of the extinction equation (1.3) in order to know the exact value of \mathbf{q} .

Using (1.6), the extinction equation (1.3) becomes

$$\begin{aligned} \mathbf{s} &= (-\Delta)^{-1} \mathbf{d} + (-\Delta)^{-1} (D_0 - \Delta) \mathbf{s} + (-\Delta)^{-1} \sum_{m \geq 1} B_m \mathbf{s}^{(m+1)} \\ \Leftrightarrow \mathbf{0} &= \mathbf{d} + D_0 \mathbf{s} + \sum_{m \geq 1} B_m \mathbf{s}^{(m+1)} \\ \Leftrightarrow \mathbf{s} &= \boldsymbol{\theta} + \sum_{m \geq 1} \Psi_m \mathbf{s}^{(m+1)}, \end{aligned} \quad (1.14)$$

with the notations $\boldsymbol{\theta} = (-D_0)^{-1} \mathbf{d}$ and $\Psi_m = (-D_0)^{-1} B_m$ previously introduced. As expected, Equation (1.14) is the same as $\mathbf{s} = \mathbf{P}(\mathbf{s})$ using (1.10).

In the particular case of the MBT, (1.14) takes the simple quadratic form

$$\mathbf{s} = \boldsymbol{\theta} + \Psi(\mathbf{s} \otimes \mathbf{s}). \quad (1.15)$$

Its interpretation is as follows. For an MBT to eventually become extinct, the root must

- either die without branching, which occurs with probability θ ,
- or split in a left and a right branches, which occurs with probabilities given by the matrix Ψ , and the left and right subtrees, evolving independently, must eventually become extinct.

Equation (1.15) is a matrix quadratic equation that can generally not be solved explicitly, except in special cases such as the exponential and the phase-type MBT.

Indeed, in an exponential MBT, $n = 1$, $\mathbf{d} = \mu$, $B = \lambda$ and $D_0 = -\mu - \lambda$. The extinction probability is then trivially computed as $q = 1$ if $\mu \geq \lambda$ and $q = \mu/\lambda$ if $\mu < \lambda$.

In a phase-type MBT, the birth rates matrix takes the form $B = \mathbf{t} \cdot (\boldsymbol{\alpha} \otimes \boldsymbol{\tau})$. The extinction equation (1.15) becomes

$$\mathbf{s} = (-T)^{-1} \mathbf{d} + (-T)^{-1} \mathbf{t} (\boldsymbol{\alpha} \mathbf{s}) (\boldsymbol{\tau} \mathbf{s}). \quad (1.16)$$

By pre-multiplying (1.16) once by $\boldsymbol{\alpha}$ and once by $\boldsymbol{\tau}$, we obtain a system of two scalar equations with two unknowns $\boldsymbol{\alpha} \mathbf{s}$ and $\boldsymbol{\tau} \mathbf{s}$. If we define $k_1 = \boldsymbol{\alpha} (-T)^{-1} \mathbf{d}$ and $k_2 = \boldsymbol{\tau} (-T)^{-1} \mathbf{d}$, then the extinction probability vector \mathbf{q} is easily shown to be $\mathbf{q} = \mathbf{1}$ if $k_1 + k_2 \geq 1$, and

$$\mathbf{q} = (-T)^{-1} \mathbf{d} + (-T)^{-1} \mathbf{t} \frac{k_1 k_2}{k_1 k_2 - k_1 - k_2 + 1}$$

if $k_1 + k_2 < 1$. Note that $\boldsymbol{\alpha} (-T)^{-1} \mathbf{t} = 1 - k_1$, and $\boldsymbol{\tau} (-T)^{-1} \mathbf{t} = 1 - k_2$.

Remark 1.6.1. It is not surprising that the criticality threshold is $k_1 + k_2$ here, since the mean progeny matrix (1.13) takes the special form

$$M^* = (-T)^{-1} \mathbf{t} \cdot (\boldsymbol{\alpha} + \boldsymbol{\tau}),$$

of which the maximal eigenvalue is $\rho = (\boldsymbol{\alpha} + \boldsymbol{\tau}) (-T)^{-1} \mathbf{t} = 2 - (k_1 + k_2)$.

Generally, we need numerical tools in order to compute the minimal nonnegative solution of the extinction equations (1.14) and (1.15). This is the subject of the next two chapters.

CHAPTER 2

Linear functional algorithms

We propose a first approach to numerically compute the probability that a population modelled by a Markovian tree eventually becomes extinct. This approach is based on linear functional iterations applied to the matrix extinction equation.

We first focus on the MBT case. We start by recalling two algorithms developed by Bean, Kontoleon and Taylor [9], named the *Depth* and the *Order* algorithms. Then, we describe a third linear algorithm, called the *Thickneses* algorithm. We emphasize its probabilistic interpretation, which allows us to prove its convergence.

Then, we study the convergence rate of all linear algorithms and we compare their performance on a few numerical examples. Finally, a section is devoted to the generalization of the linear algorithms to the GMT case.

A major part of this chapter is presented in Hautphenne, Latouche and Remiche [28].

2.1 The Depth and the Order algorithms

The Depth algorithm is based on functional iterations applied to (1.15), and proceeds as follows:

$$\ell(0) = \theta, \quad \ell(k) = \theta + \Psi(\ell(k-1) \otimes \ell(k-1)), \quad k \geq 1. \quad (2.1)$$

The *depth* of a tree may be defined as the number of branching points along the longest branch of the tree (see Figure 2.1 for an example, where the label w identifies a leaf at the end of a longest branch). With this, $\ell(k)$ is the probability that the tree eventually becomes extinct with a depth at most equal to k . This shows that the sequence $\ell(k)$ monotonically converges to \mathbf{q} .

Using (1.5), Equation (1.15) may be rewritten as $[I - \Psi(\mathbf{s} \otimes I)] \mathbf{s} = \boldsymbol{\theta}$ or

$$\mathbf{s} = [I - \Psi(\mathbf{s} \otimes I)]^{-1} \boldsymbol{\theta}, \quad (2.2)$$

provided that the inverse matrix in the right-hand side of (2.2) exists. This suggests another iterative algorithm based on functional iterations:

$$\mathbf{s}(0) = \boldsymbol{\theta}, \quad \mathbf{s}(k) = [I - \Psi(\mathbf{s}(k-1) \otimes I)]^{-1} \boldsymbol{\theta}, \quad k \geq 1. \quad (2.3)$$

The approximation $\mathbf{s}(k)$ can be interpreted as the probability that the tree eventually becomes extinct with an *order* at most equal to k . We give a precise definition below but at this point it suffices to write that the order of a tree is the maximal number of children generations. Since a tree which becomes extinct has finite order, it is clear that the sequence (2.3) monotonically converges to \mathbf{q} .

Our definition of the order of a tree is slightly different from that in [9]; it will make it easier to compare the Order algorithm to the Thicknesses algorithm.

In the sequel, we do not make any difference between the MBT process and its representation as a binary tree. Let \mathcal{T} be a given binary tree. We mark with a 1 each child arc and with a 0 each parental arc. If \mathcal{T} is made up of the root and one leaf only, that is if the tree eventually becomes extinct without any branching point, then that unique arc is marked with a 0. Finally, we associate to every node $x \in \mathcal{T}$ (that is, every branching point or leaf) the string of 0's and 1's which mark the shortest path from x to the root and we define $L(x)$ as the number of 1's in this sequence. The order of \mathcal{T} , denoted by $\mathbb{O}(\mathcal{T})$, is defined as

$$\mathbb{O}(\mathcal{T}) = \max \{L(x) : x \in \mathcal{T}\}.$$

For instance, take the leaf w on Figure 2.1. One observes by exhaustive examination of all the nodes, that $\mathbb{O}(\mathcal{T}) = L(w) = 5$.

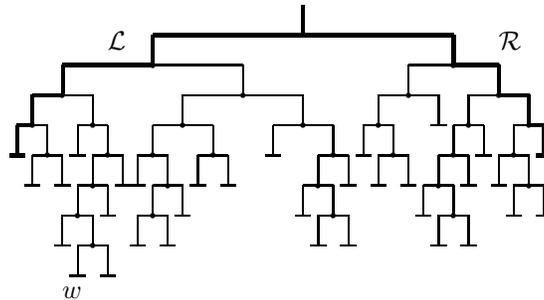


Figure 2.1: A tree with depth 8 (a longest branch leads to w), order 5 (w is a fifth generation child of the first parent), left thickness 5, and right thickness 6.

For later reference, we call the *parental branch* of the tree \mathcal{T} , that branch from the root made up of parental arcs only. It is the rightmost branch of \mathcal{T} and will be denoted by \mathcal{R} . Similarly, we call the *first child branch* of the tree \mathcal{T} , that branch from the root made up of child arcs only. It is the leftmost branch of \mathcal{T} and will be denoted by \mathcal{L} .

Remark 2.1.1. We can actually consider two Order algorithms: instead of (2.2), we may transform (1.15) as

$$\mathbf{s} = [I - \Psi(I \otimes \mathbf{s})]^{-1} \boldsymbol{\theta}. \quad (2.4)$$

This leads to another algorithm which goes as follows

$$\mathbf{s}(0) = \boldsymbol{\theta}, \quad \mathbf{s}(k) = [I - \Psi(I \otimes \mathbf{s}(k-1))]^{-1} \boldsymbol{\theta}, \quad k \geq 1. \quad (2.5)$$

It is completely symmetric to the Order algorithm, and the probabilistic interpretation is easily adapted: one merely counts 0's instead of 1's in the path associated to a node.

For later use, the first Order algorithm will be called the *Order-1* algorithm, and the latter will be called the *Order-0* algorithm. When not specified, the Order algorithm refers to the Order-1 algorithm.

More details about the Depth and the Order algorithms are to be found in Kontoleon's thesis [43], and in Bean, Kontoleon and Taylor [9].

2.2 The Thicknesses algorithm

The Thicknesses algorithm proceeds by functional iterations, *alternatively* using (2.2) and (2.4). We define

$$\mathbf{q}_0(0) = \boldsymbol{\theta}, \quad (2.6)$$

$$\mathbf{q}_1(2k-1) = [I - \Psi(I \otimes \mathbf{q}_0(2k-2))]^{-1} \boldsymbol{\theta}, \quad k \geq 1, \quad (2.7)$$

$$\mathbf{q}_0(2k) = [I - \Psi(\mathbf{q}_1(2k-1) \otimes I)]^{-1} \boldsymbol{\theta}, \quad k \geq 1. \quad (2.8)$$

The sequences $\{\mathbf{q}_1(2k-1)\}$ and $\{\mathbf{q}_0(2k)\}$ are well-defined and monotonically converge to the extinction probability \mathbf{q} . Before showing this, we need to define the *thicknesses* of a tree.

Like we did in the previous section, we give a label 0 or 1 to the arcs of the tree. To each node $x \in \mathcal{T}$, we now associate two sequences, $\text{path}_1(x)$ and $\text{path}_0(x)$: $\text{path}_1(x)$ is the string of 0's and 1's which mark the shortest path to the first child branch \mathcal{L} , and $\text{path}_0(x)$ is the string of 0's and 1's to the parental branch \mathcal{R} .

Next, we define $N_1(x)$ and $N_0(x)$ respectively as the number of blocks in the sequences $\text{path}_1(x)$ and $\text{path}_0(x)$, where a *block* is a sequence of consecutive 0's or consecutive 1's. Briefly stated, these count the number of direction changes on the paths from a node to \mathcal{L} and to \mathcal{R} .

The left thickness $\mathbb{S}_1(\mathcal{T})$ and the right thickness $\mathbb{S}_0(\mathcal{T})$ of a tree \mathcal{T} are defined as follows:

$$\mathbb{S}_1(\mathcal{T}) = \max \{N_1(x) : x \in \mathcal{T}\}, \quad \mathbb{S}_0(\mathcal{T}) = \max \{N_0(x) : x \in \mathcal{T}\};$$

if \mathcal{T} consists of a root only, then $\mathbb{S}_1(\mathcal{T}) = \mathbb{S}_0(\mathcal{T}) = 0$.

We see on Figure 2.1 that $N_1(w) = 4$ and $N_0(w) = 5$ and, by exhaustive examination of all the nodes, that $\mathbb{S}_1(\mathcal{T}) = 5$ and $\mathbb{S}_0(\mathcal{T}) = 6$.

Lemma 2.2.1. *If \mathcal{T} is the representation of an MBT which becomes extinct, then $\mathbb{S}_1(\mathcal{T}) < \infty$ and $\mathbb{S}_0(\mathcal{T}) < \infty$.*

Proof. Suppose that a tree \mathcal{T} dies out. It necessarily contains a finite number of branching points, say n . Then, $\mathbb{S}_1(\mathcal{T}) \leq n$ since, starting from any $x \in \mathcal{T}$, the length of the sequence $\text{path}_1(x)$ is at most n and thus $N_1(x) \leq n$. The same argument applies to $\mathbb{S}_0(\mathcal{T})$. \square

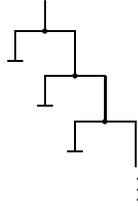


Figure 2.2: An infinite tree with finite thicknesses

However, it is possible for a tree with infinitely many nodes to have finite thicknesses, see Figure 2.2.

We denote by $[\mathcal{T} < \infty]$ the event that the MBT eventually becomes extinct. Thus, $q_i = \text{P}[\mathcal{T} < \infty | \varphi_0 = i]$, where φ_0 denotes the initial phase of the MBT, and we write, in short, that $\mathbf{q} = \text{P}[\mathcal{T} < \infty | \varphi_0]$.

We further define, for $k \geq 0$, the probability vectors

$$\mathbf{r}_1(2k+1) = \text{P}[\mathcal{T} < \infty \cap \mathbb{S}_1(\mathcal{T}) \leq 2k+1 | \varphi_0], \quad (2.9)$$

$$\mathbf{r}_0(2k) = \text{P}[\mathcal{T} < \infty \cap \mathbb{S}_0(\mathcal{T}) \leq 2k | \varphi_0]. \quad (2.10)$$

Theorem 2.2.2. *The sequences $\{\mathbf{r}_1(2k+1), k \geq 0\}$ and $\{\mathbf{r}_0(2k), k \geq 0\}$ satisfy the equations (2.6–2.8). They are monotonically increasing and converge to \mathbf{q} . Furthermore, $\mathbf{r}_0(2k) \leq \mathbf{r}_1(2k+1) \leq \mathbf{r}_0(2k+2)$, for all $k \geq 0$.*

Proof. Let us show that $[\mathbb{S}_0(\mathcal{T}) \leq 2k] \subseteq [\mathbb{S}_1(\mathcal{T}) \leq 2k+1]$, so that $\mathbf{r}_0(2k) \leq \mathbf{r}_1(2k+1)$. If a tree has a right thickness at most equal to $2k$, its left thickness is at most equal to $2k+1$ because one additional block of 0's only is required to reach the leftmost branch \mathcal{L} , after having reached the rightmost branch \mathcal{R} . The proof that $\mathbf{r}_1(2k+1) \leq \mathbf{r}_0(2k+2)$ is similar.

We now prove that the sequence $\{\mathbf{r}_1(2k+1), k \geq 0\}$ converges to \mathbf{q} . Using (2.9), we have

$$\begin{aligned} \lim_{k \rightarrow \infty} \mathbf{r}_1(2k+1) &= \lim_{k \rightarrow \infty} \text{P}[\mathcal{T} < \infty \cap \mathbb{S}_1(\mathcal{T}) \leq 2k+1 | \varphi_0] \\ &= \text{P}[\mathcal{T} < \infty \cap \mathbb{S}_1(\mathcal{T}) < \infty | \varphi_0] \\ &= \text{P}[\mathcal{T} < \infty | \varphi_0] \end{aligned}$$

by Lemma 2.2.1. The proof for the second sequence is similar.

Finally, we need to show that the two sequences $\{\mathbf{r}_1(2k+1), k \geq 0\}$ and $\{\mathbf{r}_0(2k), k \geq 0\}$ actually satisfy (2.6–2.8).

By definition, $\mathbb{S}_0(\mathcal{T}) = 0$ if and only if the root dies before any birth, which happens with probability θ , so that $\mathbf{r}_0(0) = \mathbf{q}_0(0)$.

There exist two cases where a tree eventually gets extinct with a left thickness at most equal to $2k + 1$: either death occurs before the first birth or a birth occurs first. In the latter case,

- the left subtree \mathcal{T}^l eventually becomes extinct with a left thickness at most equal to $2k + 1$, since the leftmost branch of \mathcal{T}^l is part of the leftmost branch of the entire tree \mathcal{T} ;
- the right subtree \mathcal{T}^r eventually becomes extinct with a right thickness at most equal to $2k$ since, in order to reach the leftmost branch \mathcal{L} of the whole tree \mathcal{T} with at most $2k + 1$ changes of direction, we first have to reach the rightmost branch of \mathcal{T}^r with at most $2k$ changes of direction, and then add one change of direction to reach \mathcal{L} .

The probability that there is a birth before a death is given by Ψ ; the random trees \mathcal{T}^l and \mathcal{T}^r are independent given their initial phases defined by Ψ , thus

$$\begin{aligned} \mathbf{r}_1(2k + 1) &= \theta + \Psi[\mathbf{r}_1(2k + 1) \otimes \mathbf{r}_0(2k)] \\ &= \theta + \Psi[I \otimes \mathbf{r}_0(2k)]\mathbf{r}_1(2k + 1) \\ &= \theta + \Psi[I \otimes \mathbf{r}_0(2k)]\theta + (\Psi[I \otimes \mathbf{r}_0(2k)])^2\mathbf{r}_1(2k + 1) \\ &= \dots = \sum_{n=0}^{\infty} (\Psi[I \otimes \mathbf{r}_0(2k)])^n \theta. \end{aligned}$$

Since the series converges, it is equal to $(I - \Psi[I \otimes \mathbf{r}_0(2k)])^{-1}$, and thus (2.7) is proved. A similar argument is used to prove (2.8). \square

We thus see that the Thicknesses algorithm somewhat alternates between child and parental branches.

In order to illustrate the differences between the Order and the Thicknesses algorithms, we show on Figure 2.3 a portion of the biggest trees corresponding to the third stage of the two algorithms.

The tree on top corresponds to the Order algorithm; it is the most complete binary tree with order 3. It is made up of an unbounded rightmost branch to which are attached identical copies of a tree, which actually is the tree from stage two. The important point is that branches to the left are limited, their length are at most 3.

The tree at the bottom corresponds to the Thicknesses algorithm; it is the most complete binary tree with a left thickness equal to 3. By contrast, it is more balanced and has unbounded branches in both the left and the right directions.

These observations generalize to every stage of the two algorithms. Consequently, the Order algorithm may be expected to converge fast in situations where trees grow with long branches in one direction only. On the other hand, the Thicknesses algorithm may be expected to converge faster in situations where the MBT has very long branches

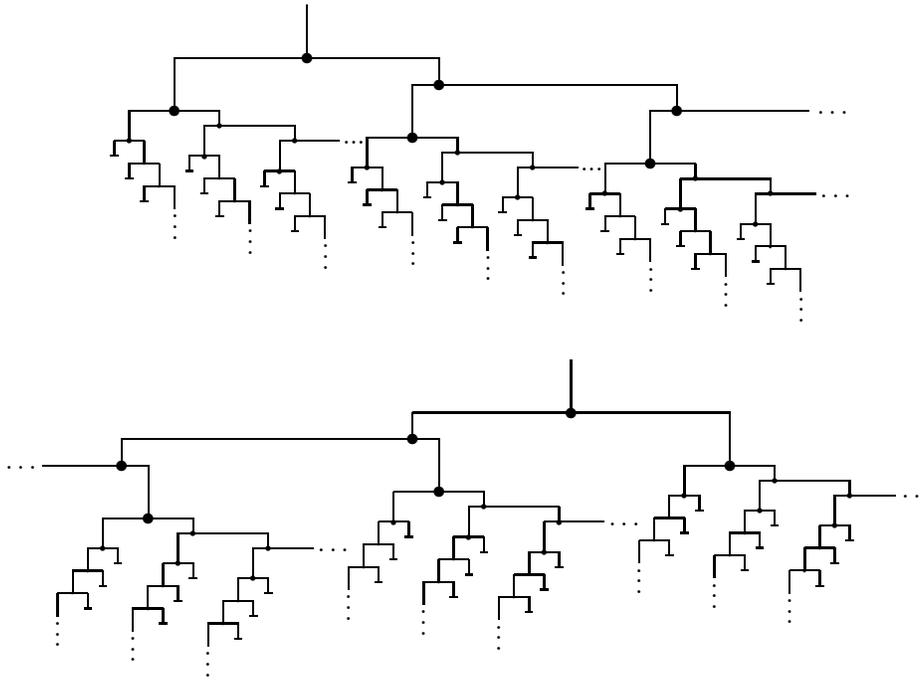


Figure 2.3: A portion of the biggest tree corresponding to the third stage of the Order algorithm (top) and the Thicknesses algorithm (bottom).

both to the left and to the right. This is numerically illustrated with Example 2.4.1. in Section 2.4.

2.3 Convergence rates

If the MBT is controlled by a MAP with n phases, then by making use of the structure of the matrices considered in the expression of the algorithms, in particular Kronecker products with an identity matrix, we obtain a complexity of $2n^3 + \mathcal{O}(n^2)$ flops per iteration for the Depth algorithm, and a complexity of $(8/3)n^3 + \mathcal{O}(n^2)$ flops for the Order and the Thicknesses algorithms. Therefore, the convergence rate of the three sequences is the key factor in comparing the efficiency of the linear algorithms.

In the sequel, we need the theorem below. Recall that an MBT is irreducible if the mean progeny matrix (1.9) is irreducible. In that case, either $\mathbf{q} = \mathbf{1}$ or $\mathbf{q} < \mathbf{1}$.

Theorem 2.3.1. *Assume that the MBT is irreducible. In the subcritical and supercritical cases,*

$$sp[\Psi(\mathbf{q} \oplus \mathbf{q})] < 1,$$

so that $[I - \Psi(\mathbf{q} \oplus \mathbf{q})]^{-1}$ exists and is nonnegative. In the critical case,

$$sp[\Psi(\mathbf{q} \oplus \mathbf{q})] = 1.$$

Proof. Let $\mathbf{P}^{(1)}(\mathbf{s}) = \mathbf{P}(\mathbf{s})$ and $\mathbf{P}^{(k)}(\mathbf{s}) = \mathbf{P}(\mathbf{P}^{(k-1)}(\mathbf{s}))$, where $\mathbf{P}(\mathbf{s})$ is the progeny generating function defined in (1.12). Define $M_k(\mathbf{s}) = (m_{ij}^{(k)}(\mathbf{s}))$, $1 \leq i, j \leq n$, where $m_{ij}^{(k)}(\mathbf{s}) = \partial(\mathbf{P}^{(k)}(\mathbf{s}))_i / \partial s_j$. One shows by induction that

$$M_k(\mathbf{s}) = M(\mathbf{P}^{(k-1)}(\mathbf{s})) M_{k-1}(\mathbf{s}), \quad (2.11)$$

with $M_1(\mathbf{s}) = M(\mathbf{s}) = \Psi(\mathbf{s} \oplus \mathbf{s})$. The mean progeny matrix of the branching process is $M = M(\mathbf{1}) = \Psi(\mathbf{1} \oplus \mathbf{1})$, and the matrix of interest in the statement of the theorem is

$$M(\mathbf{q}) = \Psi(\mathbf{q} \oplus \mathbf{q}). \quad (2.12)$$

The vector \mathbf{q} being the extinction probability, we have $\mathbf{P}(\mathbf{q}) = \mathbf{q} = \mathbf{P}^{(k)}(\mathbf{q})$ for all $k \geq 1$. Thus, by (2.11),

$$M_k(\mathbf{q}) = M(\mathbf{q}) M_{k-1}(\mathbf{q}) = M^k(\mathbf{q}). \quad (2.13)$$

By Theorem 1.2.5, $\lim_{k \rightarrow \infty} \mathbf{P}^{(k)}(\mathbf{s}) = \mathbf{q}$ for all \mathbf{s} such that $0 \leq s_i < 1, i = 1, \dots, n$, which implies that

$$\lim_{k \rightarrow \infty} M_k(\mathbf{s}) = 0 \quad \text{for any given } \mathbf{s} < \mathbf{1}. \quad (2.14)$$

Thus, we conclude from (2.13,2.14), that

- if the MBT (which is irreducible) is supercritical, then $\mathbf{q} < \mathbf{1}$, $\lim_{k \rightarrow \infty} M^k(\mathbf{q}) = \lim_{k \rightarrow \infty} M_k(\mathbf{q}) = 0$, and $\text{sp}[M(\mathbf{q})] < 1$;
- if the process is subcritical, then $\mathbf{q} = \mathbf{1}$, $M(\mathbf{q}) = M(\mathbf{1}) = M$, and $\text{sp}[M(\mathbf{q})] = \text{sp}[M] < 1$, as stated in Theorem 1.2.1;
- if the process is critical, then $\mathbf{q} = \mathbf{1}$, $M(\mathbf{q}) = M(\mathbf{1}) = M$, and $\text{sp}[M(\mathbf{q})] = \text{sp}[M] = 1$.

It follows from the Neumann Lemma [58, Proposition 2.3.1] that in the subcritical and supercritical cases, $[I - \Psi(\mathbf{q} \oplus \mathbf{q})]^{-1}$ exists and

$$[I - \Psi(\mathbf{q} \oplus \mathbf{q})]^{-1} = \sum_{i=0}^{\infty} [\Psi(\mathbf{q} \oplus \mathbf{q})]^i \geq 0.$$

□

In the rest of the section, we assume that the MBT is irreducible.

Corollary 2.3.2. *In the subcritical and supercritical cases, $\text{sp}[\Psi(\mathbf{q} \otimes I)] < 1$ and $\text{sp}[\Psi(I \otimes \mathbf{q})] < 1$, both $[I - \Psi(\mathbf{q} \otimes I)]^{-1}$ and $[I - \Psi(I \otimes \mathbf{q})]^{-1}$ exist and are nonnegative. In the critical case, $\text{sp}[\Psi(\mathbf{q} \otimes I)] \leq 1$ and $\text{sp}[\Psi(I \otimes \mathbf{q})] \leq 1$.*

Proof. This immediately follows from $\Psi(\mathbf{q} \otimes I) \leq \Psi(\mathbf{q} \oplus \mathbf{q})$ and $\Psi(I \otimes \mathbf{q}) \leq \Psi(\mathbf{q} \oplus \mathbf{q})$, and from the monotonicity properties of the spectral radius for nonnegative matrices.

□

Let us denote by $\langle \mathbf{0}, \mathbf{q} \rangle$ the set of vectors \mathbf{x} such that $\mathbf{0} \leq \mathbf{x} \leq \mathbf{q}$.

Corollary 2.3.3. *In the subcritical and supercritical cases, the matrix $[I - \Psi(\mathbf{x} \oplus \mathbf{x})]^{-1}$ exists and is nonnegative for all $\mathbf{x} \in \langle \mathbf{0}, \mathbf{q} \rangle$. Furthermore, $[I - \Psi(\mathbf{x} \oplus \mathbf{x})]^{-1} \leq [I - \Psi(\mathbf{y} \oplus \mathbf{y})]^{-1}$ for $\mathbf{0} \leq \mathbf{x} \leq \mathbf{y} \leq \mathbf{q}$.*

Proof. If $\mathbf{0} \leq \mathbf{x} \leq \mathbf{q}$, then, $\mathbf{0} \leq \Psi(\mathbf{x} \oplus \mathbf{x}) \leq \Psi(\mathbf{q} \oplus \mathbf{q})$, so that, in the subcritical and supercritical cases

$$\mathbf{0} \leq \sum_{i=0}^{\infty} [\Psi(\mathbf{x} \oplus \mathbf{x})]^i \leq \sum_{i=0}^{\infty} [\Psi(\mathbf{q} \oplus \mathbf{q})]^i < \infty$$

and thus $[I - \Psi(\mathbf{x} \oplus \mathbf{x})]^{-1}$ exists and is nonnegative. The second statement is proved by a similar argument. \square

We denote by $\mathbf{q}_n^{(d)}$, $\mathbf{q}_n^{(o)}$, and $\mathbf{q}_n^{(t)}$ the n th approximation produced by the Depth, the Order and the Thicknesses algorithm respectively, and we define the approximation errors

$$\mathbf{E}_n^{(d)} = \mathbf{q} - \mathbf{q}_n^{(d)}, \quad \mathbf{E}_n^{(o)} = \mathbf{q} - \mathbf{q}_n^{(o)}, \quad \mathbf{E}_n^{(t)} = \mathbf{q} - \mathbf{q}_n^{(t)}.$$

Theorem 2.3.4. *If the MBT is not critical, then upper bounds of the approximation errors for the three algorithms are as follows. For the Depth algorithm,*

$$\mathbf{E}_n^{(d)} \leq \Psi(\mathbf{q} \oplus \mathbf{q}) \mathbf{E}_{n-1}^{(d)}, \quad (2.15)$$

for the Order algorithm,

$$\mathbf{E}_n^{(o)} \leq [I - \Psi(\mathbf{q} \otimes I)]^{-1} \Psi(I \otimes \mathbf{q}) \mathbf{E}_{n-1}^{(o)}, \quad (2.16)$$

and for the Thicknesses algorithm,

$$\mathbf{E}_{2n-1}^{(t)} \leq [I - \Psi(I \otimes \mathbf{q})]^{-1} \Psi(\mathbf{q} \otimes I) \mathbf{E}_{2n-2}^{(t)} \quad (2.17)$$

$$\mathbf{E}_{2n}^{(t)} \leq [I - \Psi(\mathbf{q} \otimes I)]^{-1} \Psi(I \otimes \mathbf{q}) \mathbf{E}_{2n-1}^{(t)}. \quad (2.18)$$

Proof. We prove (2.16) only, the other inequalities being proved in a similar manner. We rewrite (2.3) as

$$\mathbf{q}_n^{(o)} = [I - \Psi(\mathbf{q}_{n-1}^{(o)} \otimes I)]^{-1} \boldsymbol{\theta} = \boldsymbol{\theta} + \Psi(\mathbf{q}_{n-1}^{(o)} \otimes \mathbf{q}_n^{(o)}).$$

Then,

$$\begin{aligned} \mathbf{E}_n^{(o)} &= \Psi(\mathbf{q} \otimes \mathbf{q}) - \Psi(\mathbf{q}_{n-1}^{(o)} \otimes \mathbf{q}_n^{(o)}) \\ &= \Psi((\mathbf{q} - \mathbf{q}_{n-1}^{(o)}) \otimes \mathbf{q}) + \Psi(\mathbf{q}_{n-1}^{(o)} \otimes (\mathbf{q} - \mathbf{q}_n^{(o)})) \\ &= \Psi(\mathbf{E}_{n-1}^{(o)} \otimes \mathbf{q}) + \Psi(\mathbf{q}_{n-1}^{(o)} \otimes \mathbf{E}_n^{(o)}) \\ &\leq \Psi(I \otimes \mathbf{q}) \mathbf{E}_{n-1}^{(o)} + \Psi(\mathbf{q} \otimes I) \mathbf{E}_n^{(o)} \end{aligned}$$

since $\mathbf{q}_{n-1}^{(o)} \leq \mathbf{q}$. Thus,

$$(I - \Psi(\mathbf{q} \otimes I)) \mathbf{E}_n^{(o)} \leq \Psi(I \otimes \mathbf{q}) \mathbf{E}_{n-1}^{(o)}.$$

We premultiply both sides by $[I - \Psi(\mathbf{q} \otimes I)]^{-1}$, which exists and is nonnegative, by Corollary 2.3.2, and this concludes the proof of (2.16). \square

As a result, in the noncritical case, all three algorithms converge linearly. Indeed, if we denote by $\gamma^{(d)}$, $\gamma^{(o)}$ and $\gamma^{(t)}$ their convergence rates, we immediately see that

$$\gamma^{(d)} \leq \text{sp}[M(\mathbf{q})], \quad (2.19)$$

where $M(\mathbf{q})$ is defined in (2.12), and that

$$\begin{aligned} \gamma^{(o)} &\leq \text{sp}[R_1(\mathbf{q})], \\ \gamma^{(t)} &\leq \{\text{sp}[R_1(\mathbf{q}) R_2(\mathbf{q})]\}^{1/2}, \end{aligned} \quad (2.20)$$

where

$$R_1(\mathbf{q}) = [I - \Psi(\mathbf{q} \otimes I)]^{-1} \Psi(I \otimes \mathbf{q}) \quad (2.21)$$

and

$$R_2(\mathbf{q}) = [I - \Psi(I \otimes \mathbf{q})]^{-1} \Psi(\mathbf{q} \otimes I) \quad (2.22)$$

(Ortega and Rheinboldt [58, Section 9.2]). Notice that, for the Order-1 algorithm, by symmetry we have $\gamma^{(o-1)} \leq \text{sp}[R_2(\mathbf{q})]$.

We need to recall the following definitions and theorem from Varga [72] that are useful in the proof of the next result.

Definition 2.3.5. *Let $B \geq 0$ be an $n \times n$ matrix. The matrix $A = \alpha I - B$ is an M-matrix if $\text{sp}(B) \leq \alpha$.*

As consequences of Theorem 2.3.1 and Corollary 2.3.2, the matrices $I - \Psi(\mathbf{q} \oplus \mathbf{q})$, $I - \Psi(I \otimes \mathbf{q})$, and $I - \Psi(\mathbf{q} \otimes I)$ are M-matrices.

Definition 2.3.6. *Let A be an M-matrix. The splitting $A = B - C$ of A is called a regular splitting if the matrices B and C are such that B is an M-matrix and $C \geq 0$.*

Theorem 2.3.7. *If $A = B_1 - C_1$ and $A = B_2 - C_2$ are two regular splittings of the M-matrix A , and if $C_1 \leq C_2$ and B_1 and B_2 are nonsingular, then $\text{sp}(B_1^{-1} C_1) \leq \text{sp}(B_2^{-1} C_2)$. If A is singular, then $\text{sp}(B_1^{-1} C_1) = \text{sp}(B_2^{-1} C_2) = 1$. \square*

The next theorem allows us to compare the spectral radius of the matrices $M(\mathbf{q})$, $R_1(\mathbf{q})$, and $R_2(\mathbf{q})$, and shows that the Depth and the Order algorithms are linearly convergent in the noncritical case.

Theorem 2.3.8. *If the process is noncritical, then*

$$\text{sp}[R_1(\mathbf{q})] \leq \text{sp}[M(\mathbf{q})] < 1, \quad (2.23)$$

and

$$\text{sp}[R_2(\mathbf{q})] \leq \text{sp}[M(\mathbf{q})] < 1. \quad (2.24)$$

If the process is critical and if $[I - \Psi(\mathbf{q} \otimes I)]^{-1}$ and $[I - \Psi(I \otimes \mathbf{q})]^{-1}$ both exist, then

$$\text{sp}[M(\mathbf{q})] = \text{sp}[R_1(\mathbf{q})] = \text{sp}[R_2(\mathbf{q})] = 1. \quad (2.25)$$

Proof. In order to compare the spectral radius of the matrices $M(\mathbf{q})$, $R_1(\mathbf{q})$ and $R_2(\mathbf{q})$, we use the following three regular splittings of the M-matrix $A = I - M(\mathbf{q})$:

$$\begin{aligned} A &= B_1 - C_1 \quad \text{with} \quad B_1 = I, & C_1 &= M(\mathbf{q}), \\ A &= B_2 - C_2 \quad \text{with} \quad B_2 = I - \Psi(\mathbf{q} \otimes I), & C_2 &= \Psi(I \otimes \mathbf{q}), \\ A &= B_3 - C_3 \quad \text{with} \quad B_3 = I - \Psi(I \otimes \mathbf{q}), & C_3 &= \Psi(\mathbf{q} \otimes I). \end{aligned}$$

In the noncritical case, B_2 and B_3 are invertible by Corollary 2.3.2. Since $C_1 \geq C_2$ and $C_1 \geq C_3$, it results from Theorem 2.3.7 that

$$\text{sp}[B_2^{-1} C_2] \leq \text{sp}[C_1] \quad \text{and} \quad \text{sp}[B_3^{-1} C_3] \leq \text{sp}[C_1].$$

This, together with Theorem 2.3.1 and (2.21,2.22), proves (2.23,2.24).

If the process is critical, then A is singular since $\text{sp}[M(\mathbf{q})] = 1$. Theorem 2.3.7 is still applicable if B_2 and B_3 are nonsingular and (2.25) results. \square

Since both $\text{sp}[R_1(\mathbf{q})] \leq \text{sp}[M(\mathbf{q})]$ and $\text{sp}[R_2(\mathbf{q})] \leq \text{sp}[M(\mathbf{q})]$, this theorem, together with (2.19) and (2.20), explain in an analytical manner why the Order algorithms converge faster than the Depth algorithm, a fact which is proved by probabilistic arguments in [8, 43].

The same kind of probabilistic arguments show that the Thicknesses algorithm converges faster than the Depth algorithm. Indeed, the set of trees considered at the k th stage of the Depth algorithm is included in the set of trees considered at the k th stage of the Thicknesses algorithm since, if a tree has a depth at most equal to k , then its left and right thicknesses are at most equal to k (the depth of a tree may be defined as the maximum number of labels in the paths from the nodes to the root).

We can show the linear convergence of the Thicknesses algorithm in the noncritical case with the same arguments than those used in the proof of the previous theorem.

Corollary 2.3.9. *If the process is noncritical, then*

$$\{\text{sp}[R_1(\mathbf{q}) R_2(\mathbf{q})]\}^{1/2} < 1 \tag{2.26}$$

If the process is critical and if $[I - \Psi(\mathbf{q} \otimes I)]^{-1}$ and $[I - \Psi(I \otimes \mathbf{q})]^{-1}$ both exist, then

$$\{\text{sp}[R_1(\mathbf{q}) R_2(\mathbf{q})]\}^{1/2} = 1. \tag{2.27}$$

Proof. We use the two regular splittings of the M-matrix $A = I - M(\mathbf{q})$: $A = B_1 - C_1$ with $B_1 = I - \Psi(\mathbf{q} \otimes I)$ and $C_1 = \Psi(I \otimes \mathbf{q})$, and $A = B_2 - C_2$ with $B_2 = [I - \Psi(I \otimes \mathbf{q})][I - \Psi(\mathbf{q} \otimes I)]$, and $C_2 = \Psi(I \otimes \mathbf{q})\Psi(\mathbf{q} \otimes I)$.

We get

$$\text{sp}[R_1(\mathbf{q}) R_2(\mathbf{q})] \leq \text{sp}[R_1(\mathbf{q})],$$

as, by probabilistic arguments, we can show that $C_2 \leq C_1$. This, together with Theorem 2.3.8, provide the statement of the corollary. \square

However, to prove analytically that $\{\text{sp}[R_1(\mathbf{q}) R_2(\mathbf{q})]\}^{1/2} \leq \text{sp}[M(\mathbf{q})]$ is much more difficult. There is, in addition, no comparison to be made in all generality between the

speed of convergence of the Order and of the Thicknesses algorithms, since we have no general relation between the spectral radius of $R_1(\mathbf{q})$ and $R_2(\mathbf{q})$ on the one hand, and that of the product $R_1(\mathbf{q})R_2(\mathbf{q})$ on the other hand. We explained at the end of the previous section under which circumstances one may expect the Thicknesses algorithm to be faster; we illustrate it in the next section with Example 2.4.1.

Another consequence of Theorem 2.3.8 and Corollary 2.3.9 is that one should expect slow convergence for all linear algorithms in the case where the process is nearly critical, that is, when $\text{sp}[M(\mathbf{q})]$ is very close to 1. This is demonstrated in the next section too.

2.4 Numerical examples

Let us now apply the linear algorithms on two examples of MBTs controlled by one parameter, in order to compare their efficiency. In the first example, the parameter influences the length of the branches of the tree in one direction, and in the second example, it controls the criticality of the MBT.

Example 2.4.1 (Branches of varying length). We analyze here the effect of the shape of the tree on the functional algorithms examined so far.

In this example, individuals have the opportunity to have many children, so that the tree has long branches in the parental (right) direction. The number of generations, which translates into number of nodes in the left direction, is controlled by the parameter δ .

The birth rates matrix has the form $B_{i,jk} = (D_1)_{ik}(P_1)_{ij}$ (see Section 1.5). Here, the entry $(D_1)_{ik}$ may be decomposed in a product $\beta_i(P_0)_{ik}$, where the vector β gives the effective birth rate in each phase, and the stochastic matrix P_0 gives the conditional probabilities for the parental phase after a birth, given its phase before the birth.

There are nine phases. An individual may only die when it is in phase 5, and

$$\mathbf{d} = [0 \ 0 \ 0 \ 0 \mid 1 \mid 0 \ 0 \ 0 \ 0]^T;$$

we set $d_5 = 1$, so that the unit of time is the expected time until death when in phase 5.

An individual which is in phase 1 cycles through the phases 1 to 4; whenever it is in phase 4, it may also move to phase 5, where it is likely that it will die, or to phase 6 where its behaviour will be very different. Phases 6 to 9 also form a cycle, and from phase 9, an individual may move to phase 5 or phase 1. The matrix D_0 is as follows

$$D_0 = 10^{-3} \cdot \left[\begin{array}{cccc|cccc} * & 6 & \cdot \\ \cdot & * & 6 & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & * & 6 & \cdot & \cdot & \cdot & \cdot & \cdot \\ 6 & \cdot & \cdot & * & 1 & 1 & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & * & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & * & 6 & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & * & 6 & \cdot \\ \cdot & * & 6 \\ 1 & \cdot & \cdot & \cdot & 1 & 6 & \cdot & \cdot & * \end{array} \right];$$

its diagonal is such that $D_0\mathbf{1} + \beta + \mathbf{d} = \mathbf{0}$.

In the phases 6 to 9, the birth rate is high, and upon birth, the parent stays in the same phase, so that branches to the right are very long. The children start in phase 5, however, where they have a high probability of dying without giving birth, so that children branches to the left are very short.

The opposite is true in phases 1 to 4: after giving birth, the parent moves to phase 5, so that right branches do not grow much, while the child inherits the phase of its parent, so that left branches have the potential to grow. Birth rates are parameterized by δ , so that if δ is large, left branches have the opportunity to grow, while if δ is small, left branches will not become very long. In summary,

$$\beta = 10^{-2} [\delta \ \delta \ \delta \ \delta \mid 5 \mid 4 \ 4 \ 4 \ 4]^T.$$

The matrices P_0 and P_1 are given by

$$P_0 = \left[\begin{array}{cccc|c|cccc} \cdot & \cdot & \cdot & \cdot & 1 & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & 1 & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & 1 & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & 1 & \cdot & \cdot & \cdot & \cdot \\ \hline 0.1 & \cdot & \cdot & \cdot & 0.9 & \cdot & \cdot & \cdot & \cdot \\ \hline \cdot & \cdot & \cdot & \cdot & \cdot & 1 & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & 1 & \cdot & \cdot \\ \cdot & 1 & \cdot \\ \cdot & 1 \end{array} \right], \quad P_1 = \left[\begin{array}{cccc|c|cccc} 1 & \cdot \\ \cdot & 1 & \cdot \\ \cdot & \cdot & 1 & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & 1 & \cdot & \cdot & \cdot & \cdot & \cdot \\ \hline 0.1 & \cdot & \cdot & \cdot & 0.9 & \cdot & \cdot & \cdot & \cdot \\ \hline \cdot & \cdot & \cdot & \cdot & \cdot & 1 & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & 1 & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & 1 & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & 1 & \cdot & \cdot & \cdot \end{array} \right].$$

The expected time E spent in each set of four phases is given by

$$E = \frac{3}{6 \cdot 10^{-3}} + \frac{1}{6 \cdot 10^{-3} + 2 \cdot 10^{-3}} + E \frac{6 \cdot 10^{-3}}{6 \cdot 10^{-3} + 2 \cdot 10^{-3}}$$

leading to $E = 2500$ units of time. The expected number of children during a sojourn in the first set of phases is $a = 2500 \cdot 10^{-2} \delta = 25 \delta$, and the expected number of children during a sojourn in the second set of phases is $2500 \times 4 \cdot 10^{-2} = 100$.

For $\delta = 0$, the spectral radius of the mean matrix $M = \Psi(\mathbf{1} \oplus \mathbf{1})$ is $\rho = 0.998$ and the process is subcritical. As δ increases, ρ increases as well, the process becomes critical for $\delta = 0.83$ approximately, and it becomes supercritical beyond that.

We show on Figure 2.4 the number of iterations needed to compute the vector \mathbf{q} with the four linear algorithms as a function of δ varying in $[0, 7]$. As predicted by the convergence rates analysis given in the previous section, we observe that the number of iterations sharply increases around $\delta = 0.83$, where the process is nearly critical.

We see that the Thicknesses algorithm performs more efficiently than the other linear algorithms, especially for large values of δ . Indeed, recall from the end of Section 2.2 that we expect the Thicknesses algorithm to converge faster for MBTs with long branches in both directions, which is the case in the present example. For small values of δ , things are better for the Order-1 algorithm, although the Thicknesses algorithm remains the fastest of the four.

On Figure 2.5, we show the solution \mathbf{q} as a function of δ . In the supercritical case, the probability q_5 is never exactly 1, because there is a small probability, for an individual in phase 5, of giving birth and moving to phase 1.

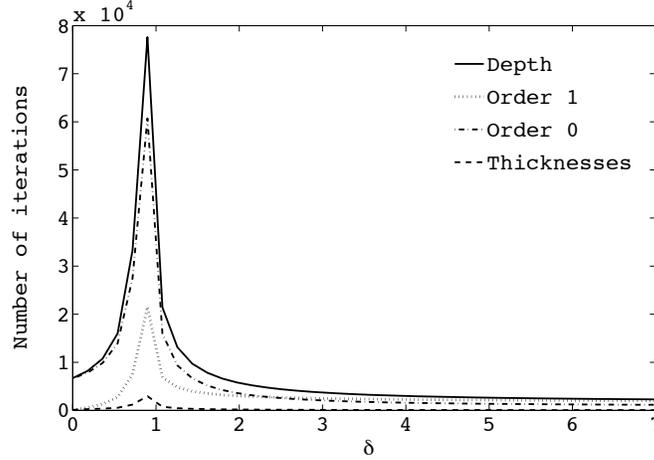


Figure 2.4: Comparison of the number of iterations for the Depth, the Order-1 and 0, and for the Thickesses algorithms, as a function of δ .

Example 2.4.2 (Nearly-critical MBT). For our second example, we take a model inspired from Kontoleon [43]. The characterizing matrices are

$$D_0 = \begin{bmatrix} -10 & 0 & 0 \\ 0 & -10 & 0 \\ 0 & 1 & -10 \end{bmatrix}, \quad \mathbf{d} = \begin{bmatrix} 1 \\ 1 \\ 9 \end{bmatrix},$$

$$B = \left[\begin{array}{ccc|ccc|ccc} 0 & 0 & 0 & 0 & 9(1-p) & 0 & 4.5p & 0 & 4.5p \\ 9p & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 9(1-p) \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{array} \right],$$

and the parameter p varies between 0 and 1.

On Figure 2.6, we plot the value of $\rho = \text{sp}(M)$ and we see that the process changes from being subcritical to critical, supercritical, critical and finally subcritical again. On Figure 2.7, we plot the number of iterations required with the four linear algorithms. Here, there is not much difference between the two Order algorithms and the Thickesses algorithm. We very clearly see the slowdown of each algorithm, as predicted by the convergence rate study, when the process gets close to being critical.

Finally, Figure 2.8 shows the solution \mathbf{q} as a function of p .

2.5 General Markovian Trees

We now investigate the generalization of the linear algorithms to the GMT case, where multiple births are allowed. Recall that in that case, the extinction equation is given by (1.14).

The Depth algorithm in [9, Equations (23–24)] is a generalization of (2.1):

$$\ell(0) = \boldsymbol{\theta}, \quad \ell(k) = \boldsymbol{\theta} + \sum_{m \geq 1} \Psi_m \ell^{(m+1)}(k-1), \quad k \geq 1. \quad (2.28)$$

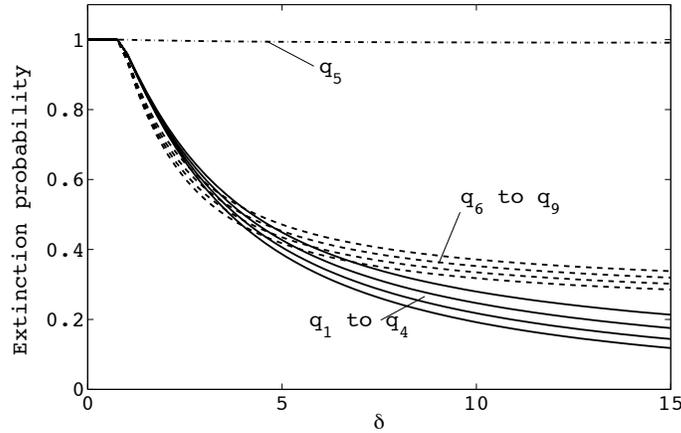


Figure 2.5: The vector \mathbf{q} of extinction probability for $\delta = 0$ to 15.

The Order algorithm in [9, Equations (40–42)] is a generalization of (2.3): after splitting $\mathbf{s}^{(m+1)}$ as $\mathbf{s}^{(m+1)} = (\mathbf{s}^{(m)} \otimes I)\mathbf{s}$, one rewrites (1.14) as

$$\mathbf{s} = \boldsymbol{\theta} + \sum_{m \geq 1} \Psi_m(\mathbf{s}^{(m)} \otimes I)\mathbf{s} = [I - \sum_{m \geq 1} \Psi_m(\mathbf{s}^{(m)} \otimes I)]^{-1}\boldsymbol{\theta}, \quad (2.29)$$

which leads to the functional iteration

$$\mathbf{s}(0) = \boldsymbol{\theta}, \quad \mathbf{s}(k) = [I - \sum_{m \geq 1} \Psi_m(\mathbf{s}^{(m)}(k-1) \otimes I)]^{-1}\boldsymbol{\theta}, \quad k \geq 1. \quad (2.30)$$

The sequences (2.28) and (2.30) monotonically converge to \mathbf{q} , and the interpretation of the successive approximations is the same as their analogue in the MBT case.

To generalize the Thicknesses algorithm is more complex. Recall that in the MBT case, we assumed that after any branching point, the left arc is the child arc, the right arc is the parental arc, and the Thicknesses algorithm alternates between child and parental branches.

Similarly, we assume here that after any branching point, the rightmost arc is the parental arc, and is labeled 0, and the other arcs are all children arcs and are labeled from 1 to the number of children, from left to right. The Thicknesses algorithm thus now needs to cycle through the different children branches and the parental branch.

Observe that the power $\mathbf{s}^{(m+1)}$ may also be decomposed as $\mathbf{s}^{(m+1)} = (\mathbf{s}^{(i-1)} \otimes I \otimes \mathbf{s}^{(m-i+1)})\mathbf{s}$ for any $1 \leq i \leq m$. This allows us to write (1.14) as

$$\mathbf{s} = \boldsymbol{\theta} + \sum_{1 \leq m \leq i-1} \Psi_m \mathbf{s}^{(m+1)} + \sum_{m \geq i} \Psi_m(\mathbf{s}^{(i-1)} \otimes I \otimes \mathbf{s}^{(m-i+1)})\mathbf{s}, \quad (2.31)$$

for all $i \geq 1$ (where an empty sum corresponds to zero), from which (1.14) may be rewritten as

$$\mathbf{s} = \mathcal{V}_i(\mathbf{s}) \quad (2.32)$$

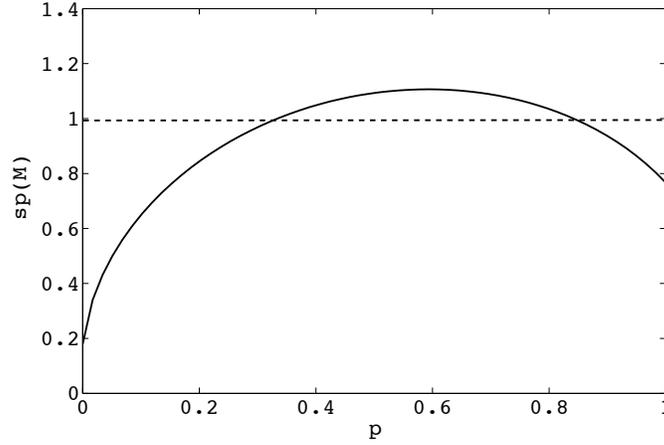


Figure 2.6: The maximal eigenvalue ρ of the mean matrix M , as a function of p .

where

$$\mathcal{V}_i(\mathbf{s}) = \left[I - \sum_{m \geq i} \Psi_m(\mathbf{s}^{(i-1)} \otimes I \otimes \mathbf{s}^{(m-i+1)}) \right]^{-1} \left[\boldsymbol{\theta} + \sum_{1 \leq m \leq i-1} \Psi_m \mathbf{s}^{(m+1)} \right]. \quad (2.33)$$

Let $\mathcal{W}_M(\mathbf{s})$ be the right-hand-side of (2.29), that is

$$\mathcal{W}_M(\mathbf{s}) = \left[I - \sum_{m \geq 1} \Psi_m(\mathbf{s}^{(m)} \otimes I) \right]^{-1} \boldsymbol{\theta}. \quad (2.34)$$

Now, let us choose some finite $M \geq 2$ which may not be greater than the maximum number of branches which follow a birth. To generalize the sequence (2.6–2.8), we cycle through the first $M - 1$ fixed-point equations (2.32) and Equation (2.29), and we obtain a sequence which converges to the extinction probability; this is the object of the next theorem.

Theorem 2.5.1. *The sequence*

$$\mathbf{q}_0 = \boldsymbol{\theta}, \quad \mathbf{q}_{Mk+i} = \mathcal{V}_i(\mathbf{q}_{Mk+i-1}), \quad \mathbf{q}_{M(k+1)} = \mathcal{W}_M(\mathbf{q}_{Mk+M-1}), \quad (2.35)$$

for $k \geq 0$, $1 \leq i \leq M - 1$, monotonically converges to \mathbf{q} , where $\mathcal{V}_i(\cdot)$ and $\mathcal{W}_M(\cdot)$ are defined in (2.33) and (2.34) respectively.

Proof. The proof that the sequence is monotone is not complicated but quite involved. We define the functions

$$\begin{aligned} \mathcal{T}_M(\mathbf{x}, \mathbf{y}) &= \boldsymbol{\theta} + \sum_{m \geq 1} \Psi_m(\mathbf{x}^{(m)} \otimes \mathbf{y}) \\ \mathcal{S}_i(\mathbf{x}, \mathbf{y}) &= \boldsymbol{\theta} + \sum_{1 \leq m \leq i-1} \Psi_m \mathbf{x}^{(m+1)} + \sum_{m \geq i} \Psi_m(\mathbf{x}^{(i-1)} \otimes \mathbf{y} \otimes \mathbf{x}^{(m-i+1)}), \end{aligned}$$

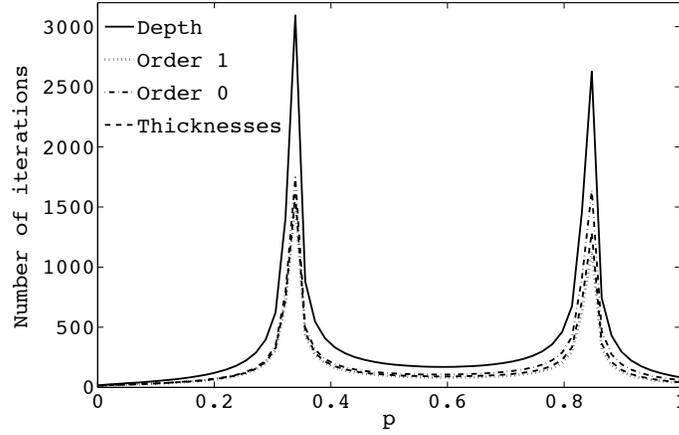


Figure 2.7: Comparison of the number of iterations for the four linear algorithms, as a function of p .

for $1 \leq i \leq M-1$.

For $\mathbf{x}' \geq \mathbf{y} \geq \mathbf{x}$ and $\mathbf{y}' \geq \mathbf{x}$, we have the inequalities

$$\mathcal{S}_j(\mathbf{x}', \mathbf{y}') \geq \mathcal{S}_i(\mathbf{x}, \mathbf{y}), \quad (2.36)$$

$$\mathcal{T}_M(\mathbf{x}', \mathbf{y}') \geq \mathcal{S}_i(\mathbf{x}, \mathbf{y}) \quad \text{and} \quad \mathcal{S}_i(\mathbf{x}', \mathbf{y}') \geq \mathcal{T}_M(\mathbf{x}, \mathbf{y}), \quad (2.37)$$

for $1 \leq i \neq j \leq M-1$. To prove (2.36) for $j > i$, we proceed as follows:

$$\begin{aligned} \mathcal{S}_j(\mathbf{x}', \mathbf{y}') &= \boldsymbol{\theta} + \sum_{1 \leq m \leq i-1} \Psi_m \mathbf{x}'^{(m+1)} + \sum_{i \leq m \leq j-1} \Psi_m \mathbf{x}'^{(m+1)} \\ &\quad + \sum_{m \geq j} \Psi_m (\mathbf{x}'^{(j-1)} \otimes \mathbf{y}' \otimes \mathbf{x}'^{(m-j+1)}) \\ &\geq \boldsymbol{\theta} + \sum_{1 \leq m \leq i-1} \Psi_m \mathbf{x}^{(m+1)} + \sum_{i \leq m \leq j-1} \Psi_m \mathbf{x}'^{(m+1)} \\ &\quad + \sum_{m \geq j} \Psi_m (\mathbf{x}^{(i-1)} \otimes \mathbf{y} \otimes \mathbf{x}^{(m-i+1)}) \\ &\geq \boldsymbol{\theta} + \sum_{1 \leq m \leq i-1} \Psi_m \mathbf{x}^{(m+1)} + \sum_{m \geq i} \Psi_m (\mathbf{x}^{(i-1)} \otimes \mathbf{y} \otimes \mathbf{x}^{(m-i+1)}) \\ &= \mathcal{S}_i(\mathbf{x}, \mathbf{y}). \end{aligned}$$

The other inequalities are proved in a similar manner through a comparison term by term and, for each term, a comparison factor by factor.

Next, we prove that the sequence $\{\mathbf{q}_k\}$ is monotone up to \mathbf{q}_{M-1} . Assume that $\mathbf{q}_0 \leq \mathbf{q}_1 \leq \dots \leq \mathbf{q}_{i-1}$ for some $i \leq M-1$; we need to show that $\mathbf{q}_{i-1} \leq \mathbf{q}_i$. Now, it

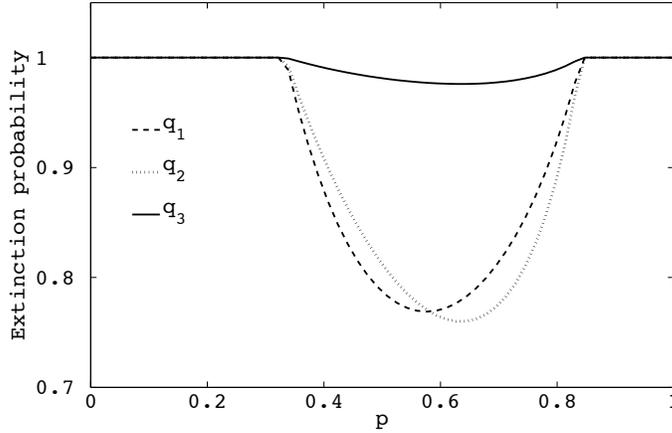


Figure 2.8: The vector \mathbf{q} of extinction probability, as a function of p .

results from (2.35) that we may write

$$\begin{aligned} \mathbf{q}_i &= \boldsymbol{\theta} + \sum_{1 \leq m \leq i-1} \Psi_m \mathbf{q}_{i-1}^{(m+1)} + \sum_{m \geq i} \Psi_m (\mathbf{q}_{i-1}^{(i-1)} \otimes \mathbf{q}_i \otimes \mathbf{q}_{i-1}^{(m-i+1)}), \\ &= \mathcal{S}_i(\mathbf{q}_{i-1}, \mathbf{q}_i) \end{aligned}$$

and it also results that $\mathbf{q}_i \geq \boldsymbol{\theta}$.

From the inequalities $\mathbf{q}_{i-1} \geq \mathbf{q}_1 \geq \boldsymbol{\theta}$ and $\mathbf{q}_i \geq \boldsymbol{\theta}$, it results from (2.36) that $\mathbf{q}_i = \mathcal{S}_i(\mathbf{q}_{i-1}, \mathbf{q}_i) \geq \mathcal{S}_1(\boldsymbol{\theta}, \mathbf{q}_1) = \mathbf{q}_1$. We use this inequality and iterate the argument, finding that $\mathbf{q}_i = \mathcal{S}_i(\mathbf{q}_{i-1}, \mathbf{q}_i) \geq \mathcal{S}_2(\mathbf{q}_1, \mathbf{q}_2) = \mathbf{q}_2$. In this fashion, we successively prove that \mathbf{q}_i is greater than $\mathbf{q}_3, \dots, \mathbf{q}_{i-1}$. This procedure is similar to climbing a ladder one rung at a time, we repeatedly use it in the remainder of the proof.

We make the first induction assumption that $\mathbf{q}_0 \leq \mathbf{q}_1 \leq \dots \leq \mathbf{q}_{Mk+i-1}$ for some $k \geq 1$, $1 \leq i \leq M-1$ and prove that $\mathbf{q}_{Mk+i} \geq \mathbf{q}_{Mk+i-1}$. The equation (2.33) may also be written as

$$\mathcal{V}_i(\mathbf{s}) = \sum_{\nu \geq 0} \left[\sum_{m \geq i} \Psi_m (\mathbf{s}^{(i-1)} \otimes I \otimes \mathbf{s}^{(m-i+1)}) \right]^\nu \left[\boldsymbol{\theta} + \sum_{1 \leq m \leq i-1} \Psi_m \mathbf{s}^{(m+1)} \right]$$

which show that $\mathcal{V}_i(\mathbf{s})$ is a nondecreasing function of \mathbf{s} for $\mathbf{s} \geq \mathbf{0}$. This allows us to conclude that $\mathbf{q}_{Mk+i} \geq \mathbf{q}_{M(k-1)+i}$, thereby giving us a first step on the ladder. Next, we use (2.36) and eventually prove that $\mathbf{q}_{Mk+i} \geq \mathbf{q}_{Mk-1}$. At this stage, we use the second inequality in (2.37) and write that $\mathbf{q}_{Mk+i} = \mathcal{S}_i(\mathbf{q}_{Mk+i-1}, \mathbf{q}_{Mk+i}) \geq \mathcal{T}_M(\mathbf{q}_{Mk-1}, \mathbf{q}_{Mk}) = \mathbf{q}_{Mk}$. From then on, we use (2.36) again.

We make the second induction assumption that $\mathbf{q}_0 \leq \mathbf{q}_1 \leq \dots \leq \mathbf{q}_{Mk+M-1}$ for some $k \geq 0$, and we prove in the same fashion that $\mathbf{q}_{M(k+1)} \geq \mathbf{q}_{Mk+M-1}$. The function $\mathcal{W}_M(\mathbf{s})$ may be written as

$$\mathcal{W}_M(\mathbf{s}) = \sum_{\nu \geq 0} \left[\sum_{m \geq 1} \Psi_m (\mathbf{s}^{(m)} \otimes I) \right]^\nu \boldsymbol{\theta},$$

so that it is clear that $\mathbf{q}_{M(k+1)} \geq \mathbf{q}_{Mk}$. Having established that first step, we repeatedly use the first inequality in (2.37).

The last part of the proof is easy: the functions $\mathcal{V}_i(\cdot)$ and $\mathcal{W}(\cdot)$ are non-decreasing, therefore the fact that $\mathbf{q}_0 = \boldsymbol{\theta} \leq \mathbf{q}$ implies by induction that $\mathbf{q}_j \leq \mathbf{q}$ for all j . The sequence, being monotone and bounded, is convergent and since \mathbf{q} is the minimal nonnegative solution, the convergence is to \mathbf{q} . \square

Like in the MBT case, the ℓ th approximation \mathbf{q}_ℓ of the Thicknesses algorithm (2.35) may be interpreted as the probability that the tree becomes extinct with some “distance” to the leaves being bounded by a function of ℓ . The precise expressions, however, are more involved than in the MBT case.

Let us first assume that the number of branches after a birth is bounded by M . We consider the case $M = 4$, from which the general case will be clear enough. This means that a parent may have at most three children at a time.

In order to better show the parallelism with the Thicknesses algorithm for MBTs, we rewrite the successive approximations of \mathbf{q} by adding the indices of the branches we successively cycle through: $\mathbf{q}_0(0) = \mathbf{q}_0$, and for $k \geq 1$,

$$\begin{aligned} \mathbf{q}_1(4k-3) &= \mathbf{q}_{4k-3} \quad (= \mathbf{q}_{4(k-1)+1}) \\ \mathbf{q}_2(4k-2) &= \mathbf{q}_{4k-2} \quad (= \mathbf{q}_{4(k-1)+2}) \\ \mathbf{q}_3(4k-1) &= \mathbf{q}_{4k-1} \quad (= \mathbf{q}_{4(k-1)+3}) \\ \mathbf{q}_0(4k) &= \mathbf{q}_{4k}. \end{aligned}$$

We define four thicknesses measures for a tree \mathcal{T} , that we note $\mathbb{S}_1(\mathcal{T})$, $\mathbb{S}_2(\mathcal{T})$, $\mathbb{S}_3(\mathcal{T})$ and $\mathbb{S}_0(\mathcal{T})$, such that the successive approximations of the Thicknesses algorithm have the following interpretation

$$\begin{aligned} \mathbf{q}_1(4k-3) &= \mathbb{P}[\mathcal{T} < \infty \cap \mathbb{S}_1(\mathcal{T}) \leq 4k-3 \mid \varphi_0], \\ \mathbf{q}_2(4k-2) &= \mathbb{P}[\mathcal{T} < \infty \cap \mathbb{S}_2(\mathcal{T}) \leq 4k-2 \mid \varphi_0], \\ \mathbf{q}_3(4k-1) &= \mathbb{P}[\mathcal{T} < \infty \cap \mathbb{S}_3(\mathcal{T}) \leq 4k-1 \mid \varphi_0], \\ \mathbf{q}_0(4k) &= \mathbb{P}[\mathcal{T} < \infty \cap \mathbb{S}_0(\mathcal{T}) \leq 4k \mid \varphi_0]. \end{aligned}$$

As before, these distances are defined as $\mathbb{S}_i(\mathcal{T}) = \max\{N_i(x) : x \in \mathcal{T}\}$, for $i = 1, 2, 3, 0$, where $N_i(x)$ counts a number of blocks in a sequence associated to the node x .

We first need to label the arcs of the tree. As before, we mark with a 0 each parental arc. Now, at a birth there may be up to 3 children. Going from left to right, we give the mark 1 to the first child arc, 2 to the second child arc (if any), and 3 to the third one (if any).

As before, the first child branch is made up of arcs with label 1 only, starting from the root, and we denote it as \mathcal{L}_1 . Similarly, recall that the parental branch \mathcal{R} is made up of arcs will label 0 only, starting from the root. Now, let us note by \mathcal{L}_2 the branch starting from the root and formed of second child arcs only, and by \mathcal{L}_3 the branch

starting from the root and formed of third child arcs only. If one of these principal branches is empty, which happens if the first birth generates less than the maximum number of children, then it will be assumed to be constituted of the root arc only, the root thus belonging to $\mathcal{L}_1, \mathcal{L}_2, \mathcal{L}_3$, and \mathcal{R} .

To each node $x \in \mathcal{T}$, we associate now four sequences, $\text{path}_i(x)$ for $i = 1, 2, 3, 0$. The sequence $\text{path}_i(x)$ is the string of labels which mark the shortest path from x to the branch \mathcal{L}_i for $i = 1, 2, 3$, or to the branch \mathcal{R} for $i = 0$. The counter $N_i(x)$ is equal to the number of blocks in the sequence $\text{path}_i(x)$, but here the definition of a *block* is a bit more involved than for the MBT case.

Let us introduce some notations in the form of regular expressions. We use ℓ^* to represent a succession (which can be empty) of an unspecified number of copies of the symbol ℓ ; the concatenation ℓm is read as “ ℓ followed by m ”; and finally $\ell + m$ is read as “ ℓ or m ”.

In order to form the blocks in the sequences $\text{path}_i(x)$, we need the following diagram that we skim through following the direction of the arrows (that is, *from right to left*), and in which we have four principal types of blocks: B_0, B_1, B_2 and B_3 . The order in which we consider the blocks reflects the order in which the successive equations of the Thicknesses algorithm are applied.

$$\underbrace{1^*(1+3+0)}_{B_1} \leftarrow \underbrace{2^*(1+2+0)}_{B_2} \leftarrow \underbrace{3^*(1+2+3)}_{B_3} \leftarrow \underbrace{0^*(2+3+0)}_{B_0} \quad (2.38)$$

The block of B_0 -type is constituted of a single 2 or 3 or 0, possibly followed by a string of 0’s. Similarly, the block of B_3 -type is constituted of a single 1 or 2 or 3, possibly succeeded by a string of 3’s. In the same idea we define the blocks of B_2 - and B_1 -types.

Now, let us show how to aggregate the labels into blocks in the sequences $\text{path}_i(x)$, $i = 1, 2, 3, 0$. We give the details for $i = 1$. Take for example the string

$$\text{path}_1(x) = 210033203212003 \quad (2.39)$$

associated with a node x . The identification of the blocks is made using the scheme (2.38), by considering each label of the sequence, starting from *the right* and scanning it *from right to left*. For $i = 1$, we start by identifying a first block of B_0 -type; indeed, the rightmost label in $\text{path}_1(x)$ is always different from 1 since $\text{path}_1(x)$ represents the sequence of labels from x to \mathcal{L}_1 . Then, we cyclically identify blocks of types B_3, B_2, B_1 , and B_0 .

The first block of B_0 -type in the sequence $\text{path}_1(x)$ is constituted of the first label with all the possibly succeeding 0’s. We obtain for the sequence (2.39)

$$\text{path}_1(x) = 210033203212 \quad \underbrace{003}_{\text{First block of } B_0\text{-type}} \quad .$$

Once the first block is identified, the following label (if there is any) taken in the sequence, still traversing it from right to left, now belongs to a block of B_3 -type, which

is also constituted of all the possibly succeeding 3's. For our example, we get

$$\text{path}_1(x) = 21003320321 \quad \underbrace{2}_{\text{Second block of } B_3\text{-type}} \quad \underbrace{003}_{\text{First block of } B_0\text{-type}} .$$

The next label and all the possibly succeeding 2's belong to a block of B_2 -type, and so on. We finally obtain for the sequence (2.39)

$$\text{path}_1(x) = \underbrace{2}_{B_0} \underbrace{10}_{B_1} \underbrace{0}_{B_2} \underbrace{332}_{B_3} \underbrace{0}_{B_0} \underbrace{3}_{B_1} \underbrace{21}_{B_2} \underbrace{2}_{B_3} \underbrace{003}_{B_0} .$$

For $i = 2, 3, 0$, the aggregation of $\text{path}_i(x)$ into blocks works exactly the same as for $i = 1$, the only difference being the first block considered when starting from the right of the sequence: it must be

- a B_1 -type block for $i = 2$,
- a B_2 -type block for $i = 3$,
- a B_3 -type block for $i = 0$.

The order of consideration of the different blocks still follows the scheme (2.38).

The quantity $N_i(x)$ is then defined as the number of blocks formed in the sequence $\text{path}_i(x)$ associated with the node x . In the example above, we see that $N_1(x) = 9$.

With the probabilistic interpretation of each stage of the Thicknesses algorithm and the definition of the four thicknesses, we can now justify, for instance, the step $\mathbf{q}_2(4k - 2)$ of the algorithm. It may be rewritten as

$$\begin{aligned} \mathbf{q}_2(4k - 2) &= \boldsymbol{\theta} + \Psi_1 [\mathbf{q}_1(4k - 3) \otimes \mathbf{q}_1(4k - 3)] \\ &\quad + \Psi_2 [\mathbf{q}_1(4k - 3) \otimes \mathbf{q}_2(4k - 2) \otimes \mathbf{q}_1(4k - 3)] \\ &\quad + \Psi_3 [\mathbf{q}_1(4k - 3) \otimes \mathbf{q}_2(4k - 2) \otimes \mathbf{q}_1(4k - 3) \otimes \mathbf{q}_1(4k - 3)]. \end{aligned}$$

Let us interpret the right-hand side. There exist two cases where a tree \mathcal{T} eventually gets extinct with a thickness $\mathbb{S}_2(\mathcal{T})$ at most equal to $4k - 2$: either death occurs before the first birth, or a birth occurs first. In the latter case,

- whatever the number of children, there is always a first child subtree \mathcal{T}^{l_1} and a parental subtree \mathcal{T}^r , which eventually become extinct with a thickness $\mathbb{S}_1(\mathcal{T}^{l_1})$ and $\mathbb{S}_1(\mathcal{T}^r)$ at most equal to $4k - 3$; indeed, in order to reach the branch \mathcal{L}_2 of the whole tree \mathcal{T} with at most $4k - 2$ blocks, we first have to reach the branch \mathcal{L}_1 in \mathcal{T}^{l_1} , and in \mathcal{T}^r , with at most $4k - 3$ blocks, and then add one block of B_1 -type to reach \mathcal{L}_2 ; this happens with probability $\mathbf{q}_1(4k - 3)$;
- if there is a second child, then the associated subtree \mathcal{T}^{l_2} eventually becomes extinct with a thickness $\mathbb{S}_2(\mathcal{T}^{l_2})$ at most equal to $4k - 2$, since the branch \mathcal{L}_2 in \mathcal{T}^{l_2} is part of the branch \mathcal{L}_2 in the entire tree \mathcal{T} ;

- finally, if there is a third child, its associated subtree \mathcal{T}^{l_3} eventually becomes extinct with a thickness $\mathbb{S}_1(\mathcal{T}^{l_3})$ at most equal to $4k - 3$, for the same reasons as for the subtrees \mathcal{T}^{l_1} and \mathcal{T}^r .

As for the MBT case, one proves that the event $[\mathcal{T} < \infty]$ implies the four events $[\mathbb{S}_1(\mathcal{T}) < \infty]$, $[\mathbb{S}_2(\mathcal{T}) < \infty]$, $[\mathbb{S}_3(\mathcal{T}) < \infty]$ and $[\mathbb{S}_0(\mathcal{T}) < \infty]$, so that

$$\lim_{k \rightarrow \infty} \mathbf{q}_1(4k - 3) = \lim_{k \rightarrow \infty} \mathbf{q}_2(4k - 2) = \lim_{k \rightarrow \infty} \mathbf{q}_3(4k - 1) = \lim_{k \rightarrow \infty} \mathbf{q}_0(4k) = \mathbf{q}.$$

Now, we consider the case where $2 \leq M < \infty$ is smaller than the maximal number of branches after a birth (for instance if that number is unbounded).

The parental arcs of the tree still take the label 0, and the $M - 1$ first children arcs take the labels 1 to $M - 1$; now, we give the common label \blacktriangle to the other children arcs.

As previously, we define M principal branches: the parental branch \mathcal{R} , and the children branches \mathcal{L}_i , for $i = 1, 2, \dots, M - 1$. They are associated with M thicknesses measures $\mathbb{S}_i(\mathcal{T})$, $i = 0, 1, \dots, M - 1$, and the interpretation of the Thicknesses algorithm still goes as

$$\mathbf{q}_{Mk+i} = \mathbb{P}[\mathcal{T} < \infty \cap \mathbb{S}_i(\mathcal{T}) \leq Mk + i \mid \varphi_0], \quad k \geq 0, 0 \leq i \leq M - 1.$$

The definition of the M thicknesses of a tree is exactly the same as before, the only difference being that the sequences $\text{path}_i(\cdot)$ associated to the nodes of the tree may include the label \blacktriangle . The rule of labels aggregation in blocks must then take the label \blacktriangle into account, and becomes, in the case $M = 4$ for instance,

$$\underbrace{1^* (1 + 3 + \blacktriangle + 0)}_{B_1} \leftarrow \underbrace{2^* (1 + 2 + \blacktriangle + 0)}_{B_2} \leftarrow \underbrace{3^* (1 + 2 + 3 + \blacktriangle)}_{B_3} \leftarrow \underbrace{0^* (2 + 3 + \blacktriangle + 0)}_{B_0},$$

to compare with (2.38). This generalizes to any $M \geq 2$.

CHAPTER 3

Quadratic algorithms

We apply Newton's method to the quadratic matrix extinction equation for MBTs, and we prove that the resulting sequence is globally and quadratically convergent. Each iteration may be interpreted as the extinction probability of the branching process, under a set of constraints which become weaker at each step.

We use the Newton algorithm on the two examples described in Section 2.4. We also return to the demographic application and we compute, for each country, the extinction probability of a female family. We compare the performances of the Newton algorithm and of the linear algorithms studied in the preceding chapter on all these examples.

Finally, we show that we can obtain at least three other quadratic sequences by modifying the formulation of the extinction equation. We study in detail the convergence properties of one of them, that is shown to be more efficient than the Newton algorithm in terms of the number of iterations required to converge.

The material in this chapter is published with somewhat more details in Hautphenne, Latouche and Remiche [27] and in Hautphenne and van Houdt [32].

3.1 The Newton algorithm

Let us rewrite the extinction equation (1.15) as $\mathcal{F}(\mathbf{x}) = \mathbf{0}$, where

$$\mathcal{F}(\mathbf{x}) = \mathbf{x} - \boldsymbol{\theta} - \Psi(\mathbf{x} \otimes \mathbf{x}). \quad (3.1)$$

The function \mathcal{F} is a mapping from \mathbb{R}^n into itself. In order to apply Newton's method to solve $\mathcal{F}(\mathbf{x}) = \mathbf{0}$, we need the following definition from Ortega and Rheinboldt [58].

Definition 3.1.1. The mapping $\mathbf{F} : D \subset \mathbb{R}^n \rightarrow \mathbb{R}^m$ is Fréchet-differentiable at $\mathbf{x} \in \text{int}(D)$ if there exists a linear operator A from \mathbb{R}^n to \mathbb{R}^m such that

$$\lim_{\mathbf{h} \rightarrow \mathbf{0}} \frac{\|\mathbf{F}(\mathbf{x} + \mathbf{h}) - \mathbf{F}(\mathbf{x}) - A\mathbf{h}\|}{\|\mathbf{h}\|} = 0.$$

The linear operator A is denoted by F'_x and is called the Fréchet derivative of \mathbf{F} at \mathbf{x} .

The Fréchet derivative of \mathcal{F} at \mathbf{x} is a linear map \mathcal{F}'_x given by

$$\mathcal{F}'_x : \mathbf{z} \mapsto [I - \Psi(\mathbf{x} \oplus \mathbf{x})] \mathbf{z} = \mathbf{z} - \Psi(\mathbf{z} \otimes \mathbf{x} + \mathbf{x} \otimes \mathbf{z}).$$

For a given \mathbf{x}_0 , the Newton sequence for the solution of $\mathcal{F}(\mathbf{x}) = \mathbf{0}$ is

$$\mathbf{x}_{k+1} = \mathbf{x}_k - (\mathcal{F}'_{\mathbf{x}_k})^{-1} \mathcal{F}(\mathbf{x}_k) \tag{3.2}$$

$$= \mathbf{x}_k - [I - \Psi(\mathbf{x}_k \oplus \mathbf{x}_k)]^{-1} [\mathbf{x}_k - \boldsymbol{\theta} - \Psi(\mathbf{x}_k \otimes \mathbf{x}_k)] \tag{3.3}$$

$$= [I - \Psi(\mathbf{x}_k \oplus \mathbf{x}_k)]^{-1} [\boldsymbol{\theta} - \Psi(\mathbf{x}_k \otimes \mathbf{x}_k)], \tag{3.4}$$

for $k \geq 0$, provided that $\mathcal{F}'_{\mathbf{x}_k}$ is invertible for all k .

Theorem 3.1.2. For any \mathbf{x}_0 in $\langle \mathbf{0}, \boldsymbol{\theta} \rangle$, the Newton iteration (3.4) is such that

- (a) the sequence $\{\mathbf{x}_k\}$ is well defined,
- (b) $\mathbf{x}_0 \leq \mathbf{x}_1 \leq \mathbf{x}_2 \leq \dots$, and
- (c) $\lim_{k \rightarrow \infty} \mathbf{x}_k = \mathbf{q}$.

Moreover, there exists a positive constant c such that

$$\|\mathbf{x}_{k+1} - \mathbf{q}\| \leq c \|\mathbf{x}_k - \mathbf{q}\|^2, \tag{3.5}$$

so that the Newton algorithm converges (at least) quadratically.

Before proving this theorem, we need a few preliminary results.

Lemma 3.1.3. Assume that the process is supercritical and irreducible. We have

$$\mathcal{F}(\mathbf{x}) - \mathcal{F}(\mathbf{y}) \geq \mathcal{F}'_{\mathbf{x}}(\mathbf{x} - \mathbf{y}), \tag{3.6}$$

for all $\mathbf{x} \leq \mathbf{y}$ in $\langle \mathbf{0}, \mathbf{q} \rangle$.

The inverse $P(\mathbf{x}) = [I - \Psi(\mathbf{x} \oplus \mathbf{x})]^{-1}$ of $\mathcal{F}'_{\mathbf{x}}$ exists for all \mathbf{x} in $\langle \mathbf{0}, \mathbf{q} \rangle$ and is non negative. Furthermore, $P(\mathbf{x}) \leq P(\mathbf{y})$ for all $\mathbf{x} \leq \mathbf{y}$ in $\langle \mathbf{0}, \mathbf{q} \rangle$.

Proof. Firstly,

$$\begin{aligned} \mathcal{F}(\mathbf{x}) - \mathcal{F}(\mathbf{y}) &= (\mathbf{x} - \mathbf{y}) - \Psi(\mathbf{x} \otimes \mathbf{x}) + \Psi(\mathbf{y} \otimes \mathbf{y}) \\ &= (\mathbf{x} - \mathbf{y}) - \Psi(\mathbf{x} \otimes (\mathbf{x} - \mathbf{y})) - \Psi((\mathbf{x} - \mathbf{y}) \otimes \mathbf{y}) \\ &\geq \mathcal{F}'_{\mathbf{x}}(\mathbf{x} - \mathbf{y}) \end{aligned}$$

since $\mathbf{x} \leq \mathbf{y}$.

It follows from Corollary 2.3.3 that $\text{sp}[\Psi(\mathbf{x} \oplus \mathbf{x})] < 1$ for all \mathbf{x} in $\langle \mathbf{0}, \mathbf{q} \rangle$, so that the inverse $P(\mathbf{x})$ does exist, and

$$P(\mathbf{y}) = \sum_{n \geq 0} [\Psi(\mathbf{y} \oplus \mathbf{y})]^n \geq \sum_{n \geq 0} [\Psi(\mathbf{x} \oplus \mathbf{x})]^n = P(\mathbf{x}) \geq 0$$

for all $\mathbf{x} \leq \mathbf{y}$ in $\langle \mathbf{0}, \mathbf{q} \rangle$. \square

The proposition below is norm-independent, although it will sometimes be convenient to use the L^∞ -norm for vectors and matrices.

Lemma 3.1.4. *The operator \mathcal{F}' is Lipschitz-continuous on $\langle \mathbf{0}, \mathbf{q} \rangle$, that is, there exists a constant γ such that*

$$\|\mathcal{F}'_{\mathbf{x}} - \mathcal{F}'_{\mathbf{y}}\| \leq \gamma \|\mathbf{x} - \mathbf{y}\| \quad \forall \mathbf{x}, \mathbf{y} \in \langle \mathbf{0}, \mathbf{q} \rangle. \quad (3.7)$$

Proof. Assume that \mathbf{h} is a vector of norm 1, and that \mathbf{x}, \mathbf{y} are two vectors in $\langle \mathbf{0}, \mathbf{q} \rangle$. We may write

$$[\mathcal{F}'_{\mathbf{x}} - \mathcal{F}'_{\mathbf{y}}] \mathbf{h} = \Psi((\mathbf{y} - \mathbf{x}) \oplus (\mathbf{y} - \mathbf{x})) \mathbf{h}.$$

Thus, we have

$$\|[\mathcal{F}'_{\mathbf{x}} - \mathcal{F}'_{\mathbf{y}}] \mathbf{h}\| \leq 2c \|\Psi\| \|\mathbf{x} - \mathbf{y}\|$$

where c is a finite constant, since $\|\mathbf{h}\| = 1$ and since $\|\mathbf{x} \otimes I\|_\infty = \|I \otimes \mathbf{x}\|_\infty = \|\mathbf{x}\|_\infty$. This proves (3.7) with $\gamma = 2c \|\Psi\| < \infty$. \square

We are now in a position to prove Theorem 3.1.2.

Proof of Theorem 3.1.2 It closely follows those of Propositions 13.2.3 and of the Monotone Newton Theorem 13.3.4 in [58].

We start by showing that if $\mathbf{0} \leq \mathbf{x}_0 \leq \boldsymbol{\theta}$, then $\mathbf{0} \leq \mathbf{x}_k \leq \mathbf{x}_{k+1} \leq \mathbf{q}$, and $\mathcal{F}(\mathbf{x}_k) \leq \mathbf{0}$, for all k .

First, it results from (3.6) that $\mathcal{F}(\mathbf{0}) - \mathcal{F}(\mathbf{x}_0) \geq \mathcal{F}'_{\mathbf{0}}(\mathbf{0} - \mathbf{x}_0)$, which shows that $\mathcal{F}(\mathbf{x}_0) \leq \mathbf{0}$, since $\mathcal{F}(\mathbf{0}) = -\boldsymbol{\theta}$ and $\mathcal{F}'_{\mathbf{0}}$ is the identity operator.

Now, make the induction assumption that $\mathbf{0} \leq \mathbf{x}_k \leq \mathbf{q}$, and that $\mathcal{F}(\mathbf{x}_k) \leq \mathbf{0}$, for some $k \geq 0$. This implies that $P(\mathbf{x}_k) \geq 0$, by Lemma 3.1.3. Furthermore, $\mathbf{x}_k \leq \mathbf{x}_{k+1}$ by (3.2).

Using (3.2) and Lemma 3.1.3 again, we find that, for any $\mathbf{z} \in \langle \mathbf{x}_k, \mathbf{q} \rangle$,

$$\begin{aligned} \mathbf{z} - P(\mathbf{x}_k) \mathcal{F}(\mathbf{z}) &= \mathbf{x}_{k+1} - (\mathbf{x}_k - \mathbf{z}) + P(\mathbf{x}_k)(\mathcal{F}(\mathbf{x}_k) - \mathcal{F}(\mathbf{z})) \\ &\geq \mathbf{x}_{k+1} - [I - P(\mathbf{x}_k) \mathcal{F}'_{\mathbf{x}_k}](\mathbf{x}_k - \mathbf{z}) \\ &= \mathbf{x}_{k+1} \end{aligned}$$

and, in particular, this implies that $\mathbf{q} = \mathbf{q} - P(\mathbf{x}_k) \mathcal{F}(\mathbf{q}) \geq \mathbf{x}_{k+1}$. Thus $\mathbf{0} \leq \mathbf{x}_k \leq \mathbf{x}_{k+1} \leq \mathbf{q}$.

Finally, by Lemma 3.1.3 and (3.2),

$$\mathcal{F}(\mathbf{x}_{k+1}) \leq \mathcal{F}(\mathbf{x}_k) + \mathcal{F}'_{\mathbf{x}_k}(\mathbf{x}_{k+1} - \mathbf{x}_k) = [I - \mathcal{F}'_{\mathbf{x}_k} P(\mathbf{x}_k)] \mathcal{F}(\mathbf{x}_k) = \mathbf{0},$$

which completes the induction.

As a bounded, nondecreasing sequence, $\{\mathbf{x}_k\}$ has a limit $\mathbf{x}^* \leq \mathbf{q}$. We now show that $\mathcal{F}(\mathbf{x}^*) = \mathbf{0}$.

Using Lemma 3.1.3, we observe that $0 \leq P(\mathbf{x}_0) \leq P(\mathbf{x}_k)$, since $\mathbf{x}_0 \leq \mathbf{x}_k$ for all $k \geq 0$; also, $\mathcal{F}(\mathbf{x}_k) \leq \mathbf{0}$, so that

$$\mathbf{x}_k - \mathbf{x}_{k+1} = P(\mathbf{x}_k) \mathcal{F}(\mathbf{x}_k) \leq P(\mathbf{x}_0) \mathcal{F}(\mathbf{x}_k) \leq \mathbf{0}.$$

We know that $\lim_{k \rightarrow \infty} (\mathbf{x}_k - \mathbf{x}_{k+1}) = \mathbf{0}$, so that $\lim_{k \rightarrow \infty} P(\mathbf{x}_0) \mathcal{F}(\mathbf{x}_k) = \mathbf{0}$. As a consequence of Lemma 3.1.4 above and Propositions 3.2.8 and 3.1.6 in [58], the operator \mathcal{F} is continuous at \mathbf{x}^* , and $P(\mathbf{x}_0) \mathcal{F}(\mathbf{x}^*) = \mathbf{0}$. Since $P(\mathbf{x}_0)$ is nonsingular, it follows that $\mathcal{F}(\mathbf{x}^*) = \mathbf{0}$ and we have proved that $\mathbf{x}^* \leq \mathbf{q}$ is a solution of $\mathcal{F}(\mathbf{x}) = \mathbf{0}$.

We also know that \mathbf{q} is the smallest nonnegative solution of $\mathcal{F}(\mathbf{x}) = \mathbf{0}$. This implies that $\mathbf{x}^* = \mathbf{q}$ and that $\lim_{k \rightarrow \infty} \mathbf{x}_k = \mathbf{q}$.

It remains for us to prove (3.5). By Lemmas 3.1.3 and 3.1.4, the operator \mathcal{F}' is nonsingular and continuous on $\langle \mathbf{0}, \mathbf{q} \rangle$, therefore, there exists a β such that $\|P(\mathbf{x})\| \leq \beta$, for all \mathbf{x} in $\langle \mathbf{0}, \mathbf{q} \rangle$, and

$$\begin{aligned} \|\mathbf{x}_{k+1} - \mathbf{q}\| &= \|\mathbf{x}_k - \mathbf{q} - P(\mathbf{x}_k)(\mathcal{F}(\mathbf{x}_k) - \mathcal{F}(\mathbf{q}))\| \\ &\leq \beta \|\mathcal{F}'_{\mathbf{x}_k}(\mathbf{x}_k - \mathbf{q}) - (\mathcal{F}(\mathbf{x}_k) - \mathcal{F}(\mathbf{q}))\| \\ &\leq \frac{1}{2} \beta \gamma \|\mathbf{x}_k - \mathbf{q}\|^2, \end{aligned}$$

by the mean-value Theorem [58, Proposition 3.2.12], and we take $c = \frac{1}{2} \beta \gamma$. \square

In principle, the starting point \mathbf{x}_0 might thus be chosen anywhere in $\langle \mathbf{0}, \boldsymbol{\theta} \rangle$ but, in practise, one would choose a point as close as possible to the solution \mathbf{q} , and set $\mathbf{x}_0 = \boldsymbol{\theta}$.

Convergence rate

Let us now investigate more accurately the convergence rate of the Newton algorithm. Noting by \mathbf{q}_n the n th approximation of \mathbf{q} , and by $\mathbf{E}_n = \mathbf{q} - \mathbf{q}_n$ its approximation error, we easily obtain an upper bound:

$$\mathbf{E}_n \leq [I - \Psi(\mathbf{q} \oplus \mathbf{q})]^{-1} \Psi(\mathbf{E}_{n-1} \otimes \mathbf{E}_{n-1}). \quad (3.8)$$

By Theorem 2.3.1, we know that in the critical case the matrix $I - \Psi(\mathbf{q} \oplus \mathbf{q})$ in (3.8) is singular, and the upper-bound of \mathbf{E}_n is thus not well-defined. Like for the linear algorithms, we should expect that the Newton algorithm converges slowly when the process is nearly critical.

Otherwise, Theorem 3.1.2 shows that the convergence is at least quadratic. With (3.8), we see that it is likely to be exactly quadratic since the error \mathbf{E}_{n-1} appears in a quadratic form. In order to prove this precisely, we call upon the Newton attraction Theorem [58, Theorem 10.2.2], three of its assumptions being readily seen to hold:

- \mathcal{F}' is continuous at \mathbf{q} by Lemma 3.1.4;

- $\mathcal{F}'_q = I - \Psi(\mathbf{q} \oplus \mathbf{q})$ is nonsingular by Theorem 2.3.1;
- there is a constant $\alpha < \infty$ such that $\|\mathcal{F}'_x - \mathcal{F}'_q\| \leq \alpha \|\mathbf{x} - \mathbf{q}\|$, for all x in $\langle \mathbf{0}, \mathbf{q} \rangle$ by (3.7).

The fourth required assumption is that $\mathcal{F}''(\mathbf{q})\mathbf{h}\mathbf{h} = -2\Psi(\mathbf{h} \otimes \mathbf{h})$ should be different from $\mathbf{0}$ for $\mathbf{h} \neq \mathbf{0}$, which is not true in all generality. To give one example only, assume that there is a phase (call it the phase “1”) such that $B_{i,1,1} = 0$ for all i , meaning that it is not possible at a time of birth that both the parent and the child should enter into phase 1; if the vector \mathbf{h} has only its first component different from zero, then $\mathcal{F}''(\mathbf{q})\mathbf{h}\mathbf{h} = \mathbf{0}$.

Nevertheless, if we assume that from each phase there is a path to extinction (Assumption (1.2.2)), then we are led to $\mathbf{q} > \mathbf{0}$. In that case, it is likely that the sequence $\{\mathbf{x}_k\}$ will stay in the interior of $\langle \mathbf{0}, \mathbf{q} \rangle$, so that $\mathbf{q} - \mathbf{x}_k > \mathbf{0}$ and

$$\mathcal{F}''(\mathbf{q})(\mathbf{q} - \mathbf{x}_k)(\mathbf{q} - \mathbf{x}_k) \neq \mathbf{0},$$

which is the property really needed in [58, Theorem 10.2.2].

3.2 Probabilistic interpretation

We now give a probabilistic interpretation of the Newton algorithm when $\mathbf{x}_0 = \boldsymbol{\theta}$. Each iteration may then be interpreted as the probability that the MBT eventually becomes extinct under some constraint. More precisely, we show that at each stage, the Newton algorithm computes the probability that the MBT becomes extinct *and* that the associated binary tree belongs to an increasing sequence \mathcal{X}_k of sets of trees.

The sequence is defined below, but first we need to introduce some notations. Let $\Delta_k = \mathbf{x}_k - \mathbf{x}_{k-1}$, with $\Delta_0 = \boldsymbol{\theta}$, be the increment between the $(k-1)$ th and the k th approximations of the algorithm, for $k \geq 1$. We know that $\Delta_k \geq \mathbf{0}$ for all k . Using (3.3), we can write

$$\Delta_k = [I - \Psi(\mathbf{x}_{k-1} \oplus \mathbf{x}_{k-1})]^{-1} \boldsymbol{\epsilon}_k, \quad k \geq 1, \quad (3.9)$$

where

$$\begin{aligned} \boldsymbol{\epsilon}_k &= \boldsymbol{\theta} + \Psi(\mathbf{x}_{k-1} \otimes \mathbf{x}_{k-1}) - \mathbf{x}_{k-1} \\ &= \boldsymbol{\theta} + \Psi(\mathbf{x}_{k-2} \oplus \mathbf{x}_{k-2})\mathbf{x}_{k-1} - \Psi(\mathbf{x}_{k-2} \otimes \mathbf{x}_{k-2}) \\ &\quad + \Psi(\Delta_{k-1} \otimes \Delta_{k-1}) - \mathbf{x}_{k-1} \\ &= \Psi(\Delta_{k-1} \otimes \Delta_{k-1}), \end{aligned} \quad (3.10)$$

by (3.4).

The sets of trees are recursively defined as follows: we start with \mathcal{X}_0 which is the set of trees made up of one leaf only, and $\mathcal{D}_0 = \mathcal{X}_0$. Then, for $k \geq 1$,

- a tree is in \mathcal{E}_k if it is finite and has two subtrees, both belonging to \mathcal{D}_{k-1} ;

- a tree is in \mathcal{D}_k if it is finite and, in addition, either it is in \mathcal{E}_k , or it has two subtrees, one in \mathcal{X}_{k-1} and one in \mathcal{D}_k itself;
- the set \mathcal{X}_k is the union of $\mathcal{D}_0, \mathcal{D}_1, \dots, \mathcal{D}_k$.

These relations may be summarized as follows, for $k \geq 1$,

$$\begin{aligned} \mathcal{X}_k &= \mathcal{X}_{k-1} \cup \mathcal{D}_k \\ \mathcal{D}_k &= \begin{array}{c} | \\ \text{---} \bullet \text{---} \\ | \quad | \\ \mathcal{D}_{k-1} \quad \mathcal{D}_{k-1} \end{array} \cup \begin{array}{c} | \\ \text{---} \bullet \text{---} \\ | \quad | \\ \mathcal{X}_{k-1} \quad \mathcal{D}_k \end{array} \cup \begin{array}{c} | \\ \text{---} \bullet \text{---} \\ | \quad | \\ \mathcal{D}_k \quad \mathcal{X}_{k-1} \end{array} \end{aligned}$$

Theorem 3.2.1. *If $\mathbf{x}_0 = \boldsymbol{\theta}$, then the vector \mathbf{x}_k in the Newton sequence (3.4) is, for all $k \geq 0$, the vector of probabilities $P[\mathcal{T} \in \mathcal{X}_k | \varphi_0]$, that is, the conditional probability that the MBT \mathcal{T} belongs to \mathcal{X}_k and becomes extinct, given its initial phase. Furthermore, $\Delta_k = P[\mathcal{T} \in \mathcal{D}_k | \varphi_0]$.*

Proof. The proof is by induction. For $k = 0$, the property holds by definition. Assume that it holds up to $k - 1$.

We immediately find that

$$P[\mathcal{T} \in \mathcal{E}_k | \varphi_0] = \Psi(\Delta_{k-1} \otimes \Delta_{k-1}) = \boldsymbol{\epsilon}_k,$$

by (3.10). Indeed, the initial phases of the two subtrees are chosen with the matrix Ψ , they both belong to \mathcal{D}_{k-1} and become extinct with probability Δ_{k-1} , by the induction assumption.

Now, if we denote by \mathbf{z} the vector of probabilities $P[\mathcal{T} \in \mathcal{D}_k | \varphi_0]$, we find that

$$\begin{aligned} \mathbf{z} &= \boldsymbol{\epsilon}_k + \Psi(\mathbf{x}_{k-1} \otimes \mathbf{z}) + \Psi(\mathbf{z} \otimes \mathbf{x}_{k-1}) \\ &= \boldsymbol{\epsilon}_k + \Psi(\mathbf{x}_{k-1} \oplus \mathbf{x}_{k-1})\mathbf{z} \\ &= [I - \Psi(\mathbf{x}_{k-1} \oplus \mathbf{x}_{k-1})]^{-1} \boldsymbol{\epsilon}_k \\ &= \Delta_k \end{aligned}$$

by (3.9).

Finally, if we can show that the sets \mathcal{X}_{k-1} and \mathcal{D}_k are disjoint, then

$$P[\mathcal{T} \in \mathcal{X}_k | \varphi_0] = \mathbf{x}_{k-1} + \Delta_k = \mathbf{x}_k$$

by definition of Δ_k .

By definition of \mathcal{X}_{k-1} , it is disjoint from \mathcal{D}_k for all $k \geq 1$ if and only if \mathcal{D}_k and \mathcal{D}_i are disjoint for all $k \geq 1$ and all $i \leq k - 1$. This is equivalent to the claim that all the sets \mathcal{D}_k are disjoint, $k \geq 0$. We show this by induction on k .

We proceed as follows: let us assume that for all $i \leq k - 1$ and for all $j \geq i + 1$, $\mathcal{D}_i \cap \mathcal{D}_j = \emptyset$. This is true for $k = 1$ since the trees in \mathcal{D}_0 do not have any branching point. We have to show that for all $j \geq k + 1$, $\mathcal{D}_k \cap \mathcal{D}_j = \emptyset$.

Assume that there exists some tree \mathcal{T} with $\mathcal{T} \in \mathcal{D}_k$ and $\mathcal{T} \in \mathcal{D}_j$, for some $j \geq k+1$. The tree \mathcal{T} being in \mathcal{D}_k , it has two subtrees and either both are in \mathcal{D}_{k-1} , or one of the left or right subtrees is in \mathcal{D}_k with the other one being anywhere in $\mathcal{X}_{k-1} = \mathcal{D}_0 \cup \mathcal{D}_1 \cup \dots \cup \mathcal{D}_{k-1}$. A similar conclusion is drawn from the fact that \mathcal{T} is in \mathcal{D}_j : both subtrees are in \mathcal{D}_{j-1} or one is in \mathcal{D}_j and the other is in $\mathcal{X}_{j-1} = \mathcal{D}_0 \cup \mathcal{D}_1 \cup \dots \cup \mathcal{D}_{j-1}$.

By exhaustive enumeration of all nine possible consequences, we are led to one of two cases. In the first case, there exist some indices ℓ and n such that $\ell \leq k-1 < k \leq n$ and $\mathcal{D}_\ell \cap \mathcal{D}_n \neq \emptyset$. But this contradicts the induction assumption.

In the second case, one of the subtrees, call it \mathcal{T}^* , belongs to both \mathcal{D}_k and \mathcal{D}_j , $j \geq k+1$. We thus repeat the same argument with \mathcal{T}^* . Since the initial tree is finite and every subtree contains a number of nodes which is strictly finite, it is impossible to indefinitely be left with the only conclusion that one of the subtrees belongs to both \mathcal{D}_k and \mathcal{D}_j . Thus, we will eventually find a contradiction like in the first case. This concludes our proof. \square

3.3 Numerical examples

Let us take again the two examples discussed in Section 2.4. For the linear and quadratic algorithms, we compare the approximation errors, two residuals and the mean CPU execution time (over a set of 100 simulations, using Matlab with Intel 2.4 GHz).

For Example 2.4.1 (branches of varying length), we depict on Figure 3.1 the number of iterations needed to compute \mathbf{q} with the Newton algorithm, as a function of δ . As expected, we see that it is greatest when the process is nearly critical.

On Figure 3.2, we plot $\log_{10} \|\mathbf{E}_n\|_\infty$ and we compare the convergence rates of the algorithms when $\delta = 2$. Since we do not know a priori the exact value of \mathbf{q} , we do not have the exact value of \mathbf{E}_n neither. Instead, we use the difference $\mathbf{q}^* - \mathbf{q}_n$ where \mathbf{q}^* is the value of \mathbf{q} obtained numerically. Here, and in all examples, we have used $\|\mathbf{q}_n - \mathbf{q}_{n-1}\|_\infty < 10^{-10}$ as the stopping criterion. We see that after a very few iterations, the Newton algorithm has converged, and that the Thicknesses algorithm is really faster than the other linear algorithms, as already emphasized in Section 2.4.

One usually computes two types of residuals: the absolute residual

$$r_1 = \|\mathbf{q}^* - \boldsymbol{\theta} - \Psi(\mathbf{q}^* \otimes \mathbf{q}^*)\|_\infty,$$

and the relative residual

$$r_2 = \frac{\|\mathbf{q}^* - \boldsymbol{\theta} - \Psi(\mathbf{q}^* \otimes \mathbf{q}^*)\|_1}{\|\mathbf{q}^*\|_1 + \|\boldsymbol{\theta}\|_1 + \|\Psi(\mathbf{q}^* \otimes \mathbf{q}^*)\|_1}.$$

Table 3.1 shows the number of iterations and the residuals for each algorithm, as well as the CPU time expressed in seconds.

Algorithm	Iterations	r_1	r_2	CPU time
Newton	9	$2.00 \cdot 10^{-14}$	$1.00 \cdot 10^{-14}$	0.002
Thicknesses	181	$2.03 \cdot 10^{-12}$	$4.50 \cdot 10^{-13}$	0.026
Order-1	3002	$9.87 \cdot 10^{-11}$	$2.76 \cdot 10^{-11}$	0.8038
Order-0	3529	$9.90 \cdot 10^{-11}$	$2.76 \cdot 10^{-11}$	1.0263
Depth	5705	$9.96 \cdot 10^{-11}$	$5.07 \cdot 10^{-11}$	2.1077

Table 3.1: Comparison of the number of iterations, the residuals, and the CPU time (in seconds) for the algorithms with $\delta = 2$.

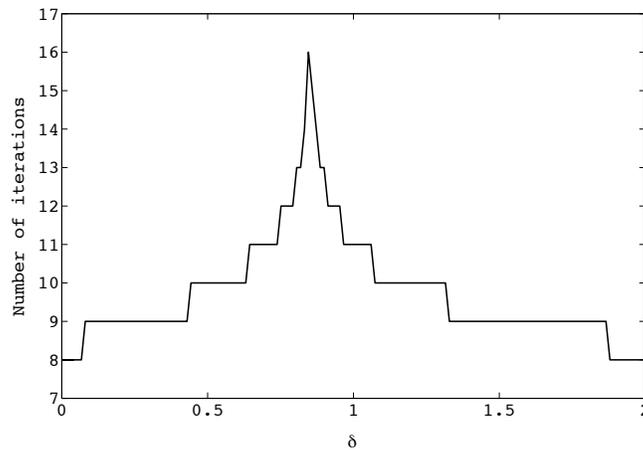


Figure 3.1: Number of iterations for the Newton algorithm as a function of δ .

For Example 2.4.2 (nearly-critical MBT), Figure 3.3 depicts the number of iterations required with the Newton algorithm, as a function of the parameter p . This number is again very small compared to the linear algorithms. We see that when p gets close to the critical case (that is, around the values $p = 0.34$ and $p = 0.84$), the algorithm convergence is increasingly slow.

We note from Figure 2.6 that the process seems to be the most supercritical for p about 0.6. For this value, we give in Table 3.2 the number of iterations and the residuals for each algorithm. The CPU time here is much less meaningful than for the first example as it is quite small; we give these numbers for completeness sake only.

3.4 Application in demography

In this section, we return to our demographic application, and we compute the probability that the female family generated by a first woman eventually becomes extinct. This corresponds to the extinction probability of the MBT modelling a woman's family,

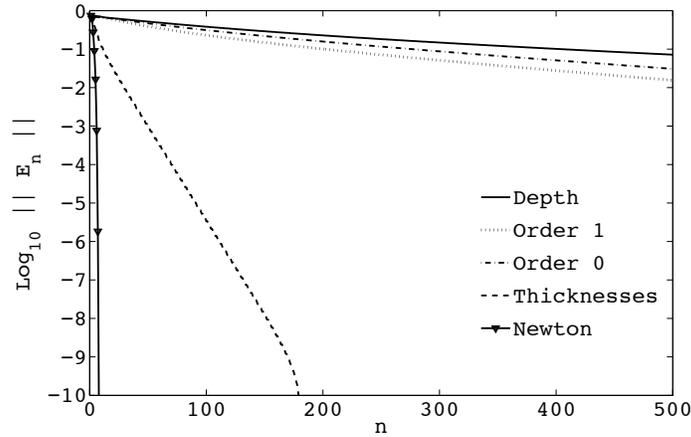


Figure 3.2: Logarithm of $\|\mathbf{E}_n\|_\infty$ for the five algorithms with $\delta = 2$.

Algorithm	Iterations	r_1	r_2	CPU time
Newton	9	$2.66 \cdot 10^{-15}$	$8.51 \cdot 10^{-16}$	0.0013
Order-1	82	$4.38 \cdot 10^{-11}$	$1.60 \cdot 10^{-11}$	0.0048
Thicknesses	91	$4.40 \cdot 10^{-11}$	$1.53 \cdot 10^{-11}$	0.0061
Order-0	107	$4.93 \cdot 10^{-11}$	$1.85 \cdot 10^{-11}$	0.0063
Depth	170	$8.89 \cdot 10^{-11}$	$3.69 \cdot 10^{-11}$	0.0188

Table 3.2: Comparison of the number of iterations and of the residuals for the five algorithms with $p = 0.6$.

as described in Example 1.5.2 of Section 1.5. Notice that this MBT is not irreducible, since once a woman reaches the age class 50 – 54, she is not able to produce any child anymore. But as we will see later in Section 4.4, this does not affect our results.

The extinction probability vector \mathbf{q} may be computed with any of the linear or quadratic algorithms. Figure 3.4 shows each entry of \mathbf{q} , that is the extinction probability of the female family generated by a single woman, given her age class at initial time. We only plot the results for the supercritical countries, as the extinction probability is one in the other countries, regardless the age class of the initial woman.

We see here again the infant mortality effect which was already discussed in Section 1.4: for instance, the family generated by a Congolese girl aged between 1 and 4 years has a higher probability of eventually becoming extinct than for a girl aged between 15 and 19 years, because the first girl has a lower probability than the second one of reaching adulthood.

Let us now compare the convergence speed and the accuracy of the linear algorithms and the Newton algorithm on the case of Belgium, for which we know that $\mathbf{q} = \mathbf{1}$.

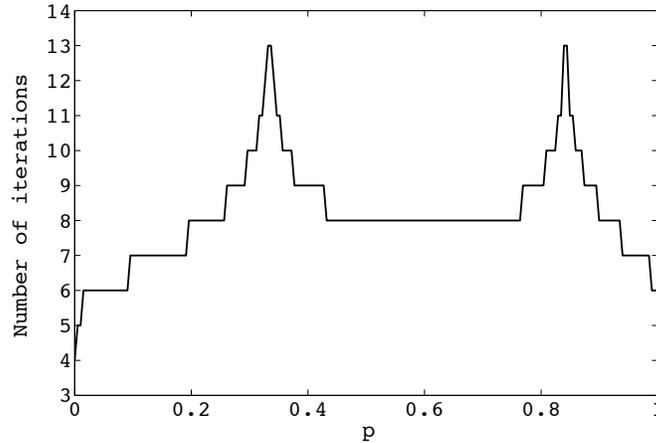


Figure 3.3: Number of iterations for the Newton algorithm as a function of p .

We give in Table 3.3 the number of iterations, the two residuals, and the CPU time expressed in seconds, for the five algorithms. On Figure 3.5, we give the logarithm of the error $\|E_n\|_\infty = \|\mathbf{1} - \mathbf{q}_n\|_\infty$ for the five algorithms. The linear and quadratic convergences are very clear and, as expected, the Depth algorithm is significantly slower than the other three linear algorithms.

Algorithm	Iterations	r_1	r_2	CPU time
Newton	8	$4.44 \cdot 10^{-16}$	$3.83 \cdot 10^{-17}$	0.0040
Order-0	60	$2.53 \cdot 10^{-11}$	$3.96 \cdot 10^{-12}$	0.0115
Thicknesses	74	$4.40 \cdot 10^{-11}$	$7.52 \cdot 10^{-12}$	0.0149
Order-1	87	$4.54 \cdot 10^{-11}$	$7.75 \cdot 10^{-12}$	0.0168
Depth	131	$8.59 \cdot 10^{-11}$	$1.42 \cdot 10^{-11}$	0.0219

Table 3.3: Comparison of the number of iterations, the residuals and the CPU time (in seconds) for the five algorithms.

When moving from the raw to the gap model with $n = 136$ phases, in which after-birth gap periods are taken into account, some supercritical countries become subcritical, so that the extinction probability of their female families becomes $\mathbf{q} = \mathbf{1}$. It is the case for Brazil, South Africa and Turkey, for instance. We gather in Table 3.4 the spectral radius of the mean progeny matrix with $n = 22$ and $n = 136$ phases for these three countries. We thus see again how sensitive the results are to the data, and that it may be of high interest to consider these gap periods when looking at the extinction probability of a population.

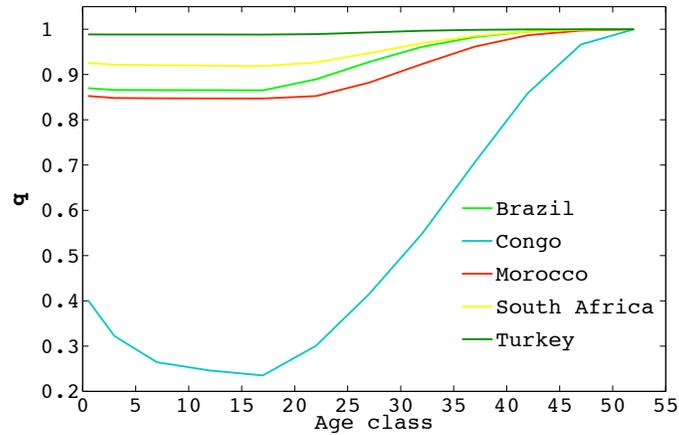


Figure 3.4: Extinction probability of the family generated by first woman as a function of her age class

Country	raw	gap
Brazil	1.0539	0.9932
South Africa	1.0315	0.9793
Turkey	1.0045	0.9384

Table 3.4: Comparison of the spectral radius of the mean matrix M in the raw and in the gap models

3.5 Alternate Newton sequences

We end the chapter by discussing other quadratic algorithms which may be obtained from the Newton method applied to the extinction equation. We first introduce the way these alternate algorithms came to our attention.

In a given binary tree representation of an MBT, we can visit all the nodes and the arcs in a *pre-order* way, that is, in a *depth-first* traversal (Sedgewick [63]). If the MBT eventually becomes extinct, then, starting from its root, we will cover all the nodes of the corresponding tree in a finite time.

Such a traversal of the binary tree has led to a correspondence between MBTs and *tree-like QBD* processes, that we describe in Hautphenne and Van Houdt [32]. Without going into the details here, it is shown there that the linear algorithms to compute the extinction probability of MBTs coincide with linear algorithms developed to compute some particular first passage probability matrices in tree-like QBD processes.

However, a quadratic algorithm based on the Newton iteration method, developed by Bini, Latouche and Meini [10] for tree-like QBD processes, did not seem to have

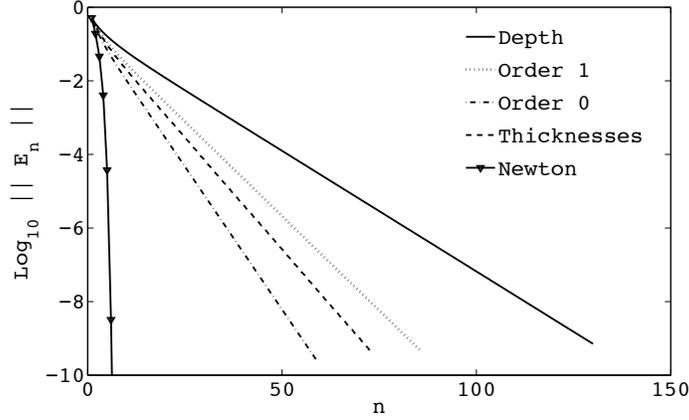


Figure 3.5: Logarithms of the errors of the five algorithms.

any correspondence in the MBT context. Indeed, this quadratic algorithm is different from the algorithm in Section 3.1. In [32], we show that it actually corresponds to the Newton method applied on a different formulation of (1.15) for MBTs.

Indeed, recall from (2.2) and (2.4) that (1.15) may be equivalently rewritten as $\mathbf{s} = [I - \Psi(\mathbf{s} \otimes I)]^{-1} \boldsymbol{\theta}$ or $\mathbf{s} = [I - \Psi(I \otimes \mathbf{s})]^{-1} \boldsymbol{\theta}$. We can thus apply the Newton method on the equation $\mathcal{F}(\mathbf{x}) = \mathbf{0}$, where

$$\mathcal{F}(\mathbf{x}) = \mathbf{x} - [I - \Psi(\mathbf{x} \otimes I)]^{-1} \boldsymbol{\theta}, \quad (3.11)$$

or

$$\mathcal{F}(\mathbf{x}) = \mathbf{x} - [I - \Psi(I \otimes \mathbf{x})]^{-1} \boldsymbol{\theta}. \quad (3.12)$$

The two resulting algorithms may be termed as “Newton-Order” sequences, since the structure of $\mathcal{F}(\mathbf{x})$ reminds us of the structure of the two Order algorithms discussed in Section 2.1. The Newton algorithm from [10] for tree-like QBDs corresponds to the Newton-Order-0 algorithm arising from (3.12).

Similarly, the Newton algorithm in Section 3.1 may be seen as a “Newton-Depth” sequence, and we may also construct the “Newton-Thicknesses” sequence, by applying the Newton iteration method alternatively on (3.11) and on (3.12).

In the rest of this section, we show that Theorem 3.1.2 still holds for the Newton-Order-0 algorithm, and that this sequence requires fewer iterations than the Newton-Depth sequence. However, the complexity of the new iteration is a little higher, which is reflected by the CPU time comparison reported in [32].

The Fréchet derivative of \mathcal{F} at \mathbf{x} , where $\mathcal{F}(\mathbf{x})$ is given by (3.12), is a linear map $\mathcal{F}'_{\mathbf{x}} : \mathbb{R}^n \rightarrow \mathbb{R}^n$ given by

$$\mathcal{F}'_{\mathbf{x}} : \mathbf{z} \mapsto [I - S_{\mathbf{x}} \Psi(S_{\mathbf{x}} \boldsymbol{\theta} \otimes I)] \mathbf{z} = [\mathbf{z} - S_{\mathbf{x}} \Psi(S_{\mathbf{x}} \boldsymbol{\theta} \otimes \mathbf{z})],$$

with $S_{\mathbf{x}} = [I - \Psi(I \otimes \mathbf{x})]^{-1}$.

For a given \mathbf{x}_0 , the Newton-Order-0 sequence for the solution of $\mathcal{F}(\mathbf{x}) = \mathbf{0}$ is

$$\begin{aligned} \mathbf{x}_{k+1} &= \mathbf{x}_k - (\mathcal{F}'_{\mathbf{x}_k})^{-1} \mathcal{F}(\mathbf{x}_k) \\ &= \mathbf{x}_k - [I - S_{\mathbf{x}_k} \Psi(S_{\mathbf{x}_k} \boldsymbol{\theta} \otimes I)]^{-1} [\mathbf{x}_k - S_{\mathbf{x}_k} \boldsymbol{\theta}] \end{aligned} \quad (3.13)$$

for $k \geq 0$, provided that $\mathcal{F}'_{\mathbf{x}_k}$ is invertible for all k . The proof of Theorem 3.1.2 for the sequence (3.13) follows the same steps as for (3.4) and is thus omitted. It requires an equivalent series of lemmas, whose proofs are more involved here, as well as the following lemma, which is the analogue of Theorem 2.3.1.

Lemma 3.5.1. *If the MBT is noncritical and irreducible, then $\text{sp}[S_{\mathbf{q}} \Psi(S_{\mathbf{q}} \boldsymbol{\theta} \otimes I)] < 1$, and $[I - S_{\mathbf{q}} \Psi(S_{\mathbf{q}} \boldsymbol{\theta} \otimes I)]^{-1}$ exists and is nonnegative. In the critical case, $\text{sp}[S_{\mathbf{q}} \Psi(S_{\mathbf{q}} \boldsymbol{\theta} \otimes I)] = 1$.*

Proof. Consider the following branching process embedded in the MBT: the leftmost branch of the MBT represents the lifetime of the first individual of this branching process, and each right branch coming from the leftmost branch represents a new child from the initial individual, which may itself generate new individuals, and so on. For this process, we see that the progeny generating function of an individual is given by

$$\mathbf{G}(\mathbf{x}) = \sum_{n \geq 0} [\Psi(I \otimes \mathbf{x})]^n \boldsymbol{\theta} = [I - \Psi(I \otimes \mathbf{x})]^{-1} \boldsymbol{\theta}.$$

We now repeat the proof of Theorem 2.3.1 with this new progeny generating function, and with $M(\mathbf{x}) = S_{\mathbf{x}} \Psi(S_{\mathbf{x}} \boldsymbol{\theta} \otimes I)$. In the subcritical and supercritical cases, we get $\text{sp}[S_{\mathbf{q}} \Psi(S_{\mathbf{q}} \boldsymbol{\theta} \otimes I)] < 1$, and in the critical case, $\text{sp}[S_{\mathbf{q}} \Psi(S_{\mathbf{q}} \boldsymbol{\theta} \otimes I)] = 1$. \square

In the sequel we shall often use the notation $\Psi_{\mathbf{x}} = \Psi(I \otimes \mathbf{x})$. In order to make the similarities more apparent, we write in parenthesis the label of the analogous property for the sequence (3.4).

Lemma 3.5.2 (3.1.3). *Assume that the process is supercritical and irreducible. We have*

$$\mathcal{F}(\mathbf{x}) - \mathcal{F}(\mathbf{y}) \geq \mathcal{F}'_{\mathbf{x}}(\mathbf{x} - \mathbf{y}),$$

for all $\mathbf{x} \leq \mathbf{y}$ in $\langle \mathbf{0}, \mathbf{q} \rangle$.

The inverse $P(\mathbf{x}) = [I - S_{\mathbf{x}} \Psi(S_{\mathbf{x}} \boldsymbol{\theta} \otimes I)]^{-1}$ of $\mathcal{F}'_{\mathbf{x}}$ exists for all \mathbf{x} in $\langle \mathbf{0}, \mathbf{q} \rangle$ and is nonnegative. Furthermore, $P(\mathbf{x}) \leq P(\mathbf{y})$ for all $\mathbf{x} \leq \mathbf{y}$ in $\langle \mathbf{0}, \mathbf{q} \rangle$.

Proof. First, remark that $S_{\mathbf{x}} = I + S_{\mathbf{x}} \Psi_{\mathbf{x}} = I + \Psi_{\mathbf{x}} S_{\mathbf{x}}$. Note also that if $\mathbf{x} \leq \mathbf{y}$, then $S_{\mathbf{x}} \leq S_{\mathbf{y}}$.

Thus, if $\mathbf{x} \leq \mathbf{y}$, then

$$\begin{aligned}
\mathcal{F}'_{\mathbf{x}}(\mathbf{x} - \mathbf{y}) &= \mathbf{x} - \mathbf{y} + S_{\mathbf{x}} \Psi [I \otimes (\mathbf{y} - \mathbf{x})] S_{\mathbf{x}} \boldsymbol{\theta} \\
&= \mathbf{x} - \mathbf{y} + S_{\mathbf{x}} (\Psi_{\mathbf{y}} - \Psi_{\mathbf{x}}) S_{\mathbf{x}} \boldsymbol{\theta} \\
&\leq \mathbf{x} - \mathbf{y} + S_{\mathbf{y}} (\Psi_{\mathbf{y}} - \Psi_{\mathbf{x}}) S_{\mathbf{x}} \boldsymbol{\theta} \\
&= \mathbf{x} - \mathbf{y} + (S_{\mathbf{y}} - I) S_{\mathbf{x}} \boldsymbol{\theta} - S_{\mathbf{y}} (S_{\mathbf{x}} - I) \boldsymbol{\theta} \\
&= \mathbf{x} - \mathbf{y} + (S_{\mathbf{y}} - S_{\mathbf{x}}) \boldsymbol{\theta} \\
&= \mathcal{F}(\mathbf{x}) - \mathcal{F}(\mathbf{y}).
\end{aligned}$$

It follows from Lemma 3.5.1 that $\text{sp}[S_{\mathbf{x}} \Psi (S_{\mathbf{x}} \boldsymbol{\theta} \otimes I)] < 1$ for all \mathbf{x} in $\langle \mathbf{0}, \mathbf{q} \rangle$, since $S_{\mathbf{x}} \leq S_{\mathbf{q}}$ and thus $S_{\mathbf{x}} \Psi (S_{\mathbf{x}} \boldsymbol{\theta} \otimes I) \leq S_{\mathbf{q}} \Psi (S_{\mathbf{q}} \boldsymbol{\theta} \otimes I)$. So, the inverse $P(\mathbf{x})$ does exist. Moreover,

$$P(\mathbf{y}) = \sum_{n \geq 0} [S_{\mathbf{y}} \Psi (S_{\mathbf{y}} \boldsymbol{\theta} \otimes I)]^n \geq \sum_{n \geq 0} [S_{\mathbf{x}} \Psi (S_{\mathbf{x}} \boldsymbol{\theta} \otimes I)]^n = P(\mathbf{x}) \geq 0$$

for all $\mathbf{x} \leq \mathbf{y}$ in $\langle \mathbf{0}, \mathbf{q} \rangle$. □

Lemma 3.5.3 (3.1.4). *Assume that the process is supercritical and irreducible. The operator \mathcal{F}' is Lipschitz-continuous on $\langle \mathbf{0}, \mathbf{q} \rangle$, that is, there exists a constant γ such that*

$$\|\mathcal{F}'_{\mathbf{x}} - \mathcal{F}'_{\mathbf{y}}\| \leq \gamma \|\mathbf{x} - \mathbf{y}\| \quad \forall \mathbf{x}, \mathbf{y} \in \langle \mathbf{0}, \mathbf{q} \rangle.$$

Proof. Assume that \mathbf{h} is a vector of norm 1, and that \mathbf{x}, \mathbf{y} are two vectors in $\langle \mathbf{0}, \mathbf{q} \rangle$. We may write

$$[\mathcal{F}'_{\mathbf{x}} - \mathcal{F}'_{\mathbf{y}}] \mathbf{h} = S_{\mathbf{y}} \Psi_{\mathbf{h}} S_{\mathbf{y}} \boldsymbol{\theta} - S_{\mathbf{x}} \Psi_{\mathbf{h}} S_{\mathbf{x}} \boldsymbol{\theta}.$$

By adding and subtracting the term $S_{\mathbf{y}} \Psi_{\mathbf{h}} S_{\mathbf{x}} \boldsymbol{\theta}$, we obtain

$$[\mathcal{F}'_{\mathbf{x}} - \mathcal{F}'_{\mathbf{y}}] \mathbf{h} = S_{\mathbf{y}} \Psi_{\mathbf{h}} (S_{\mathbf{y}} - S_{\mathbf{x}}) \boldsymbol{\theta} + (S_{\mathbf{y}} - S_{\mathbf{x}}) \Psi_{\mathbf{h}} S_{\mathbf{x}} \boldsymbol{\theta}.$$

Thus, we have

$$\begin{aligned}
\|[\mathcal{F}'_{\mathbf{x}} - \mathcal{F}'_{\mathbf{y}}] \mathbf{h}\| &\leq \|S_{\mathbf{y}} \Psi_{\mathbf{h}} (S_{\mathbf{y}} - S_{\mathbf{x}}) \boldsymbol{\theta}\| + \|(S_{\mathbf{y}} - S_{\mathbf{x}}) \Psi_{\mathbf{h}} S_{\mathbf{x}} \boldsymbol{\theta}\| \\
&\leq \|S_{\mathbf{y}}\| \cdot \|\Psi_{\mathbf{h}}\| \cdot \|S_{\mathbf{y}} - S_{\mathbf{x}}\| \cdot \|\boldsymbol{\theta}\| \\
&\quad + \|S_{\mathbf{x}}\| \cdot \|\Psi_{\mathbf{h}}\| \cdot \|S_{\mathbf{y}} - S_{\mathbf{x}}\| \cdot \|\boldsymbol{\theta}\|.
\end{aligned}$$

Now, $\forall \mathbf{x}, \mathbf{y} \in \langle \mathbf{0}, \mathbf{q} \rangle$, $\|S_{\mathbf{x}}\| \leq \|S_{\mathbf{q}}\| = C$ and $\|S_{\mathbf{y}}\| \leq \|S_{\mathbf{q}}\| = C$. Since $\|\mathbf{h}\| = 1$ and since $\|I \otimes I\|_{\infty} = \|I \otimes \mathbf{x}\|_{\infty} = \|\mathbf{x}\|_{\infty}$, then $\|\Psi_{\mathbf{h}}\| \leq \|\Psi\| = C'$. Finally, $\|\boldsymbol{\theta}\| = C''$. Thus,

$$\|[\mathcal{F}'_{\mathbf{x}} - \mathcal{F}'_{\mathbf{y}}] \mathbf{h}\| \leq 2 C C' C'' \|S_{\mathbf{y}} - S_{\mathbf{x}}\|.$$

But

$$\begin{aligned}
\|S_{\mathbf{y}} - S_{\mathbf{x}}\| &= \|\Psi_{\mathbf{y}} S_{\mathbf{y}} - \Psi_{\mathbf{x}} S_{\mathbf{x}}\| \\
&= \|\Psi_{\mathbf{y}} S_{\mathbf{y}} - \Psi_{\mathbf{x}} S_{\mathbf{x}} + \Psi_{\mathbf{x}} S_{\mathbf{y}} - \Psi_{\mathbf{x}} S_{\mathbf{y}}\| \\
&= \|(\Psi_{\mathbf{y}} - \Psi_{\mathbf{x}}) S_{\mathbf{y}} + \Psi_{\mathbf{x}} (S_{\mathbf{y}} - S_{\mathbf{x}})\| \\
&\leq \|\Psi_{\mathbf{y}} - \Psi_{\mathbf{x}}\| C + \|\Psi_{\mathbf{x}}\| \cdot \|S_{\mathbf{y}} - S_{\mathbf{x}}\|,
\end{aligned}$$

so that

$$(1 - \|\Psi_{\mathbf{x}}\|) \|S_{\mathbf{y}} - S_{\mathbf{x}}\| \leq C \|\Psi_{\mathbf{y}} - \Psi_{\mathbf{x}}\|.$$

Since $(1 - \|\Psi_{\mathbf{q}}\|) \leq (1 - \|\Psi_{\mathbf{x}}\|)$ for $\mathbf{x} \in \langle \mathbf{0}, \mathbf{q} \rangle$ and $\|\Psi_{\mathbf{q}}\| \leq \|\Psi\| \cdot \|\mathbf{q}\| < 1$ as $\|\Psi\|_{\infty} \leq 1$ and $\|\mathbf{q}\|_{\infty} < 1$ by irreducibility of the MBT, we obtain

$$\begin{aligned} \|S_{\mathbf{y}} - S_{\mathbf{x}}\| &\leq C (1 - \|\Psi_{\mathbf{q}}\|)^{-1} \|\Psi_{\mathbf{y}} - \Psi_{\mathbf{x}}\| \\ &= C (1 - \|\Psi_{\mathbf{q}}\|)^{-1} \|\Psi [I \otimes (\mathbf{y} - \mathbf{x})]\| \\ &\leq C (1 - \|\Psi_{\mathbf{q}}\|)^{-1} C' \|\mathbf{y} - \mathbf{x}\|. \end{aligned}$$

So,

$$\|\mathcal{F}'_{\mathbf{x}} - \mathcal{F}'_{\mathbf{y}}\| \leq \gamma \|\mathbf{x} - \mathbf{y}\|$$

with $\gamma = 2 C^2 C'^2 C'' (1 - \|\Psi_{\mathbf{q}}\|)^{-1} < \infty$. \square

Let us now compare the Newton-Depth and the Newton-Order-0 sequences, both starting with $\mathbf{x}_0 = \boldsymbol{\theta}$. Let us write $\tilde{\mathbf{x}}_k$ for the k th approximation of the Newton-Depth algorithm (3.3), to distinguish from that of the Newton-Order-0 algorithm (3.13).

Denote the difference between the k th iteration in the two Newton algorithms by $\Upsilon_k = \mathbf{x}_k - \tilde{\mathbf{x}}_k$. Let us show that at each iteration, the Newton-Order-0 algorithm is closer to the solution \mathbf{q} than the Newton-Depth algorithm, which implies that the Newton-Order-0 algorithm converges faster towards the solution than the Newton-Depth, in terms of the number of iterations.

Proposition 3.5.4. *The difference Υ_k is nonnegative for all $k \geq 0$.*

Proof. The proof goes by induction. First, $\Upsilon_0 = \mathbf{x}_0 - \tilde{\mathbf{x}}_0 = \boldsymbol{\theta} - \boldsymbol{\theta} = \mathbf{0}$. Now, suppose that $\Upsilon_k \geq \mathbf{0}$. Let us show that we still have $\Upsilon_{k+1} \geq \mathbf{0}$.

By multiplying both sides of (3.13) on the left by $[I - S_{\mathbf{x}_k} \Psi (S_{\mathbf{x}_k} \boldsymbol{\theta} \otimes I)]$, the Newton-Order-0 sequence may be rewritten as

$$\mathbf{x}_{k+1} = S_{\mathbf{x}_k} \Psi_{\mathbf{x}_{k+1}} S_{\mathbf{x}_k} \boldsymbol{\theta} - S_{\mathbf{x}_k} \Psi_{\mathbf{x}_k} S_{\mathbf{x}_k} \boldsymbol{\theta} + S_{\mathbf{x}_k} \boldsymbol{\theta}. \quad (3.14)$$

Let us now multiply both sides of (3.14) on the left by $(I - \Psi(I \otimes \mathbf{x}_k))$. We obtain

$$\mathbf{x}_{k+1} = \Psi(\mathbf{x}_{k+1} \otimes \mathbf{x}_k) + \Psi(S_{\mathbf{x}_k} \boldsymbol{\theta} \otimes \mathbf{x}_{k+1}) - \Psi(S_{\mathbf{x}_k} \boldsymbol{\theta} \otimes \mathbf{x}_k) + \boldsymbol{\theta}. \quad (3.15)$$

Similarly, for the Newton-Depth sequence we have

$$\tilde{\mathbf{x}}_{k+1} = \Psi(\tilde{\mathbf{x}}_k \otimes \tilde{\mathbf{x}}_{k+1}) + \Psi(\tilde{\mathbf{x}}_{k+1} \otimes \tilde{\mathbf{x}}_k) - \Psi(\tilde{\mathbf{x}}_k \otimes \tilde{\mathbf{x}}_k) + \boldsymbol{\theta}. \quad (3.16)$$

Now, by subtracting (3.16) from (3.15) we get

$$\begin{aligned} \Upsilon_{k+1} &= \Psi(\mathbf{x}_{k+1} \otimes \mathbf{x}_k) + \Psi(S_{\mathbf{x}_k} \boldsymbol{\theta} \otimes (\mathbf{x}_{k+1} - \mathbf{x}_k)) - \Psi(\tilde{\mathbf{x}}_{k+1} \otimes \tilde{\mathbf{x}}_k) \\ &\quad - \Psi(\tilde{\mathbf{x}}_k \otimes (\tilde{\mathbf{x}}_{k+1} - \tilde{\mathbf{x}}_k)). \end{aligned}$$

By adding and subtracting the quantities $\Psi(\mathbf{x}_{k+1} \otimes \tilde{\mathbf{x}}_k)$ and $\Psi(S_{\mathbf{x}_k} \boldsymbol{\theta} \otimes (\tilde{\mathbf{x}}_{k+1} - \tilde{\mathbf{x}}_k))$, and regrouping the terms, we obtain

$$\begin{aligned}
\Upsilon_{k+1} &= \Psi(S_{\mathbf{x}_k} \boldsymbol{\theta} \oplus \tilde{\mathbf{x}}_k) \Upsilon_{k+1} + \Psi[(\mathbf{x}_{k+1} - S_{\mathbf{x}_k} \boldsymbol{\theta}) \otimes I] \Upsilon_k \\
&\quad + \Psi[(S_{\mathbf{x}_k} \boldsymbol{\theta} - \tilde{\mathbf{x}}_k) \otimes (\tilde{\mathbf{x}}_{k+1} - \tilde{\mathbf{x}}_k)] \\
&= \underbrace{[I - \Psi(S_{\mathbf{x}_k} \boldsymbol{\theta} \oplus \tilde{\mathbf{x}}_k)]^{-1}}_{(I)} \left\{ \underbrace{\Psi[(\mathbf{x}_{k+1} - S_{\mathbf{x}_k} \boldsymbol{\theta}) \otimes I]}_{(II)} \underbrace{\Upsilon_k}_{(III)} \right. \\
&\quad \left. + \Psi \left[\underbrace{(S_{\mathbf{x}_k} \boldsymbol{\theta} - \tilde{\mathbf{x}}_k)}_{(IV)} \otimes \underbrace{(\tilde{\mathbf{x}}_{k+1} - \tilde{\mathbf{x}}_k)}_{(V)} \right] \right\} \\
&\geq \mathbf{0}.
\end{aligned}$$

Indeed, (I) is a positive matrix, since it is equal to a infinite sum of positive terms; (II) is positive by Equation (3.14) and the increase of the Newton-Order-0 sequence; (III) is positive by induction assumption; (IV) is positive since $\tilde{\mathbf{x}}_k \leq \mathbf{x}_k$ by induction assumption, and because $\mathbf{x}_k \leq S_{\mathbf{x}_k} \boldsymbol{\theta} \forall k \geq 0$. Indeed, in the proof of Theorem 3.1.2, it appears that if $\mathbf{0} \leq \mathbf{x}_0 \leq \boldsymbol{\theta}$, then $\mathcal{F}(\mathbf{x}_k) \leq 0$, for all k ; finally, (V) is positive by the increasing nature of the Newton-Depth sequence. \square

In terms of number of iterations, we thus know that the Newton-Order-0 algorithm always surpasses the Newton-Depth algorithm. Other comparisons do not lead to general conclusions and the fastest of the Newton algorithms depends on the example under consideration.

Using the particular structure of the matrices involved at each iteration, we obtain a complexity of $(20/3)n^3 + \mathcal{O}(n^2)$ flops per iteration for the Newton-Depth algorithm, against $8n^3 + \mathcal{O}(n^2)$ flops for the three other Newton algorithms. We thus expect the Newton-Depth algorithm to be somewhat faster than the other algorithms, even if it requires one or two iterations more; numerical examples are provided in [32].

Concluding remarks

Remark 3.5.5. We observe that the Newton algorithms have a greater complexity than the linear algorithms. But as the number of iterations required with the Newton algorithms is far less than with the linear algorithms, the total computational cost of the Newton algorithms is less than that of the linear ones, which was already shown in Tables 3.1 and 3.2.

Remark 3.5.6. As a final remark, we have verified that each Newton algorithm may be naturally generalized to the GMT case, but we have not yet implemented the algorithms so obtained.

CHAPTER 4

Reducible branching processes

We generally assumed in the previous chapters that the MBT was irreducible. What happens if we remove this assumption? How does a reducible multitype branching process behave?

Reducible (or *decomposable*) multitype branching processes differ in several ways from irreducible processes. In the literature, authors generally focus on the asymptotic behaviour of such branching processes without discussing extinction criteria or algorithmic questions.

For instance, let $\{\mathbf{Z}_n, n \in \mathbb{N}\}$ denote a supercritical discrete-time multitype *irreducible* branching process; let $\rho > 1$ be the eigenvalue of maximal real part of the mean progeny matrix M , and \mathbf{v} its corresponding positive left eigenvector. Kesten and Stigum [38] show that there exists a one-dimensional random variable w such that $\lim_{n \rightarrow \infty} (\mathbf{Z}_n / \rho^n) = w \cdot \mathbf{v}$ with probability 1. In this limit, the eigenvalue ρ plays thus the role of a normalizing constant, and we see that all types grow at the same rate ρ .

The same authors prove in [39] that in the reducible case, the asymptotic behaviour of the branching process \mathbf{Z}_n depends on the type of the initial individual. In addition, different subsets of the components of the vector \mathbf{Z}_n have, in general, different normalizing constants; different types may thus grow at different rates. The corresponding limit vector shows a greater variety of qualitative properties than in the irreducible case.

In this chapter, we focus on supercritical processes. The types are partitioned into equivalence classes. In this context, extinction of some classes of individuals is possible without the whole process becoming extinct. We derive criteria for the extinction of the whole process (total extinction) and of specific classes (partial extinction). We give sufficient conditions for the extinction of a class to imply the extinction of another class or even the whole process.

Then, we prove that the extinction probability of a specific class is solution of the usual extinction equation with some constraints, and that it may be seen as the total extinction probability of a modified branching process.

Finally, we discuss algorithmic methods to compute the total and the partial extinction probabilities of a reducible MBT, and we conclude with numerical examples.

4.1 Definitions and notations

Recall from Section 1.1 that a multitype branching process $\mathbf{Z}(t) = [Z_1(t), \dots, Z_n(t)]^T$ is reducible if its mean progeny matrix M is reducible, that is, if there exist indices $1 \leq i, j \leq n$ such that for all $k \geq 0$, $(M^k)_{ij} = 0$; this means that individuals of type i will never have any individual of type j among their descendants.

The matrix M may be written in a normal form, possibly after a permutation of indices (Gantmacher [21, Chapter 13]):

$$M = \begin{bmatrix} \mathcal{M}_{11} & 0 & 0 & \dots & 0 \\ \mathcal{M}_{21} & \mathcal{M}_{22} & 0 & \dots & 0 \\ \mathcal{M}_{31} & \mathcal{M}_{32} & \mathcal{M}_{33} & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \mathcal{M}_{m1} & \mathcal{M}_{m2} & \mathcal{M}_{m3} & \dots & \mathcal{M}_{mm} \end{bmatrix}, \quad (4.1)$$

where the diagonal blocks \mathcal{M}_{ii} are irreducible or equal to zero, and the sub-diagonal blocks \mathcal{M}_{ij} for $i > j$ are nonnegative. We write $\mathcal{M}_{k\ell}$ ($1 \leq k, \ell \leq m$) for the (k, ℓ) th submatrix of M , in order to distinguish it from $M_{k\ell}$, which is the *component* (k, ℓ) of M .

This decomposition reflects the fact that the n types of the branching process $\mathbf{Z}(t)$ are partitioned into m classes C_k , $1 \leq k \leq m$ (Mode [54, Section 2.3]). In this view, $\mathcal{M}_{k\ell} = (M_{ij})_{i \in C_k, j \in C_\ell}$. If i and j belong to the same class, they *communicate*, meaning that there exist nonnegative integers n_1 and n_2 such that $(M^{n_1})_{ij} > 0$ and $(M^{n_2})_{ji} > 0$. This is an equivalence relation, and the C_k 's are equivalent classes.

We define the following sets of class indices for $1 \leq k \leq m$

$$\begin{aligned} \mathcal{D}_k &= \{\ell \leq k : \exists n \geq 0, (M^n)_{ij} \neq 0 \text{ for some } i \in C_k, j \in C_\ell\} \\ \mathcal{A}_k &= \{\ell \geq k : \exists n \geq 0, (M^n)_{ji} \neq 0 \text{ for some } i \in C_k, j \in C_\ell\}, \\ \mathcal{E}_k &= \{\ell < k : \mathcal{M}_{k\ell} \neq 0\}. \end{aligned}$$

In other words, $\ell \in \mathcal{D}_k$ means that an individual in class C_k may give birth, possibly after several generations, to an individual in class C_ℓ (“ \mathcal{D} ” is for “Descendant”); conversely, $\ell \in \mathcal{A}_k$ means that an individual in class C_ℓ may generate, directly or indirectly, an individual in class C_k (“ \mathcal{A} ” is for “Ancestor”). Clearly $\ell \in \mathcal{A}_k$ if and only if $k \in \mathcal{D}_\ell$. Finally, $\ell \in \mathcal{E}_k$ means that an individual in class C_k may *directly* give birth to an individual in class C_ℓ , $k \neq \ell$.

If $\mathbf{Z}(0) = \mathbf{e}_i$ where $i \in C_k$ for some k , and if $\mathcal{M}_{kk} \neq 0$, then the subprocess $\mathbf{Z}^k(t) = (Z_i(t))_{i \in C_k}$, restricted to the individuals whose type is in C_k , is an irreducible branching process with mean progeny matrix \mathcal{M}_{kk} [39].

It is well known [21] that when a matrix M has the form given by (4.1), its spectrum is precisely the union of the spectra of the \mathcal{M}_{kk} , $1 \leq k \leq m$, so that the spectral radius of M is $\text{sp}(M) = \max_{1 \leq k \leq m} \text{sp}(\mathcal{M}_{kk})$. Therefore, one supercritical subprocess $\mathbf{Z}^k(t)$ is enough for the whole process $\mathbf{Z}(t)$ to be supercritical as well.

However, the behaviour of the reducible branching process is not determined by the spectral radius of M only; we shall demonstrate in the next sections how the criticality of the different subprocesses $\mathbf{Z}^k(t)$ influences the behaviour of the whole process $\mathbf{Z}(t)$. Let us first introduce some notations.

We denote by \mathbf{q}_k the *vector* of extinction probability of the whole process, given that the initial individual belongs to class C_k , that is

$$(\mathbf{q}_k)_i = \text{P}[\exists T > 0 : \mathbf{Z}(T) = \mathbf{0} \mid \mathbf{Z}(0) = \mathbf{e}_i, i \in C_k].$$

This is a *total* extinction: there will be *no* individual alive after time T . We shall note the total extinction event by E , that is, $E = [\exists T > 0 : \mathbf{Z}(T) = \mathbf{0}]$. With this, $\mathbf{q} = [\mathbf{q}_1, \mathbf{q}_2, \dots, \mathbf{q}_m]^T$ denotes the extinction probability of the whole process, given the class of the initial individual. Later, for short, we also write “ $\varphi_0 \in C_k$ ” for “ $\mathbf{Z}(0) = \mathbf{e}_i$ for some $i \in C_k$ ”.

Now observe that if we restrict our attention to the class C_ℓ only, the event $[\exists T > 0 : \mathbf{Z}^\ell(T) = \mathbf{0}]$ does not necessarily imply the extinction of class C_ℓ since at time T , some individual in another class might be alive and able to produce new individuals of class C_ℓ in the future.

Thus, extinction of class C_ℓ , which we term a *partial* extinction, corresponds to the event $E_\ell = [\exists T > 0 : \forall t \geq T, \mathbf{Z}^\ell(t) = \mathbf{0}]$. We denote by \mathbf{q}_k^ℓ the vector of extinction probability of class C_ℓ given that the initial individual belongs to class C_k , that is

$$\mathbf{q}_k^\ell = \text{P}[E_\ell \mid \varphi_0 \in C_k] = \text{P}[\exists T > 0 : \forall t \geq T, \mathbf{Z}^\ell(t) = \mathbf{0} \mid \varphi_0 \in C_k],$$

and $\mathbf{q}^\ell = [\mathbf{q}_1^\ell, \mathbf{q}_2^\ell, \dots, \mathbf{q}_m^\ell]^T$ denotes the partial extinction probability vector of class C_ℓ , given the class of the initial individual.

The lemma below directly results from the fact that if the whole process $\mathbf{Z}(t)$ becomes extinct, then all the classes C_ℓ become extinct too.

Lemma 4.1.1. $\mathbf{q} \leq \mathbf{q}^\ell$ for all $1 \leq \ell \leq m$. □

4.2 Extinction criteria

Recall from Section 1.2 that in an irreducible branching process, the extinction probability vector \mathbf{q} has either all its components equal to one or all its components strictly less than one.

In a reducible branching process, this dichotomy does not hold anymore: all the components of \mathbf{q} are equal to one in the subcritical and critical cases, but there might be some components equal to one in the supercritical case as well;

Actually, by irreducibility of the equivalence classes, for each $1 \leq k \leq m$, either $\mathbf{q}_k = \mathbf{1}$ or $\mathbf{q}_k < \mathbf{1}$, with at least one k such that $\mathbf{q}_k < \mathbf{1}$ if the whole process is supercritical, and for each $1 \leq \ell \leq m$, either $\mathbf{q}_k^\ell = \mathbf{1}$ or $\mathbf{q}_k^\ell < \mathbf{1}$. Here, it may thus happen that, starting from one class C_k , the whole process eventually becomes extinct, so that $\mathbf{q}_k = \mathbf{1}$, while starting from another class C_j , the explosion of the process is possible, so that $\mathbf{q}_j < \mathbf{1}$.

The first result below provides a necessary and sufficient condition for the total extinction, given the class of the first individual.

Proposition 4.2.1. *For $1 \leq k \leq m$,*

$$\mathbf{q}_k < \mathbf{1} \Leftrightarrow \exists \ell \in \mathcal{D}_k : \text{sp}(\mathcal{M}_{\ell\ell}) > 1.$$

Proof. We shall show the following equivalent statement

$$\mathbf{q}_k < \mathbf{1} \Leftrightarrow (\text{sp}(\mathcal{M}_{kk}) > 1) \text{ or } (\exists \ell \in \mathcal{E}_k : \mathbf{q}_\ell < \mathbf{1}). \quad (4.2)$$

It actually suffices to prove that

$$\exists \ell \in \mathcal{E}_k : \mathbf{q}_\ell < \mathbf{1} \Rightarrow \mathbf{q}_k < \mathbf{1}, \quad (4.3)$$

$$\forall \ell \in \mathcal{E}_k : \mathbf{q}_\ell = \mathbf{1} \Rightarrow (\mathbf{q}_k < \mathbf{1} \Leftrightarrow \text{sp}(\mathcal{M}_{kk}) > 1). \quad (4.4)$$

Then, after some formal manipulations, we get (4.2).

Recall that $\mathbf{P}(\mathbf{s})$ denotes the progeny generating function associated to the branching process $\mathbf{Z}(t)$; we decompose it as $\mathbf{P}(\mathbf{s}) = [\mathbf{P}_1(\mathbf{s}), \mathbf{P}_2(\mathbf{s}), \dots, \mathbf{P}_m(\mathbf{s})]^T$, where the index in the subvector $\mathbf{P}_i(\mathbf{s})$ indicates the class of the initial individual.

By Theorem 1.2.1, the extinction probability vector $\mathbf{q} = [\mathbf{q}_1, \mathbf{q}_2, \dots, \mathbf{q}_m]^T$ is the minimal nonnegative solution of the fixed point equation $\mathbf{s} = \mathbf{P}(\mathbf{s})$ and thus, in particular, for each $1 \leq k \leq m$, $\mathbf{q}_k = \mathbf{P}_k(\mathbf{q})$. Actually, $\mathbf{P}_k(\mathbf{q})$ only depends on \mathbf{q}_ℓ for $\ell = k$ and for all $\ell \in \mathcal{E}_k$. Let $k_1 < k_2 < \dots < k_p$ denote the elements in \mathcal{E}_k ; we may thus write

$$\mathbf{q}_k = \mathbf{P}_k(\mathbf{q}_{k_1}, \mathbf{q}_{k_2}, \dots, \mathbf{q}_{k_p}, \mathbf{q}_k).$$

First, assume that $\mathcal{E}_k \neq \emptyset$ and that there exists at least one $\ell \in \mathcal{E}_k$ such that $\mathbf{q}_\ell < \mathbf{1}$. Then, $\mathbf{P}_k(\cdot)$ being nondecreasing in each of its variables and strictly increasing in at least one variable of each subvector, we have

$$\mathbf{q}_k < \mathbf{P}_k(\mathbf{1}, \mathbf{1}, \dots, \mathbf{1}, \mathbf{q}_k) \leq \mathbf{1},$$

and we get $\mathbf{q}_k < \mathbf{1}$, which proves (4.3).

Now, if $\mathbf{q}_\ell = \mathbf{1} \forall \ell \in \mathcal{E}_k$, then

$$\begin{aligned} \mathbf{q}_k &= \mathbf{P}_k(\mathbf{1}, \mathbf{q}_k) \\ &= \tilde{\mathbf{P}}^k(\mathbf{q}_k), \end{aligned}$$

where $\tilde{\mathbf{P}}^k(\cdot)$ is the progeny generating function associated to the subprocess $\mathbf{Z}^k(t)$ restricted to class C_k . So, \mathbf{q}_k is solution of the fixed point equation $\tilde{\mathbf{P}}^k(\mathbf{s}) = \mathbf{s}$ of which the minimal nonnegative solution is the extinction probability of class C_k , given the type of the initial individual belonging to this class, that is \mathbf{q}_k^k . On the one hand, if $\text{sp}(\mathcal{M}_{kk}) \leq 1$, then $\mathbf{q}_k^k = \mathbf{1}$ and thus $\mathbf{q}_k = \mathbf{1}$. On the other hand, if $\text{sp}(\mathcal{M}_{kk}) > 1$, then $\mathbf{q}_k^k < \mathbf{1}$ and by Lemma 4.1.1 we know that $\mathbf{q}_k \leq \mathbf{q}_k^k$, which implies that $\mathbf{q}_k < \mathbf{1}$.

If $\mathcal{E}_k = \emptyset$, then the same conclusion holds by analogue reasoning. Thus, we get (4.4). \square

The second result is about partial extinction. Starting from an individual in class C_k , the survival of class C_i is possible if and only if the initial individual is able to generate (in one or several generations) an individual in class C_i through the birth of individuals in some class C_j associated to a supercritical subprocess $\mathbf{Z}^j(t)$.

Proposition 4.2.2. *For $1 \leq i \leq m$, for all $k \in \mathcal{A}_i$,*

$$\mathbf{q}_k^i < \mathbf{1} \Leftrightarrow \exists j \in \mathcal{A}_i \cap \mathcal{D}_k : \text{sp}(\mathcal{M}_{jj}) > 1.$$

If $k \notin \mathcal{A}_i$, then $\mathbf{q}_k^i = \mathbf{1}$.

Proof. If $k \notin \mathcal{A}_i$, then it is obvious that $\mathbf{q}_k^i = \mathbf{1}$ since an individual from class C_k will never generate any individual in class C_i . In particular, $\mathbf{q}_k^i = \mathbf{1}$ for all $k < i$.

Now, let us fix i . We show by induction that for all $k \in \mathcal{A}_i$, if for all $j \in \mathcal{A}_i \cap \mathcal{D}_k$ we have $\text{sp}(\mathcal{M}_{jj}) \leq 1$, then $\mathbf{q}_k^i = \mathbf{1}$. We assume without loss of generality that the ancestors of i are numbered consecutively: $\mathcal{A}_i = \{i, i+1, i+2, \dots, K\}$ up to some $K \leq m$.

We already know that $\mathbf{q}_i^i = \mathbf{1}$ if and only if $\text{sp}(\mathcal{M}_{ii}) \leq 1$. Assume that for some $k-1$ between i and K , we have that for all ℓ between i and $k-1$

$$\forall j \in \mathcal{A}_i \cap \mathcal{D}_\ell : \text{sp}(\mathcal{M}_{jj}) \leq 1 \Rightarrow \mathbf{q}_\ell^i = \mathbf{1}.$$

We shall verify that it also holds for k :

$$\forall j \in \mathcal{A}_i \cap \mathcal{D}_k : \text{sp}(\mathcal{M}_{jj}) \leq 1 \Rightarrow \mathbf{q}_k^i = \mathbf{1}.$$

We denote by \mathcal{P}^h the vector of direct progeny in each class of a individual of type h . For $h \in C_k$

$$(\mathbf{q}_k^i)_h = \sum_{\mathbf{d} \geq \mathbf{0}} \text{P}[\mathcal{P}^h = (\mathbf{d}_1, \mathbf{d}_2, \dots, \mathbf{d}_m)] \prod_{1 \leq \ell \leq m} (\mathbf{q}_\ell^i)^{\mathbf{d}_\ell}.$$

Now, if $\ell \neq k$, $\ell \notin \mathcal{E}_k$, then $\mathbf{d}_\ell = \mathbf{0}$ with probability one. If $\ell \in \mathcal{E}_k$, then $\mathcal{D}_\ell \subset \mathcal{D}_k$, and by the induction assumption, $\mathbf{q}_\ell^i = \mathbf{1}$. So, we find that

$$\begin{aligned} (\mathbf{q}_k^i)_h &= \sum_{\mathbf{d}_k \geq \mathbf{0}} \text{P}[\mathcal{P}_k^h = \mathbf{d}_k] (\mathbf{q}_k^i)^{\mathbf{d}_k} \\ &= (\tilde{\mathbf{P}}^k)_h(\mathbf{q}_k^i), \end{aligned}$$

where recall that $\tilde{\mathbf{P}}^k(\cdot)$ is the progeny generating function of the subprocess $\mathbf{Z}^k(t)$ restricted to class C_k . So, \mathbf{q}_k^i is solution of the equation $\tilde{\mathbf{P}}^k(\mathbf{s}) = \mathbf{s}$ of which the minimal nonnegative solution is \mathbf{q}_k^k . As by assumption $\text{sp}(\mathcal{M}_{kk}) \leq 1$, we get $\mathbf{q}_k^k = \mathbf{1}$, and thus $\mathbf{q}_k^i = \mathbf{1}$.

It remains for us to show that if $k \in \mathcal{A}_i$ and if there exists $j \in \mathcal{A}_i \cap \mathcal{D}_k$ such that $\text{sp}(\mathcal{M}_{jj}) > 1$, then $\mathbf{q}_k^i < \mathbf{1}$, that is

$$\mathbb{P}[\forall t, \exists T \geq t : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \varphi_0 \in C_k] > 0. \quad (4.5)$$

First, we directly conclude from the irreducibility of the subprocess $\mathbf{Z}^j(t)$ that for such a j ,

$$\mathbb{P}[\forall t, \mathbf{Z}^j(t) \neq \mathbf{0} \mid \varphi_0 \in C_j] > 0, \quad (4.6)$$

and from $j \in \mathcal{A}_i$, that

$$\mathbb{P}[\exists T \geq 0 : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \mathbf{Z}^j(0) \neq \mathbf{0}] > 0 \quad (4.7)$$

as well.

Thus,

$$\begin{aligned} & \mathbb{P}[\forall t, \exists T \geq t : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \varphi_0 \in C_j] \\ &= \lim_{t \rightarrow \infty} \mathbb{P}[\exists T \geq t : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \varphi_0 \in C_j] \\ &\geq \lim_{t \rightarrow \infty} \mathbb{P}[\mathbf{Z}^j(t) \neq \mathbf{0}, \text{ and } \exists T \geq t : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \varphi_0 \in C_j] \\ &= \lim_{t \rightarrow \infty} \mathbb{P}[\mathbf{Z}^j(t) \neq \mathbf{0} \mid \varphi_0 \in C_j] \cdot \mathbb{P}[\exists T \geq t : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \mathbf{Z}^j(t) \neq \mathbf{0}] \end{aligned}$$

by the Markov property. Then, on the one hand

$$\lim_{t \rightarrow \infty} \mathbb{P}[\mathbf{Z}^j(t) \neq \mathbf{0} \mid \varphi_0 \in C_j] = \mathbb{P}[\forall t, \mathbf{Z}^j(t) \neq \mathbf{0} \mid \varphi_0 \in C_j] > 0$$

by (4.6), and on the other hand,

$$\mathbb{P}[\exists T \geq t : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \mathbf{Z}^j(t) \neq \mathbf{0}] = \mathbb{P}[\exists T \geq 0 : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \mathbf{Z}^j(0) \neq \mathbf{0}] > 0$$

by the Markov property, and by (4.7). We thus have shown that

$$\mathbb{P}[\forall t, \exists T \geq t : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \varphi_0 \in C_j] > 0,$$

that is, $\mathbf{q}_j^i < \mathbf{1}$.

Next, we prove (4.5). By assumption, $j \in \mathcal{D}_k$, that is

$$\mathbb{P}[\exists \theta \geq 0 : \mathbf{Z}^j(\theta) \neq \mathbf{0} \mid \varphi_0 \in C_k] > 0. \quad (4.8)$$

We have

$$\begin{aligned} & \mathbb{P}[\forall t, \exists T \geq t : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \varphi_0 \in C_k] \\ &\geq \mathbb{P}[\exists \theta \geq 0 : \mathbf{Z}^j(\theta) \neq \mathbf{0} \text{ and } \forall t \geq \theta, \exists T \geq t : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \varphi_0 \in C_k] \\ &= \mathbb{P}[\exists \theta \geq 0 : \mathbf{Z}^j(\theta) \neq \mathbf{0} \mid \varphi_0 \in C_k] \\ &\quad \cdot \mathbb{P}[\forall t \geq \theta, \exists T \geq t : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \varphi_0 \in C_k, \exists \theta \geq 0 : \mathbf{Z}^j(\theta) \neq \mathbf{0}], \end{aligned} \quad (4.9)$$

and the second factor in the right-hand side is equal to

$$P[\forall t, \exists T \geq t : \mathbf{Z}^i(T) \neq \mathbf{0} \mid \mathbf{Z}^j(0) \neq \mathbf{0}]$$

by the strong Markov property, and is strictly positive since $\mathbf{q}_j^i < \mathbf{1}$. This, together with (4.8) shows that the left-hand side of (4.9) is strictly positive, which concludes the proof of (4.5). \square

A direct consequence of this proposition is the following

Corollary 4.2.3. *For $1 \leq i \leq m$*

$$\mathbf{q}^i = \mathbf{1} \Leftrightarrow \forall j \in \mathcal{A}_i : sp(\mathcal{M}_{jj}) \leq 1.$$

Now, suppose that we “observe” the extinction of some class C_i . What can we conclude about the extinction of other classes, on the basis of the structure of M ?

We examine how, by virtue of the relations between classes, knowing the extinction of class C_i may inform us of the eventual extinction of class C_j , and even of the whole process.

We shall write that $A \stackrel{a.e.}{\subseteq} B$, where A and B are two events, if $P[A \cap B^c] = 0$, and that $A \stackrel{a.e.}{\equiv} B$ if $A \stackrel{a.e.}{\subseteq} B$ and $B \stackrel{a.e.}{\subseteq} A$. With these notations, the inclusions $E_i \stackrel{a.e.}{\subseteq} E_j$ and $E_i \stackrel{a.e.}{\subseteq} E$ respectively imply that $\mathbf{q}^i \leq \mathbf{q}^j$ and $\mathbf{q}^i \leq \mathbf{q}$, and the equivalences $E_i \stackrel{a.e.}{\equiv} E_j$ and $E_i \stackrel{a.e.}{\equiv} E$ respectively imply that $\mathbf{q}^i = \mathbf{q}^j$ and $\mathbf{q}^i = \mathbf{q}$.

We first do not condition on the class of the initial individual, we merely assume that $P[\varphi_0 \in C_k] > 0$ for any k , and we give general criteria about the inclusion and equivalence of extinction events.

We show below that if an individual from class C_j may generate (in one or several generations) an individual in class C_i , then the extinction of class C_i implies almost surely that class C_j becomes extinct as well. On the other hand, the extinction of class C_j implies almost surely the extinction of class C_i if and only if each subprocess $\mathbf{Z}^k(t)$, such that an individual from class C_k may generate an individual in class C_i but not in class C_j , is subcritical.

Notice in the formulation of the second statement below that j must not necessarily belong to \mathcal{A}_i for E_j to imply E_i (see Remark 4.2.6).

Proposition 4.2.4. *For $1 \leq i, j \leq m$,*

$$(i) \quad j \in \mathcal{A}_i \Rightarrow E_i \stackrel{a.e.}{\subseteq} E_j,$$

$$(ii) \quad \forall k \in \mathcal{A}_i \setminus \mathcal{A}_j : sp(\mathcal{M}_{kk}) \leq 1 \Leftrightarrow E_j \stackrel{a.e.}{\subseteq} E_i.$$

Statements (i) and (ii) actually provide the following sufficient condition for the equivalence of extinction events

$$j \in \mathcal{A}_i \text{ and } \forall k \in \mathcal{A}_i \setminus \mathcal{A}_j : sp(\mathcal{M}_{kk}) \leq 1 \Rightarrow E_j \stackrel{a.e.}{\equiv} E_i. \quad (4.10)$$

Proof. (i) Suppose that $j \in \mathcal{A}_i$. We have to show that $E_i \stackrel{a.e.}{\subseteq} E_j$, or equivalently that $E_j^c \stackrel{a.e.}{\subseteq} E_i^c$. Let V_i be the total number of individuals born in class C_i . Then, $E_i^c \stackrel{a.e.}{\equiv} [V_i = \infty]$. Let us show that $E_j^c \stackrel{a.e.}{\subseteq} [V_i = \infty]$.

Let $t_1 \leq t_2 \leq t_3 \leq \dots$ be the successive times of birth of an individual in C_j . As we assume the survival of class C_j , this sequence is almost surely infinite. Now, let X_n denote the indicator of the event $[\exists t > t_n : \mathbf{Z}^i(t) \neq \mathbf{0}]$. The assumption $j \in \mathcal{A}_i$ implies that

$$P[X_n = 1 | \mathbf{Z}^j(t_n) \neq \mathbf{0}] > 0, \quad (4.11)$$

for all $n \geq 1$. Therefore, $V_i \geq \sum_{1 \leq n \leq \infty} X_n = \infty$ almost surely, which proves $E_j^c \stackrel{a.e.}{\subseteq} E_i^c$.

(ii) Now, assume that $\forall k \in \mathcal{A}_i \setminus \mathcal{A}_j : \text{sp}(\mathcal{M}_{kk}) \leq 1$. We have to show that $E_j \stackrel{a.e.}{\subseteq} E_i$, that is $E_i^c \cap E_j \stackrel{a.e.}{\equiv} \emptyset$. Let us assume that both events E_i^c and E_j occur simultaneously. We have to show that we obtain a contradiction.

On the first hand, $E_i^c \stackrel{a.e.}{\equiv} [V_i = \infty]$ together with $\text{sp}(\mathcal{M}_{ii}) \leq 1$ (by assumption) imply that there is at least one $k \in \bar{\mathcal{A}}_i$ such that $V_k = \infty$ almost surely, where $\bar{\mathcal{A}}_i = \mathcal{A}_i \setminus \{i\}$. On the other hand, for all $k \in \mathcal{A}_j$, E_j implies E_k , that is $V_k < \infty$ almost surely, by (i). If $\bar{\mathcal{A}}_i \setminus \mathcal{A}_j = \emptyset$, this already leads to a contradiction

If $\bar{\mathcal{A}}_i \setminus \mathcal{A}_j \neq \emptyset$, then there exists at least one $k \in \bar{\mathcal{A}}_i \setminus \mathcal{A}_j$ such that $V_k = \infty$. Let k^* be the greatest k with these properties. Then, $V_{k^*} = \infty$ and $V_\ell < \infty$ almost surely for all $\ell \in \bar{\mathcal{A}}_{k^*} \subseteq \mathcal{A}_i$. This implies that $\text{sp}(\mathcal{M}_{k^*k^*}) > 1$, which contradicts the assumptions. We thus have $E_i^c \cap E_j \stackrel{a.e.}{\equiv} \emptyset$.

Finally, let us show that if $\exists k \in \mathcal{A}_i \setminus \mathcal{A}_j : \text{sp}(\mathcal{M}_{kk}) > 1$, then $P[E_j \cap E_i^c] > 0$. Let us fix k in $\mathcal{A}_i \setminus \mathcal{A}_j$ such that $\text{sp}(\mathcal{M}_{kk}) > 1$. We have

$$P[E_j \cap E_i^c] \geq P[\varphi_0 \in C_k] \cdot P[E_j \cap E_i^c | \varphi_0 \in C_k]. \quad (4.12)$$

The second factor in the right-hand side of (4.12) is such that

$$P[E_j \cap E_i^c | \varphi_0 \in C_k] \geq P[E_k^c | \varphi_0 \in C_k] \cdot P[E_j \cap E_i^c | \varphi_0 \in C_k, E_k^c]. \quad (4.13)$$

But, by assumption, $\text{sp}(\mathcal{M}_{kk}) > 1$, thus $P[E_k^c | \varphi_0 \in C_k] > 0$, and, as $k \notin \mathcal{A}_j$, $P[E_j | \varphi_0 \in C_k, E_k^c] = 1$, so that

$$P[E_j \cap E_i^c | \varphi_0 \in C_k, E_k^c] = P[E_i^c | \varphi_0 \in C_k, E_k^c].$$

Now, since $k \in \mathcal{A}_i$, by (i) we know that $P[E_i^c | E_k^c] = 1$, so $P[E_i^c | \varphi_0 \in C_k, E_k^c] > 0$, and the right-hand side of (4.13) is strictly positive, which implies that the right-hand side of (4.12) is strictly positive as well, and thus $P[E_j \cap E_i^c] > 0$. \square

The extinction of class C_i is almost surely equivalent to the extinction of the whole process if all the classes unable to generate any individual in class C_i eventually become extinct with probability one, or if all the classes are able to generate an individual in class C_i (and thus $i = 1$).

Proposition 4.2.5. *The following sufficient conditions hold for the extinction of a class to be almost surely equivalent to the total extinction.*

- (i) For $1 \leq i \leq m$, if $\forall k \notin \mathcal{A}_i : \mathbf{q}^k = \mathbf{1}$, then $E_i \stackrel{a.e.}{\equiv} E$.
- (ii) If $\mathcal{A}_1 = \{1, 2, \dots, m\}$, then $E_1 \stackrel{a.e.}{\equiv} E$.

Proof. We already know from Lemma 4.1.1 that $E \stackrel{a.e.}{\subseteq} E_i$ for all $1 \leq i \leq m$.

(i) If $k \in \mathcal{A}_i$, then by Proposition 4.2.4 (i), $E_i \stackrel{a.e.}{\subseteq} E_k$. If $k \notin \mathcal{A}_i$, then by assumption, $\mathbf{q}^k = \mathbf{1}$, which implies that $P[E_k^c] = 0$, so that $P[E_i \cap E_k^c] = 0$, and $E_i \stackrel{a.e.}{\subseteq} E_k$.

We thus have that $E_i \stackrel{a.e.}{\subseteq} E_k$ for all $1 \leq k \leq m$, and therefore $E_i \stackrel{a.e.}{\subseteq} E$, which implies $E_i \stackrel{a.e.}{\equiv} E$.

(ii) If $\mathcal{A}_1 = \{1, 2, \dots, m\}$, we know by Proposition 4.2.4 (i) that $E_1 \stackrel{a.e.}{\subseteq} E_k$ for all $1 \leq k \leq m$, so that $E_1 \stackrel{a.e.}{\subseteq} E$, and thus $E_1 \stackrel{a.e.}{\equiv} E$. \square

Remark 4.2.6. Propositions 4.2.4 (i), and 4.2.5 only give *sufficient* conditions. Let us show with an example that they are not *necessary* conditions. Take the mean progeny matrix

$$M = \begin{bmatrix} \mathcal{M}_{11} & 0 & 0 \\ 0 & \mathcal{M}_{22} & 0 \\ \mathcal{M}_{31} & \mathcal{M}_{32} & \mathcal{M}_{33} \end{bmatrix};$$

Assume that $\text{sp}(\mathcal{M}_{22}) \leq 1$ and $\text{sp}(\mathcal{M}_{33}) > 1$. By definition, $\mathcal{A}_1 = \{1, 3\}$, $\mathcal{A}_2 = \{2, 3\}$, and $\mathcal{A}_3 = \{3\}$. We have $2 \notin \mathcal{A}_1$ but $E_1 \stackrel{a.e.}{\subseteq} E_2$ since $E_1 \stackrel{a.e.}{\subseteq} E_3$ by Proposition 4.2.4 (i), and $E_3 \stackrel{a.e.}{\subseteq} E_2$ by Proposition 4.2.4 (ii). Thus, we may have $E_i \stackrel{a.e.}{\subseteq} E_j$ with $i < j$, even if j is not in \mathcal{A}_i .

Furthermore, $E_1 \stackrel{a.e.}{\equiv} E$, but $2 \notin \mathcal{A}_1$ and $\mathbf{q}^2 \neq \mathbf{1}$, since $\mathbf{q}_3^2 < 1$ by Proposition 4.2.2. Thus Proposition 4.2.5 does not provide necessary conditions either.

Notice that if in addition $\text{sp}(\mathcal{M}_{11}) \leq 1$, then by Proposition 4.2.4 (ii), $E_2 \stackrel{a.e.}{\subseteq} E_1$, even if $2 \notin \mathcal{A}_1$ and $E_3 \stackrel{a.e.}{\subseteq} E$ by Proposition 4.2.5. Thus $E_1 \stackrel{a.e.}{\equiv} E_2 \stackrel{a.e.}{\equiv} E_3 \stackrel{a.e.}{\equiv} E$ in that case.

Sometimes, the effect of the extinction of a class on another class depends on the initial individual; if we know that it belongs to some class C_ℓ , then the assumptions of Propositions 4.2.4 and 4.2.5 must be verified for the classes in \mathcal{D}_ℓ only.

Corollary 4.2.7. *For all $1 \leq i, j, \ell \leq m$,*

(i) *If C_i, C_j , and C_ℓ are three classes such that*

- $j \in \mathcal{A}_i$,
- $(\mathcal{A}_i \setminus \mathcal{A}_j) \cap \mathcal{D}_\ell \neq \emptyset$, and
- $\forall k \in (\mathcal{A}_i \setminus \mathcal{A}_j) \cap \mathcal{D}_\ell : \text{sp}(\mathcal{M}_{kk}) \leq 1$,

then $E_j \cap [\varphi_0 \in C_\ell] \stackrel{a.e.}{\equiv} E_i \cap [\varphi_0 \in C_\ell]$.

(ii) If $\mathcal{D}_\ell \subseteq \mathcal{A}_i$ or $\forall k \in \mathcal{D}_\ell \setminus \mathcal{A}_i : \mathbf{q}_\ell^k = \mathbf{1}$, then $E_i \cap [\varphi_0 \in C_\ell] \stackrel{a.e.}{=} E \cap [\varphi_0 \in C_\ell]$.

□

The proof is very similar to those of Propositions 4.2.4 and 4.2.5, and is thus omitted.

4.3 Partial extinction

Now that we have established necessary and sufficient criteria for the almost sure extinction of classes, we characterize the vector \mathbf{q}^k of extinction probability of class C_k as one particular solution of a fixed point equation.

As usual, $\mathbf{P}(\mathbf{s})$ denotes the progeny generating vector associated to the branching process. Recall the notations $\mathbf{P}^{(1)}(\mathbf{s}) = \mathbf{P}(\mathbf{s})$, and $\mathbf{P}^{(n)}(\mathbf{s}) = \mathbf{P}(\mathbf{P}^{(n-1)}(\mathbf{s}))$, for $n \geq 2$.

Recall from Theorem 1.2.5 that in the irreducible case, for any $\mathbf{0} \leq \mathbf{a} \leq \mathbf{1}$, $\mathbf{a} \neq \mathbf{1}$, we have

$$\lim_{n \rightarrow \infty} \mathbf{P}^{(n)}(\mathbf{a}) = \mathbf{q}, \quad (4.14)$$

and, as a consequence, the only solutions of the extinction equation $\mathbf{s} = \mathbf{P}(\mathbf{s})$ in the unit cube are $\mathbf{1}$ and \mathbf{q} (Harris [26, Chapter 2, Corollary 1]). In the reducible case, this is no longer the case, each \mathbf{q}^k is also a solution of the extinction equation, which may thus have up to $m + 1$ distinct solutions. Depending on the vector \mathbf{a} , the limit of $\mathbf{P}^{(n)}(\mathbf{a})$ when n tends to infinity is one solution or another.

Theorem 4.3.1. *For each $1 \leq k \leq m$, the extinction probability \mathbf{q}^k of class C_k , given the type of the initial individual, is the smallest nonnegative solution of the extinction equation $\mathbf{s} = \mathbf{P}(\mathbf{s})$ such that $\mathbf{q}_\ell^k = \mathbf{1}$ for each $\ell \notin \mathcal{A}_k$.*

Proof. We follow the same argumentation as in Mode [54, Theorem 7.1] and consider successive generations (which does not change anything to the extinction probability).

Let $\mathbf{q}^k(n)$ denote the probability that all classes in \mathcal{A}_k become extinct no later than the n th generation. We have $\mathbf{q}^k(n) \leq \mathbf{q}^k(n + 1)$ and $\mathbf{q}^k = \lim_{n \rightarrow \infty} \mathbf{q}^k(n)$. The probabilities $\mathbf{q}^k(n)$ may be computed recursively:

$$\mathbf{q}^k(1) = \mathbf{P}(\mathbf{f}^k)$$

where \mathbf{f}^k is the indicator vector of the classes which do not lead to class C_k , that is, $\mathbf{f}_\ell^k = \mathbf{1}$ for $\ell \notin \mathcal{A}_k$, and $\mathbf{f}_\ell^k = \mathbf{0}$ for $\ell \in \mathcal{A}_k$. Indeed, for all classes in \mathcal{A}_k to become extinct at the first generation, the initial individual must not produce any individual in a class belonging to \mathcal{A}_k . For $n \geq 2$,

$$\mathbf{q}^k(n) = \mathbf{P}(\mathbf{q}^k(n - 1)).$$

Since the sequence $\{\mathbf{q}^k(n)\}_{n \geq 1}$ is non decreasing in n and the generating functions are continuous in each variable, we obtain

$$\mathbf{q}^k = \mathbf{P}(\mathbf{q}^k), \quad (4.15)$$

which shows that \mathbf{q}^k is a solution of $\mathbf{s} = \mathbf{P}(\mathbf{s})$ with the property that $\mathbf{q}_\ell^k = \mathbf{1}$ for each $\ell \notin \mathcal{A}_k$.

It remains to be shown that \mathbf{q}^k is the minimal nonnegative solution of $\mathbf{s} = \mathbf{P}(\mathbf{s})$ under the specific constraint $\mathbf{q}_\ell^k = \mathbf{1}$ for each $\ell \notin \mathcal{A}_k$. Let \mathbf{q}^* be any other such vector. We have $\mathbf{q}^* \geq \mathbf{f}^k$, and thus

$$\mathbf{q}^* = \mathbf{P}(\mathbf{q}^*) \geq \mathbf{P}(\mathbf{f}^k) = \mathbf{q}^k(1),$$

by the monotonicity of $\mathbf{P}(\cdot)$, and we finally get that $\mathbf{q}^* \geq \mathbf{P}(\mathbf{q}^k(n))$ for all $n \geq 1$. Then, letting n tend to infinity, we obtain $\mathbf{q}^* \geq \mathbf{q}^k$ and the proof is completed. \square

This shows again that $\mathbf{q} \leq \mathbf{q}^k$ for all $1 \leq k \leq m$, since \mathbf{q} is the *minimal* nonnegative solution of $\mathbf{s} = \mathbf{P}(\mathbf{s})$ *without* any constraint.

Assuming that there is a path to extinction from each type of individual (Assumption 1.2.2), the counterpart of Theorem 1.2.5 in the present case is then provided by the following theorem.

Theorem 4.3.2. *For all $1 \leq k \leq m$, for every vector $\mathbf{a}^{(k)}$ such that*

$$\mathbf{a}_\ell^{(k)} \begin{cases} = \mathbf{1} & \forall \ell \notin \mathcal{A}_k \\ < \mathbf{1} & \forall \ell \in \mathcal{A}_k \end{cases}, \quad (4.16)$$

we have

$$\lim_{n \rightarrow \infty} \mathbf{P}^{(n)}(\mathbf{a}^{(k)}) = \mathbf{q}^k. \quad (4.17)$$

Proof. Let us fix k . For the sake of clarity of the proof, we reorder the n types of the branching process in two classes, K_\bullet and K_\circ , such that $i \in K_\bullet$ if some individual of type i may have an individual belonging to class C_k among its direct or indirect descendants, and $i \in K_\circ$ otherwise. In that view, we may rewrite $\mathbf{a}^{(k)} = [\mathbf{a}_\bullet, \mathbf{a}_\circ]^T$ with $\mathbf{a}_\bullet < \mathbf{1}$ and $\mathbf{a}_\circ = \mathbf{1}$.

Like in the proof of Theorem 4.3.1, we consider successive generations and we define Z_n to be the population size at the n th generation. We have for any finite $N \in \mathbb{N}_0$

$$\begin{aligned} \mathbf{P}^{(n)}(\mathbf{a}^{(k)}) &= \sum_{\mathbf{y} \geq \mathbf{0}} \mathbf{P}[Z_n = (\mathbf{0}, \mathbf{y}) \mid \varphi_0] \\ &\quad + \sum_{\substack{\mathbf{y} \geq \mathbf{0} \\ \mathbf{x} \geq \mathbf{0}, \mathbf{x} \neq \mathbf{0} \\ \|\mathbf{x}\| \leq N}} \mathbf{P}[Z_n = (\mathbf{x}, \mathbf{y}) \mid \varphi_0] \mathbf{a}_\bullet^{\mathbf{x}} \\ &\quad + \sum_{\substack{\mathbf{y} \geq \mathbf{0} \\ \mathbf{x} \geq \mathbf{0}, \mathbf{x} \neq \mathbf{0} \\ \|\mathbf{x}\| > N}} \mathbf{P}[Z_n = (\mathbf{x}, \mathbf{y}) \mid \varphi_0] \mathbf{a}_\bullet^{\mathbf{x}}. \end{aligned}$$

The first term approaches \mathbf{q}^k as n tends to infinity. The second term tends to zero as n tends to infinity: indeed, firstly

$$\sum_{\substack{\mathbf{y} \geq \mathbf{0} \\ \mathbf{x} \geq \mathbf{0}, \mathbf{x} \neq \mathbf{0} \\ \|\mathbf{x}\| \leq N}} \mathbf{P}[Z_n = (\mathbf{x}, \mathbf{y}) \mid \varphi_0 \in K_\circ] = 0$$

since if the initial individual belongs to K_\circ , then it is unable to generate an individual in C_k , which implies that it is not able to generate an individual in K_\bullet either. Secondly,

$$\lim_{n \rightarrow \infty} \sum_{\substack{\mathbf{y} \geq \mathbf{0} \\ \mathbf{x} \geq \mathbf{0}, \mathbf{x} \neq \mathbf{0} \\ \|\mathbf{x}\| \leq N}} \mathrm{P}[\mathbf{Z}_n = (\mathbf{x}, \mathbf{y}) \mid \varphi_0 \in K_\bullet] = 0$$

since if the first individual belongs to K_\bullet , then $(\mathbf{Z}_n)_\bullet$ is the restriction of the branching process limited to the types in K_\bullet , which is another branching process, itself exploding or becoming extinct by the dichotomy stated in Theorem 1.2.3. In the limit, $\|\mathbf{x}\|$ cannot be both nonzero and less than or equal to N .

Finally, the third term tends to zero since it is dominated by $\mathrm{P}[\|\mathbf{Z}_n\| > N \mid \varphi_0]$ times the N th power of a quantity strictly less than 1, and N is arbitrary. \square

As a final remark, we observe that the extinction probability \mathbf{q}^k of class C_k also corresponds to the total extinction probability $\hat{\mathbf{q}}$ of a modified branching process $\hat{\mathbf{Z}}(t)$, in which we fix at 0 the birth rate of an individual which is not able to generate individuals in class C_k , as stated below.

Proposition 4.3.3. *The extinction probability vector \mathbf{q}^k is the minimal nonnegative solution of the extinction equation $\mathbf{s} = \hat{\mathbf{P}}(\mathbf{s})$, where $\hat{\mathbf{P}}(\mathbf{s})$ is the progeny generating function of the modified branching process $\hat{\mathbf{Z}}(t)$ in which we set $\hat{\mathbf{P}}_i(\mathbf{s}) := \mathbf{1}$ for all $i \notin \mathcal{A}_k$.*

Proof. We have

$$\begin{aligned} \mathbf{q}^k &= \mathrm{P}[\exists T_1 > 0 : \mathbf{Z}_i(T_1) = \mathbf{0} \forall i \in \mathcal{A}_k \mid \varphi_0] \\ &= \mathrm{P}[\exists T_1 > 0 : \hat{\mathbf{Z}}_i(T_1) = \mathbf{0} \forall i \in \mathcal{A}_k \mid \varphi_0] \end{aligned}$$

and, as the individuals unable to generate individuals in class C_k eventually die without any progeny in the modified branching process,

$$\begin{aligned} &\mathrm{P}[\exists T_1 > 0 : \hat{\mathbf{Z}}_i(T_1) = \mathbf{0} \forall i \in \mathcal{A}_k \mid \varphi_0] \\ &= \mathrm{P}[\exists T_2 \geq T_1 : \hat{\mathbf{Z}}_i(T_2) = \mathbf{0} \forall i \in \mathcal{A}_k, \text{ and } \hat{\mathbf{Z}}_i(T_2) = \mathbf{0} \forall i \notin \mathcal{A}_k \mid \varphi_0] \\ &= \mathrm{P}[\exists T_2 > 0 : \hat{\mathbf{Z}}(T_2) = \mathbf{0} \mid \varphi_0] \\ &= \hat{\mathbf{q}}. \end{aligned}$$

This shows that $\mathbf{q}^k = \hat{\mathbf{q}}$. \square

The extinction criteria of a class C_k are thus equivalent to the total extinction criteria of the modified branching process (still reducible).

4.4 Algorithms

We now investigate the numerical techniques to compute the total and partial extinction probabilities of a reducible MBT.

Total extinction

In the reducible case, the criticality of the branching process is still determined by the spectral radius of the mean progeny matrix M , and Theorem 1.2.1 still holds, provided there is no *final* class: a final class C is such that each individual whose type is in C almost surely generates at the next generation exactly one individual whose type is in C , and possibly other individuals with types not in C (Harris, [26, Chapter 2, Theorem 10.1]).

In practice, in the supercritical case, the total extinction probability is thus still computed as the minimal nonnegative solution of the extinction equation.

For our demographic application in Section 3.4, we compute the total extinction probability of a reducible MBT, using the linear algorithms and the Newton-Depth algorithm. There is no need for the MBT to be irreducible in order to use the linear algorithms. This assumption is required in Theorem 2.3.1, used to compare the convergence rates of the linear algorithms, as well as to prove that the Newton-Depth sequence is well-defined. Actually, we can extend Theorem 2.3.1 to the case of a reducible MBT.

Corollary 4.4.1. *Assume that the MBT is reducible, with mean progeny matrix $M = \Psi(\mathbf{1} \oplus \mathbf{1})$ structured like in (4.1).*

If none of the subprocesses $\mathbf{Z}^k(t)$ is critical, that is if $\text{sp}(\mathcal{M}_{kk}) > 1$ or $\text{sp}(\mathcal{M}_{kk}) < 1$ for all k , then $\text{sp}[\Psi(\mathbf{q} \oplus \mathbf{q})] < 1$, so that $[I - \Psi(\mathbf{q} \oplus \mathbf{q})]^{-1}$ exists and is nonnegative.

If at least one subprocess $\mathbf{Z}^k(t)$ is critical, that is there exist k such that $\text{sp}(\mathcal{M}_{kk}) = 1$, then $\text{sp}[\Psi(\mathbf{q} \oplus \mathbf{q})] \leq 1$.

Proof. Define $M(\mathbf{s}) = \Psi(\mathbf{s} \oplus \mathbf{s})$. Like the mean matrix M , $M(\mathbf{s})$ is lower-triangular, and for $1 \leq k \leq m$, $\mathcal{M}_{kk}(\mathbf{s})$ is actually a function $\mathcal{M}_{kk}(\mathbf{s}_{i_1}, \mathbf{s}_{i_2}, \dots, \mathbf{s}_{i_p}, \mathbf{s}_k)$ of the variables $\mathbf{s}_{i_1}, \mathbf{s}_{i_2}, \dots, \mathbf{s}_{i_p}$ and \mathbf{s}_k only, for $i_1 < i_2 < \dots < i_p \in \mathcal{E}_k$. Since $M(\mathbf{s})$ is increasing in \mathbf{s} ,

$$\mathcal{M}_{kk}(\mathbf{s}) \leq \mathcal{M}_{kk}(\mathbf{1}, \mathbf{1}, \dots, \mathbf{1}, \mathbf{s}_k) = \tilde{\mathcal{M}}_{kk}(\mathbf{s}_k),$$

where $\tilde{\mathcal{M}}_{kk}(\mathbf{s}_k)$ is nothing else than the matrix $M(\mathbf{s})$ associated to the irreducible subprocess $\mathbf{Z}^k(t)$.

For the process $\mathbf{Z}(t)$, we thus have

$$\text{sp}[M(\mathbf{q})] = \max_k \text{sp}[\mathcal{M}_{kk}(\mathbf{q})] \leq \max_k \text{sp}[\tilde{\mathcal{M}}_{kk}(\mathbf{q}_k)]$$

and there are three possibilities for each $1 \leq k \leq m$.

In the first case, the subprocess $\mathbf{Z}^k(t)$ is supercritical, then $\mathbf{q}_k^k < \mathbf{1}$, and by the same arguments as in the proof of Theorem 2.3.1, $\text{sp}[\tilde{\mathcal{M}}_{kk}(\mathbf{q}_k^k)] < 1$. Moreover, by Lemma 4.1.1, $\mathbf{q}_k \leq \mathbf{q}_k^k$, which implies that $\text{sp}[\tilde{\mathcal{M}}_{kk}(\mathbf{q}_k)] < 1$.

In the second case, the subprocess $\mathbf{Z}^k(t)$ is subcritical, and then $\mathbf{q}_k^k = \mathbf{1}$, and as above, $\text{sp}[\tilde{\mathcal{M}}_{kk}(\mathbf{q}_k^k)] < 1$, and $\text{sp}[\tilde{\mathcal{M}}_{kk}(\mathbf{q}_k)] < 1$.

In the final case, the subprocess $\mathbf{Z}^k(t)$ is critical, and then $\mathbf{q}_k^k = \mathbf{1}$, and again by the same argument, $\text{sp}[\tilde{\mathcal{M}}_{kk}(\mathbf{q}_k^k)] = 1$, and $\text{sp}[\tilde{\mathcal{M}}_{kk}(\mathbf{q}_k)] \leq 1$.

By taking the maximum over k of the spectral radii, we thus obtain the statement of the corollary. \square

In the irreducible case, we always assumed that we were in the noncritical case. In the present case, we have to assume that none of the irreducible subprocesses $\mathbf{Z}^k(t)$ is critical in order to be sure that everything works perfectly. Then, any of the linear algorithms or the Newton algorithm may be used to solve for the total extinction of the MBT.

To further improve the efficiency of the numerical methods in the reducible case, we can take the special structure of the birth probability matrix Ψ into account, and decompose the quadratic system $\mathbf{s} = \boldsymbol{\theta} + \Psi(\mathbf{s} \otimes \mathbf{s})$ of size n in smaller parts. To clarify this idea, let us illustrate it on an example with three classes, where the mean progeny matrix may be decomposed in the following way:

$$M = \begin{bmatrix} \mathcal{M}_{11} & 0 & 0 \\ \mathcal{M}_{21} & \mathcal{M}_{22} & 0 \\ \mathcal{M}_{31} & \mathcal{M}_{32} & \mathcal{M}_{33} \end{bmatrix},$$

with $\mathcal{M}_{ij} \neq 0$ for all $i, j = 1, 2, 3$.

In what follows, we introduce some notations to specify which part of a vector \mathbf{x} we take into account:

$$\begin{aligned} \mathbf{x}_{\bar{i}} &= (x_j : j \in C_i), \\ \mathbf{x}_{\underline{i}} &= (x_j : j \in C_1 \cup C_2 \cup \dots \cup C_i), \end{aligned}$$

and we extend these notations to matrices, for instance

$$\Psi_{\bar{3}, \bar{3} \underline{2}} = (\Psi_{i,jk} : i, j \in C_3, k \in C_1 \cup C_2).$$

With these notations, we have in particular $\mathbf{q}_{\bar{i}} = \mathbf{q}_i$ and $\mathbf{q}_{\underline{i}} = [\mathbf{q}_1, \mathbf{q}_2, \dots, \mathbf{q}_{i-1}, \mathbf{q}_i]^T$.

In the example with three classes, the extinction equation may be decomposed in three smaller equations. The first one is

$$\mathbf{s}_{\bar{1}} = \boldsymbol{\theta}_{\bar{1}} + \Psi_{\bar{1}, \bar{1} \bar{1}}(\mathbf{s}_{\bar{1}} \otimes \mathbf{s}_{\bar{1}}).$$

Solving this equation provides us with the subvector $\mathbf{q}_{\bar{1}}$. The second equation is

$$\begin{aligned} \mathbf{s}_{\bar{2}} &= [\boldsymbol{\theta}_{\bar{2}} + \Psi_{\bar{2}, \bar{1} \bar{1}}(\mathbf{q}_{\bar{1}} \otimes \mathbf{q}_{\bar{1}})] \\ &+ [\Psi_{\bar{2}, \bar{1} \bar{2}}(\mathbf{q}_{\bar{1}} \otimes I) + \Psi_{\bar{2}, \bar{2} \bar{1}}(I \otimes \mathbf{q}_{\bar{1}})] \mathbf{s}_{\bar{2}} \\ &+ \Psi_{\bar{2}, \bar{2} \bar{2}}(\mathbf{s}_{\bar{2}} \otimes \mathbf{s}_{\bar{2}}) \end{aligned}$$

which may be rewritten as

$$\mathbf{s}_{\bar{2}} = \tilde{\boldsymbol{\theta}}_{\bar{2}} + \tilde{\Psi}_{\bar{2}}(\mathbf{s}_{\bar{2}} \otimes \mathbf{s}_{\bar{2}})$$

with

$$\begin{aligned} \tilde{\boldsymbol{\theta}}_{\bar{2}} &= [I - W_2]^{-1} [\boldsymbol{\theta}_{\bar{2}} + \Psi_{\bar{2}, \bar{1} \bar{1}}(\mathbf{q}_{\bar{1}} \otimes \mathbf{q}_{\bar{1}})], \\ \tilde{\Psi}_{\bar{2}} &= [I - W_2]^{-1} \Psi_{\bar{2}, \bar{2} \bar{2}}, \\ W_2 &= [\Psi_{\bar{2}, \bar{1} \bar{2}}(\mathbf{q}_{\bar{1}} \otimes I) + \Psi_{\bar{2}, \bar{2} \bar{1}}(I \otimes \mathbf{q}_{\bar{1}})]. \end{aligned}$$

Solving this second equation provides us with the subvector $\mathbf{q}_{\bar{2}}$, and thus also with $\mathbf{q}_{\bar{2}} = [\mathbf{q}_{\bar{1}}, \mathbf{q}_{\bar{2}}]^T$. Finally, the third equation has the form

$$\mathbf{s}_{\bar{3}} = \tilde{\boldsymbol{\theta}}_{\bar{3}} + \tilde{\Psi}_{\bar{3}}(\mathbf{s}_{\bar{3}} \otimes \mathbf{s}_{\bar{3}})$$

with

$$\begin{aligned}\tilde{\boldsymbol{\theta}}_{\bar{3}} &= [I - W_3]^{-1} [\boldsymbol{\theta}_{\bar{3}} + \Psi_{\bar{3};\bar{2}\bar{2}}(\mathbf{q}_{\bar{2}} \otimes \mathbf{q}_{\bar{2}})], \\ \tilde{\Psi}_{\bar{3}} &= [I - W_3]^{-1} \Psi_{\bar{3};\bar{3}\bar{3}}, \\ W_3 &= [\Psi_{\bar{3};\bar{2}\bar{3}}(\mathbf{q}_{\bar{2}} \otimes I) + \Psi_{\bar{3};\bar{3}\bar{2}}(I \otimes \mathbf{q}_{\bar{2}})].\end{aligned}$$

Solving this last equation provides us with $\mathbf{q}_{\bar{3}}$, and thus also with the whole vector $\mathbf{q}_{\bar{3}} = \mathbf{q}$.

When using for instance the Newton algorithm, the numerical complexity may be very different if we apply it once on the whole extinction equation (1.15), or several times on its decomposition; this depends on the size of the equivalence classes C_k , and on their number. Actually, the decomposition may be really worthwhile when there are *enough* equivalence classes. Let us clarify this as follows.

Suppose that we have m classes, all being of cardinality r , that is $n = m r$. We can show that the total complexity of the method without decomposition is $(20/3) m^3 r^3 + \mathcal{O}(m^2 r^2)$ flops per iteration, while decomposing the system as described above yields a polynomial complexity with $2 m r^4 + 2 m^3 r^3 + 5 m^2 r^3 + (1/3) m^3 r^2$ as dominant terms.

Figure 4.1 illustrates the difference in the complexities for $n = 500$, when m varies from 1 to 50. We see that for $m > 5$, it becomes numerically advantageous to take the structure into account and to use the decomposition.

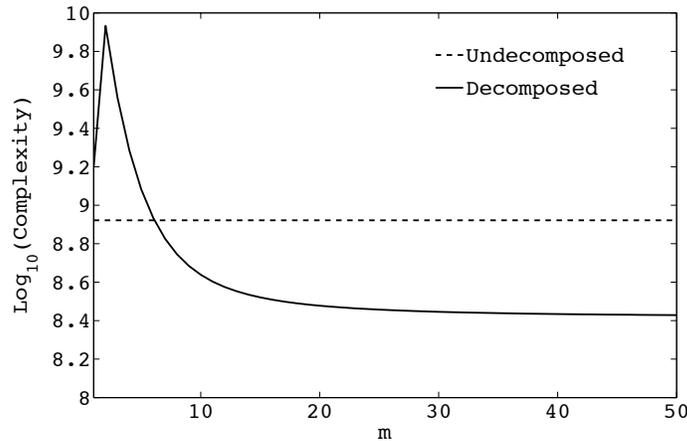


Figure 4.1: Logarithm of the numerical complexity when using the Newton algorithm with or without decomposition to solve for the extinction probability \mathbf{q} , as a function of m , when $n = m r = 500$.

Partial extinction

Recall that by partial extinction, we mean the extinction of one class, as opposed to the extinction of the whole process. We would like here to numerically evaluate the extinction probability of the class C_k , denoted by \mathbf{q}^k .

Theorems 4.3.1 and 4.3.2 suggest a method to numerically compute \mathbf{q}^k for each $1 \leq k \leq m$ in an MBT. So, starting with the initial vector $\mathbf{x}^k(0) = \mathbf{a}^{(k)}$ such that

$$\mathbf{a}_\ell^{(k)} = \begin{cases} \mathbf{1} & \forall \ell \notin \mathcal{A}_k \\ \boldsymbol{\theta}_\ell < \mathbf{1} & \forall \ell \in \mathcal{A}_k, \end{cases} \quad (4.18)$$

the functional iteration $\mathbf{x}^k(n) = \mathbf{P}(\mathbf{x}^k(n-1))$, $n \geq 1$, converges to the vector \mathbf{q}^k . We may use one of the linear algorithms discussed in Chapter 2, starting the numerical scheme with this particular initial vector $\mathbf{a}^{(k)}$.

We might also use Proposition 4.3.3 and compute \mathbf{q}^k as the total extinction probability of the modified MBT for which the birth rates matrix \hat{B} is such that $\hat{B}_{i,jk} = 0$ for all $i \notin \mathcal{A}_k$ and $1 \leq j, k \leq n$, and this with the help of one of the linear algorithms or with the Newton algorithm.

4.5 Numerical examples

We now illustrate the use of the criteria discussed in Section 4.2, as well as the computation of the total and partial extinction probabilities.

Example 4.5.1. Consider a supercritical reducible MBT with $n = 10$ phases and mean progeny matrix

$$M = \begin{bmatrix} \mathcal{M}_{11} & 0 & 0 & 0 & 0 \\ \mathcal{M}_{21} & \mathcal{M}_{22} & 0 & 0 & 0 \\ \mathcal{M}_{31} & 0 & \mathcal{M}_{33} & 0 & 0 \\ 0 & 0 & \mathcal{M}_{43} & \mathcal{M}_{44} & 0 \\ 0 & \mathcal{M}_{52} & 0 & 0 & \mathcal{M}_{55} \end{bmatrix}.$$

There are five equivalence classes, each of them of cardinality two. The submatrices are given by

$$\begin{aligned} \mathcal{M}_{11} &= \begin{bmatrix} 0.5 & 0.611 \\ 0.018 & 0.164 \end{bmatrix}, \\ \mathcal{M}_{21} &= \begin{bmatrix} 0.097 & 0.193 \\ 0.09 & 0.181 \end{bmatrix}, \quad \mathcal{M}_{22} = \begin{bmatrix} 1.545 & 0.97 \\ 0.818 & 0.727 \end{bmatrix}, \\ \mathcal{M}_{31} &= \begin{bmatrix} 0.188 & 0.188 \\ 0.177 & 0.177 \end{bmatrix}, \quad \mathcal{M}_{33} = \begin{bmatrix} 1.031 & 0.469 \\ 0.441 & 0.97 \end{bmatrix}, \\ \mathcal{M}_{43} &= \begin{bmatrix} 0.88 & 0.34 \\ 0.1 & 0.35 \end{bmatrix}, \quad \mathcal{M}_{44} = \begin{bmatrix} 0.16 & 0.32 \\ 0.25 & 0.3 \end{bmatrix}, \\ \mathcal{M}_{52} &= \begin{bmatrix} 0.481 & 0.481 \\ 0.667 & 0.667 \end{bmatrix}, \quad \mathcal{M}_{55} = \begin{bmatrix} 0.481 & 0.481 \\ 0.476 & 0.476 \end{bmatrix}. \end{aligned}$$

The spectral radius of the diagonal irreducible blocks are

i	1	2	3	4	5
$\text{sp}(\mathcal{M}_{ii})$	0.53	1.632	1.457	0.521	0.957,

so that the subprocesses $\mathbf{Z}^2(t)$ and $\mathbf{Z}^3(t)$ are supercritical, the others being subcritical. The sets \mathcal{A}_k and \mathcal{D}_k for $k = 1, 2, \dots, 5$, are given by

$$\mathcal{A}_1 = \{1, 2, 3, 4, 5\}, \mathcal{A}_2 = \{2, 5\}, \mathcal{A}_3 = \{3, 4\}, \mathcal{A}_4 = \{4\}, \mathcal{A}_5 = \{5\},$$

$$\mathcal{D}_1 = \{1\}, \mathcal{D}_2 = \{1, 2\}, \mathcal{D}_3 = \{1, 3\}, \mathcal{D}_4 = \{1, 3, 4\}, \mathcal{D}_5 = \{1, 2, 5\}.$$

According to Propositions 4.2.1 and 4.2.2, we know that

$$\mathbf{q} = \begin{bmatrix} \mathbf{1} \\ < \mathbf{1} \\ < \mathbf{1} \\ < \mathbf{1} \\ < \mathbf{1} \end{bmatrix}, \mathbf{q}^1 = \begin{bmatrix} \mathbf{1} \\ < \mathbf{1} \\ < \mathbf{1} \\ < \mathbf{1} \\ < \mathbf{1} \end{bmatrix}, \mathbf{q}^2 = \begin{bmatrix} \mathbf{1} \\ < \mathbf{1} \\ \mathbf{1} \\ \mathbf{1} \\ < \mathbf{1} \end{bmatrix}, \mathbf{q}^3 = \begin{bmatrix} \mathbf{1} \\ \mathbf{1} \\ < \mathbf{1} \\ < \mathbf{1} \\ \mathbf{1} \end{bmatrix},$$

$$\mathbf{q}^4 = \mathbf{q}^5 = \mathbf{1}$$

According to Proposition 4.2.4,

$$E_2 \stackrel{a.e.}{\subseteq} E_5, \quad E_3 \stackrel{a.e.}{\subseteq} E_4.$$

Following Proposition 4.2.5, $E_1 \stackrel{a.e.}{\equiv} E$. Moreover, by Corollary 4.2.7, we also have

$$E_2 \cap [\varphi_0 \in C_2] \stackrel{a.e.}{\equiv} E_1 \cap [\varphi_0 \in C_2], \quad E_2 \cap [\varphi_0 \in C_5] \stackrel{a.e.}{\equiv} E_1 \cap [\varphi_0 \in C_5],$$

and

$$E_3 \cap [\varphi_0 \in C_3] \stackrel{a.e.}{\equiv} E_1 \cap [\varphi_0 \in C_3], \quad E_3 \cap [\varphi_0 \in C_4] \stackrel{a.e.}{\equiv} E_1 \cap [\varphi_0 \in C_4].$$

In that case, the equivalence $E_j \cap [\varphi_0 \in C_\ell] \stackrel{a.e.}{\equiv} E_i \cap [\varphi_0 \in C_\ell]$ implies $\mathbf{q}_\ell^j = \mathbf{q}_\ell^i$.

We numerically compute the extinction probabilities with the Newton algorithm, leading to

$$\mathbf{q} = \mathbf{q}^1 = \begin{bmatrix} 1 \\ 1 \\ 0.079 \\ 0.14 \\ 0.187 \\ 0.247 \\ 0.26 \\ 0.556 \\ 0.044 \\ 0.053 \end{bmatrix}, \quad \mathbf{q}^2 = \begin{bmatrix} 1 \\ 1 \\ 0.079 \\ 0.14 \\ 1 \\ 1 \\ 1 \\ 1 \\ 0.044 \\ 0.053 \end{bmatrix}, \quad \mathbf{q}^3 = \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 0.187 \\ 0.247 \\ 0.26 \\ 0.556 \\ 1 \\ 1 \end{bmatrix},$$

$$\mathbf{q}^4 = \mathbf{q}^5 = \mathbf{1}.$$

Example 4.5.2. Consider another supercritical reducible MBT with $n = 6$ phases and mean progeny matrix

$$M = \begin{bmatrix} \mathcal{M}_{11} & 0 & 0 \\ 0 & \mathcal{M}_{22} & 0 \\ \mathcal{M}_{31} & \mathcal{M}_{32} & \mathcal{M}_{33} \end{bmatrix}.$$

There are three equivalence classes, each of them of cardinality two. The submatrices are given by

$$\mathcal{M}_{11} = \begin{bmatrix} 0.453 & 1.124 \\ 0.495 & 0.798 \end{bmatrix}, \quad \mathcal{M}_{22} = \begin{bmatrix} 1.288 & 0.698 \\ 0.89 & 1.081 \end{bmatrix},$$

$$\mathcal{M}_{31} = \begin{bmatrix} 0.363 & 0.421 \\ 0.504 & 0.389 \end{bmatrix}, \quad \mathcal{M}_{32} = \begin{bmatrix} 0.192 & 0.333 \\ 0.349 & 0.192 \end{bmatrix},$$

and

$$\mathcal{M}_{33} = \begin{bmatrix} 0.153 & 0.303 \\ 0.156 & 0.161 \end{bmatrix},$$

The spectral radius of the diagonal irreducible blocks are

i	1	2	3
$\text{sp}(\mathcal{M}_{ii})$	1.391	1.98	0.374,

so that the subprocesses $\mathbf{Z}^1(t)$ and $\mathbf{Z}^2(t)$ are supercritical, while $\mathbf{Z}^3(t)$ is subcritical. The sets \mathcal{A}_k and \mathcal{D}_k for $k = 1, 2, 3$ are given by

$$\mathcal{A}_1 = \{1, 3\}, \quad \mathcal{A}_2 = \{2, 3\}, \quad \mathcal{A}_3 = \{3\},$$

$$\mathcal{D}_1 = \{1\}, \quad \mathcal{D}_2 = \{2\}, \quad \mathcal{D}_3 = \{1, 2, 3\}.$$

According to Propositions 4.2.1, and 4.2.2, we know that

$$\mathbf{q} = \begin{bmatrix} < \mathbf{1} \\ < \mathbf{1} \\ < \mathbf{1} \end{bmatrix}, \quad \mathbf{q}^1 = \begin{bmatrix} < \mathbf{1} \\ \mathbf{1} \\ < \mathbf{1} \end{bmatrix}, \quad \mathbf{q}^2 = \begin{bmatrix} \mathbf{1} \\ < \mathbf{1} \\ < \mathbf{1} \end{bmatrix}, \quad \mathbf{q}^3 = \mathbf{1}.$$

According to Proposition 4.2.4,

$$E_1 \stackrel{a.e.}{\subseteq} E_3, \quad E_2 \stackrel{a.e.}{\subseteq} E_3.$$

Moreover, by Corollary 4.2.7,

$$E_1 \cap [\varphi_0 \in C_1] \stackrel{a.e.}{\equiv} E \cap [\varphi_0 \in C_1], \quad E_2 \cap [\varphi_0 \in C_2] \stackrel{a.e.}{\equiv} E \cap [\varphi_0 \in C_2];$$

here, the equivalence $E_i \cap [\varphi_0 \in C_\ell] \stackrel{a.e.}{\equiv} E \cap [\varphi_0 \in C_\ell]$ implies $\mathbf{q}_\ell^i = \mathbf{q}_\ell$.

The extinction probabilities are given by

$$\mathbf{q} = \begin{bmatrix} 0.366 \\ 0.473 \\ 0.007 \\ 0.015 \\ 0.173 \\ 0.181 \end{bmatrix}, \quad \mathbf{q}^1 = \begin{bmatrix} 0.366 \\ 0.473 \\ 1 \\ 1 \\ 0.443 \\ 0.447 \end{bmatrix}, \quad \mathbf{q}^2 = \begin{bmatrix} 1 \\ 1 \\ 0.007 \\ 0.015 \\ 0.424 \\ 0.455 \end{bmatrix}, \quad \mathbf{q}^3 = \mathbf{1}.$$

CHAPTER 5

Transient measures

Besides the question of the extinction probability of a population, we may also be interested in the distribution of its size at some finite time, or in the distribution of the time until its extinction. Finally, we may wonder how many individuals have been generated until some given time, or until extinction if it occurs. All these questions correspond to transient features of a Markovian tree, and are addressed in the present chapter.

Most of the results may directly be inferred from published results on multitype branching processes. Nevertheless, using probabilistic arguments as much as possible, we derive them anew within the context of MBTs, in order to present a coherent picture.

We begin by recalling some matrix derivation rules necessary to determine factorial moments from matrix probability generating functions. Then, we characterize the distribution the population size at any given time in an MBT. Its probability generating function satisfies a set of Kolmogorov backward and forward differential systems of equations. We also obtain the factorial moments as solutions of recursive matrix differential equations.

Next, we identify the distribution of the time until extinction of an MBT as the solution of a matrix differential equation, and we construct an approximation for the tail of the distribution, which we then use to evaluate the conditional mean time until extinction, given that the process does become extinct.

Finally, we consider the total progeny size up to some finite time t , and its limit as t goes to infinity. We completely characterize the asymptotic distribution, and in both cases we recursively determine all the factorial moments.

We end the chapter by a numerical illustration of the different transient measures on the MBT model in demography.

The material in this chapter is also presented in Hautphenne, Latouche and Rémiche [29].

5.1 Matrix derivatives

In this first section, we recall the rules of matrix differentiations and some of their properties. They are inspired from the matrix derivatives rules described by MacRae [52]; we particularize them to the derivative with respect to a row vector \mathbf{s}^T .

Let \mathbf{s} be a vector of size n , and let $d/d\mathbf{s}^T$ be a row vector of derivative operators $[d/ds_1, \dots, d/ds_n]$.

Definition 5.1.1 (Matrix differentiation). *If Y is a $p \times q$ matrix whose entries are function of the $n \times 1$ vector \mathbf{s} , then, the derivative of Y with respect to \mathbf{s}^T is the $p \times nq$ matrix of partial derivatives, $dY/d\mathbf{s}^T$, given by*

$$\frac{dY}{d\mathbf{s}^T} = Y \otimes d/d\mathbf{s}^T,$$

with the understanding that $Y_{ij} \cdot d/ds_k = \partial Y_{ij} / \partial s_k$.

Observe that $d\mathbf{s}/d\mathbf{s}^T = I_n$, where I_n denotes the identity matrix of size n .

We now give three general derivative theorems that will be used in the next sections to obtain the factorial moments from matrix equations for generating functions.

Theorem 5.1.2 (Sum Rule). *Let Y and Z be matrix functions of \mathbf{s} , such that their sum is defined. Then,*

$$d(Y + Z)/d\mathbf{s}^T = dY/d\mathbf{s}^T + dZ/d\mathbf{s}^T.$$

□

Theorem 5.1.3 (Product Rule). *Let Y and Z be matrix functions of \mathbf{s} , such that their product is defined. Then,*

$$d(YZ)/d\mathbf{s}^T = (dY/d\mathbf{s}^T)(Z \otimes I_n) + Y(dZ/d\mathbf{s}^T).$$

□

To give the rule for derivatives of Kronecker products, we need to introduce the permuted identity matrix $I_{(m,n)}$.

Definition 5.1.4. *The permuted identity matrix $I_{(m,n)}$ is a square matrix of size mn partitioned into $m \times n$ sub-matrices such that the (i,j) th sub-matrix has a 1 in its (j,i) th position and zeros elsewhere.*

For example,

$$I_{(2,2)} = \left[\begin{array}{cc|cc} 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ \hline 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 \end{array} \right].$$

The following identities can be verified by direct examination: $I_{(m,1)} = I_{(1,m)} = I_m$, $I_{(m,n)} = I_{(n,m)}^T$, and $I_{(m,n)} \cdot I_{(n,m)} = I_{mn}$.

The permuted identity matrix may be used to reverse the order of a Kronecker product: if A is $m \times n$, and B is $p \times q$, then

$$B \otimes A = I_{(m,p)} (A \otimes B) I_{(q,n)}.$$

Theorem 5.1.5 (Kronecker Product Rule). *If Y is an $s \times t$ matrix and Z is a $p \times q$ matrix, then*

$$\begin{aligned} d(Y \otimes Z)/ds^T &= (Y \otimes dZ/ds^T) + I_{(p,s)} (Z \otimes dY/ds^T) (I_{(t,q)} \otimes I_n) \\ &= (Y \otimes dZ/ds^T) + (dY/ds^T \otimes Z) I_{(q,tn)} (I_{(t,q)} \otimes I_n). \end{aligned}$$

□

5.2 Population size

Let $\mathbf{Z}(t) = [Z_1(t), Z_2(t), \dots, Z_n(t)]^T$ be the vector of population size at time t in an MBT, where $Z_i(t)$ is the number of branches in phase i at time t , and recall that φ_0 denotes the initial phase of the MBT.

Define the conditional vectorial generating function $\mathbf{F}(\mathbf{s}, t)$, given the phase of the first individual, as

$$F_i(\mathbf{s}, t) = \sum_{\mathbf{k} \geq \mathbf{0}} \mathbb{P}[\mathbf{Z}(t) = \mathbf{k} \mid \varphi_0 = i] \mathbf{s}^{\mathbf{k}},$$

where recall that $\mathbf{s}^{\mathbf{k}} = s_1^{k_1} s_2^{k_2} \dots s_n^{k_n}$, and $|s_i| < 1$ for all i . In the sequel, we sometimes write $\mathbf{F}(\mathbf{s}, t) = \sum_{\mathbf{k} \geq \mathbf{0}} \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = \mathbf{k}] \mathbf{s}^{\mathbf{k}}$. Note that $\mathbf{F}(\mathbf{1}, t) = \mathbf{1}$, since at any finite time t , the total population is always finite.

It is well known from the theory of multitype branching processes that the generating function $\mathbf{F}(\mathbf{s}, t)$ satisfies the backward and the forward Kolmogorov systems of equations, see for instance Harris [26, V.4.], and Athreya and Ney [6, V.7.]. We give the expressions of these differential systems in the special case of the MBT, and we show how to obtain them by probabilistic arguments in terms of the evolution of the MBT.

Theorem 5.2.1. *The forward and backward Kolmogorov equations for the generating function $\mathbf{F}(\mathbf{s}, t)$ of an MBT are respectively*

$$\frac{\partial}{\partial t} \mathbf{F}(\mathbf{s}, t) - \frac{\partial}{\partial \mathbf{s}^T} \mathbf{F}(\mathbf{s}, t) \cdot \mathbf{a}(\mathbf{s}) = \mathbf{0}, \quad (5.1)$$

where $\partial/\partial \mathbf{s}^T \mathbf{F}(\mathbf{s}, t) = \mathbf{F}(\mathbf{s}, t) \otimes \partial/\partial \mathbf{s}^T$, and

$$\frac{\partial}{\partial t} \mathbf{F}(\mathbf{s}, t) = \mathbf{a}(\mathbf{F}(\mathbf{s}, t)), \quad (5.2)$$

with $\mathbf{F}(\mathbf{s}, 0) = \mathbf{s}$ and $\mathbf{a}(\mathbf{x}) = \mathbf{d} + D_0 \mathbf{x} + B(\mathbf{x} \otimes \mathbf{x})$.

Proof. As mentioned in [6, V.7], the equations follow from the Kolmogorov equations for the Markov process $\mathbf{Z}(t)$, but (5.2) may also be justified by an argument based on the dynamics of the MBT. In order to illustrate the difference in approaches, we give the justification for (5.1) on the basis of the Kolmogorov equations, assuming that $n = 2$ in order to simplify the presentation.

The forward Kolmogorov equations for $\mathbf{Z}(t)$ are

$$\begin{aligned} \frac{d}{dt} \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (0, 0)] & \\ = d_1 \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (1, 0)] + d_2 \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (0, 1)], & \end{aligned} \quad (5.3)$$

and

$$\begin{aligned} \frac{d}{dt} \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (k_1, k_2)] = & \\ & [k_1 (B_{1,12} + B_{1,21}) + (k_2 - 1) B_{2,22}] \\ & \cdot \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (k_1, k_2 - 1)] \\ + & [k_2 (B_{2,12} + B_{2,21}) + (k_1 - 1) B_{1,11}] \\ & \cdot \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (k_1 - 1, k_2)] \\ + & (k_1 + 1) B_{1,22} \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (k_1 + 1, k_2 - 2)] \\ + & (k_2 + 1) B_{2,11} \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (k_1 - 2, k_2 + 1)] \\ + & (k_1 + 1) d_1 \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (k_1 + 1, k_2)] \\ + & (k_2 + 1) d_2 \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (k_1, k_2 + 1)] \\ + & (k_1 + 1) (D_0)_{12} \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (k_1 + 1, k_2 - 1)] \\ + & (k_2 + 1) (D_0)_{21} \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (k_1 - 1, k_2 + 1)] \\ + & [k_1 (D_0)_{11} + k_2 (D_0)_{22}] \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) = (k_1, k_2)] \end{aligned} \quad (5.4)$$

for $k_1, k_2 \geq 1$, where the probability that $Z_1(t)$ or $Z_2(t)$ takes a strictly negative value is equal to zero, by convention. Finally, $\mathbb{P}[\mathbf{Z}(0) = (1, 0) | \varphi_0 = 1] = 1$ and $\mathbb{P}[\mathbf{Z}(0) = (0, 1) | \varphi_0 = 2] = 1$.

We multiply (5.4) by $s_1^{k_1} s_2^{k_2}$, and sum over all values of k_1, k_2 , and obtain (5.1) after some algebraic manipulations.

The equation (5.2) may also be obtained from the Kolmogorov equations but a less cumbersome argument follows from conditioning on the time of the first observable event in the MBT: either the initial individual has not undergone any observable event yet at time t , which occurs with probability given by $e^{D_0 t}$, or it dies at some time $u \leq t$, which occurs with probability given by $e^{D_0 u} \mathbf{d} du$, or it has a child at some time $u \leq t$, which occurs with probability given by $e^{D_0 u} B du$, and the two sub-processes evolve independently of each others afterwards. In matrix notation, this gives

$$\begin{aligned} \mathbf{F}(\mathbf{s}, t) &= e^{D_0 t} \mathbf{s} + \int_0^t e^{D_0 u} \mathbf{d} du \\ &+ \int_0^t e^{D_0 u} B (\mathbf{F}(\mathbf{s}, t - u) \otimes \mathbf{F}(\mathbf{s}, t - u)) du. \end{aligned}$$

Now, taking the derivative with respect to t on both sides, we have

$$\frac{\partial}{\partial t} \mathbf{F}(\mathbf{s}, t) = \mathbf{d} + D_0 \mathbf{F}(\mathbf{s}, t) + B(\mathbf{F}(\mathbf{s}, t) \otimes \mathbf{F}(\mathbf{s}, t)),$$

which is (5.2). \square

In the case $n \geq 2$, none of the matrix (partial) differential equations (5.1) and (5.2) may be solved explicitly. Nevertheless, there exist powerful numerical tools to implement (5.2). We used the solver `ode45` in MATLAB, which is based on an explicit Runge-Kutta (4,5)-formula. This is a one-step solver, and its complexity is linear in the number n of phases. Further details are to be found in Dormand and Prince [17]. We are thus able to numerically evaluate $\mathbf{F}(\mathbf{s}, t)$ for any given pair (\mathbf{s}, t) .

Similarly, we can also compute the generating function

$$\mathbf{F}(s, t) = \sum_{k \geq 0} \mathbb{P}[\mathbf{Z}(t) \cdot \mathbf{1} = k | \varphi_0] s^k \quad (5.5)$$

of the *total* population size at time t by numerically solving (5.2) with $\mathbf{F}(s, 0) = s \cdot \mathbf{1}$ as initial condition (notice that here, s is scalar).

In order to get the total population size *distribution* at some given time, we may use numerical techniques for the inversion of probability generating functions, for example the algorithm proposed by Abate and Whitt [1], which is based on the trapezoid rule and a Fourier-series method for the error bound, and which we briefly present now.

Let t be fixed. Let i be the complex root of -1 , and $\text{Re}(z)$ denote the real part of z . The following theorem provides a simple algorithm, with an error bound, to approach the probabilities $\mathbf{q}_t(k) = \mathbb{P}_{\varphi_0}[\mathbf{Z}(t) \cdot \mathbf{1} = k]$, for $k \geq 1$, $\mathbf{q}_t(0)$ being computed as $\mathbf{F}(0, t)$.

Theorem 5.2.2. For $0 < r < 1$ and $k \geq 1$,

$$|\mathbf{q}_t(k) - \tilde{\mathbf{q}}_t(k)| \leq \frac{r^{2k}}{1 - r^{2k}},$$

where

$$\begin{aligned} \tilde{\mathbf{q}}_t(k) &= \frac{1}{2k r^k} \sum_{j=1}^{2k} (-1)^j \text{Re}[\mathbf{F}(r e^{\pi j i/k}, t)] \\ &= \frac{1}{2k r^k} \left\{ \mathbf{F}(r, t) + (-1)^k \mathbf{F}(-r, t) + 2 \sum_{j=1}^{k-1} (-1)^j \text{Re}[\mathbf{F}(r e^{\pi j i/k}, t)] \right\}. \end{aligned}$$

\square

In the theorem, the bound $r^{2k}/(1 - r^{2k})$ is approximately equal to r^{2k} when r^{2k} is small. Thus, to obtain a precision of $10^{-\gamma}$, we take $r = 10^{-\gamma/2k}$.

Remark 5.2.3. Theorem 5.2.2 is based on the assumption that the generating function $\mathbf{F}(s, t)$ is known exactly. Since it is numerically computed with some estimation errors, there is a risk of the error increasing when $\mathbf{F}(\cdot, t)$ is inverted. As a matter of fact, we have often obtained poor results.

Factorial moments

We can extract all the factorial moments of the population size at some given time from (5.1) and (5.2). The k th factorial moment $M^{(k)}(t)$ is an $n \times n^k$ matrix given by

$$\begin{aligned} M^{(k)}(t) &= \frac{\partial^k}{(\partial \mathbf{s}^T)^k} \mathbf{F}(\mathbf{s}, t) |_{\mathbf{s}=\mathbf{1}} \\ &= \mathbf{F}(\mathbf{s}, t) \otimes \underbrace{\frac{\partial}{\partial \mathbf{s}^T} \otimes \dots \otimes \frac{\partial}{\partial \mathbf{s}^T}}_{k \text{ times}} |_{\mathbf{s}=\mathbf{1}}. \end{aligned}$$

We define the matrix

$$\Omega = D_0 + B(\mathbf{1} \oplus \mathbf{1}), \quad (5.6)$$

which plays an important role in this chapter.

The factorial moments are recursively given by the following proposition.

Proposition 5.2.4. *The matrices $M^{(k)}(t)$, $k \geq 1$, are solutions of two recursive matrix differential equations, with initial conditions $M^{(1)}(0) = I_n$ and $M^{(k)}(0) = 0$ for $k \geq 2$. The first system is*

$$\begin{aligned} \frac{d}{dt} M^{(k)}(t) &= M^{(k)}(t) (\Omega \otimes I_{n^{k-1}}) A(k) \\ &\quad + M^{(k-1)}(t) [B(I_{n^2} + I_{(n,n)}) \otimes I_{n^{k-2}}] C(k), \end{aligned} \quad (5.7)$$

where Ω is defined in (5.6) and the $n^k \times n^k$ coefficient matrices $A(k)$ and $C(k)$ are recursively defined as

$$\begin{aligned} A(1) &= I_n \\ C(1) &= 0_n \\ A(k) &= I_{(n^{k-1}, n)} + (A(k-1) \otimes I_n), \end{aligned} \quad (5.8)$$

$$\begin{aligned} C(k) &= I_{(n^{k-2}, n^2)} (I_{(n, n^{k-2})} \otimes I_n) (A(k-1) \otimes I_n) \\ &\quad + (C(k-1) \otimes I_n), \end{aligned} \quad (5.9)$$

for $k \geq 2$.

One also has

$$\begin{aligned} \frac{d}{dt} M^{(k)}(t) &= \Omega M^{(k)}(t) \\ &\quad + \sum_{i=1}^{k-1} B(M^{(i)}(t) \otimes M^{(k-i)}(t)) C(i, k-i), \end{aligned} \quad (5.10)$$

where an empty sum is zero, and where the matrix coefficients $C(i, k-i)$ are recursively defined as

$$\begin{aligned} C(0, k-i) &= I_{n^{k-i}} \\ C(i, 0) &= I_{n^i} \\ C(i, k-i) &= I_{(n^{k-i}, n^i)} [I_{(n^{i-1}, n^{k-i})} C(i-1, k-i) \otimes I_n] \\ &\quad + [C(i, k-i-1) \otimes I_n]. \end{aligned} \quad (5.11)$$

Proof. The first recurrence is proved by taking successive derivatives of (5.1) and the second recurrence is based on (5.2). We only give details for (5.1).

First, note that

$$\begin{aligned} \mathbf{a}(\mathbf{1}) &= \mathbf{d} + D_0 \mathbf{s} + B(\mathbf{s} \otimes \mathbf{s})|_{\mathbf{s}=\mathbf{1}} = \mathbf{0} \\ \frac{d}{ds^T} \mathbf{a}(\mathbf{s})|_{\mathbf{s}=\mathbf{1}} &= D_0 + B(I_n \otimes \mathbf{s} + \mathbf{s} \otimes I_n)|_{\mathbf{s}=\mathbf{1}} = \Omega \\ \frac{d^2}{(ds^T)^2} \mathbf{a}(\mathbf{s})|_{\mathbf{s}=\mathbf{1}} &= B(I_n \otimes I_n) + B(I_n \otimes I_n)I_{(n,n)} \\ &= B(I_{n^2} + I_{(n,n)}), \end{aligned}$$

by the derivative rule of Kronecker products.

Taking derivatives of both sides of (5.1), we obtain

$$\begin{aligned} \frac{\partial}{\partial s^T} \frac{\partial}{\partial t} \mathbf{F}(\mathbf{s}, t) &= \frac{\partial^2}{(\partial s^T)^2} \mathbf{F}(\mathbf{s}, t) \cdot (\mathbf{a}(\mathbf{s}) \otimes I_n) \\ &\quad + \frac{\partial}{\partial s^T} \mathbf{F}(\mathbf{s}, t) \cdot \frac{d}{ds^T} \mathbf{a}(\mathbf{s}) \end{aligned}$$

and by setting $\mathbf{s} = \mathbf{1}$ we obtain (5.7) for $k = 1$.

Now, we make the induction assumption that

$$\begin{aligned} \frac{\partial^k}{(\partial s^T)^k} \frac{\partial}{\partial t} \mathbf{F}(\mathbf{s}, t) &= \tag{5.12} \\ &\quad \frac{\partial^{k+1}}{(\partial s^T)^{k+1}} \mathbf{F}(\mathbf{s}, t) \cdot (\mathbf{a}(\mathbf{s}) \otimes I_{n^k}) \\ &\quad + \frac{\partial^k}{(\partial s^T)^k} \mathbf{F}(\mathbf{s}, t) \cdot \left(\frac{d}{ds^T} \mathbf{a}(\mathbf{s}) \otimes I_{n^{k-1}} \right) A(k) \\ &\quad + \frac{\partial^{k-1}}{(\partial s^T)^{k-1}} \mathbf{F}(\mathbf{s}, t) \cdot \left(\frac{d^2}{(ds^T)^2} \mathbf{a}(\mathbf{s}) \otimes I_{n^{k-2}} \right) C(k) \end{aligned}$$

for some $k \geq 1$. Differentiating again with respect to \mathbf{s}^T , we obtain

$$\begin{aligned} \frac{\partial^{k+1}}{(\partial s^T)^{k+1}} \frac{\partial}{\partial t} \mathbf{F}(\mathbf{s}, t) &= \\ &\quad \frac{\partial^{k+2}}{(\partial s^T)^{k+2}} \mathbf{F}(\mathbf{s}, t) \cdot (\mathbf{a}(\mathbf{s}) \otimes I_{n^k} \otimes I_n) \\ &\quad + \frac{\partial^{k+1}}{(\partial s^T)^{k+1}} \mathbf{F}(\mathbf{s}, t) \cdot \left(\frac{d}{ds^T} \mathbf{a}(\mathbf{s}) \otimes I_{n^k} \right) I_{(n^k, n)} \\ &\quad + \frac{\partial^{k+1}}{(\partial s^T)^{k+1}} \mathbf{F}(\mathbf{s}, t) \cdot \left(\frac{d}{ds^T} \mathbf{a}(\mathbf{s}) \otimes I_{n^{k-1}} \otimes I_n \right) (A(k) \otimes I_n) \\ &\quad + \frac{\partial^k}{(\partial s^T)^k} \mathbf{F}(\mathbf{s}, t) \cdot \left(\frac{d^2}{(ds^T)^2} \mathbf{a}(\mathbf{s}) \otimes I_{n^{k-1}} \right) I_{(n^{k-1}, n^2)} \\ &\quad \cdot (I_{(n, n^{k-1})} \otimes I_n) (A(k) \otimes I_n) \\ &\quad + \frac{\partial^k}{(\partial s^T)^k} \mathbf{F}(\mathbf{s}, t) \cdot \left(\frac{d^2}{(ds^T)^2} \mathbf{a}(\mathbf{s}) \otimes I_{n^{k-1}} \right) (C(k) \otimes I_n). \end{aligned}$$

Using (5.8, 5.9), we obtain

$$\begin{aligned} \frac{\partial^{k+1}}{(\partial \mathbf{s}^T)^{k+1}} \frac{\partial}{\partial t} \mathbf{F}(\mathbf{s}, t) &= \\ & \frac{\partial^{k+2}}{(\partial \mathbf{s}^T)^{k+2}} \mathbf{F}(\mathbf{s}, t) \cdot (\mathbf{a}(\mathbf{s}) \otimes I_{n^{k+1}}) \\ & + \frac{\partial^{k+1}}{(\partial \mathbf{s}^T)^{k+1}} \mathbf{F}(\mathbf{s}, t) \cdot \left(\frac{d}{d\mathbf{s}^T} \mathbf{a}(\mathbf{s}) \otimes I_{n^k} \right) A(k+1) \\ & + \frac{\partial^k}{(\partial \mathbf{s}^T)^k} \mathbf{F}(\mathbf{s}, t) \cdot \left(\frac{d^2}{(d\mathbf{s}^T)^2} \mathbf{a}(\mathbf{s}) \otimes I_{n^{k-1}} \right) C(k+1), \end{aligned}$$

which shows that (5.12) holds for all k . The recursion formula for the factorial moments follows when we set $\mathbf{s} = \mathbf{1}$ in (5.12). \square

Remark 5.2.5. The matrix coefficients $C(i, k-i)$ in (5.11) are actually matrix generalizations of the binomial coefficients $\binom{k}{i}$.

The size of the matrices $M^{(k)}(t)$ very rapidly increases with k , which somewhat limits the usefulness of Theorem 5.2.4 beyond the first few moments, but the mean and standard deviation are easily obtained, as we show now.

Corollary 5.2.6. *The first two moments are given by*

$$M^{(1)}(t) = e^{\Omega t} \tag{5.13}$$

$$M^{(2)}(t) = X(t) (I_{n^2} + I_{(n,n)}) \tag{5.14}$$

where $X(t)$ is the solution of the Lyapunov equation

$$X(t) (\Omega \oplus \Omega) - \Omega X(t) + e^{\Omega t} B - B (e^{\Omega t} \otimes e^{\Omega t}) = 0. \tag{5.15}$$

Proof. Taking $k = 1$ in (5.10), we see that $M^{(1)}(t)$ is the solution of $(d/dt)M^{(1)}(t) = \Omega M^{(1)}(t)$, with $M^{(1)}(0) = I$. This proves (5.13).

For the second moment, (5.10, 5.13) yield

$$M^{(2)}(t) = e^{\Omega t} Y(t) (I_{n^2} + I_{(n,n)}),$$

where

$$Y(t) = \int_0^t e^{-\Omega u} B (e^{\Omega u} \otimes e^{\Omega u}) du.$$

We premultiply the integral by Ω and integrate by parts, to find that $Y(t)$ satisfies the Lyapunov equation

$$Y(t) (\Omega \oplus \Omega) - \Omega Y(t) + B - e^{-\Omega t} B (e^{\Omega t} \otimes e^{\Omega t}) = 0.$$

Writing $X(t) = e^{\Omega t} Y(t)$, we obtain (5.14). \square

The Lyapunov equation (5.15) is solved using the `lyap` solver in MATLAB. This uses a triangular decomposition approach and the complexity is $\mathcal{O}(n^3)$.

The standard deviation of the total population size at time t , given the initial phase, is thus obtained as

$$\sigma_M(t) = \left[M^{(2)}(t) \mathbf{1} + \text{diag}(M^{(1)}(t) \mathbf{1}) (\mathbf{1} - M^{(1)}(t) \mathbf{1}) \right]^{1/2}. \quad (5.16)$$

Remark 5.2.7. The matrix Ω plays a role similar to the mean progeny matrix M . Indeed, since the first moment of the population size at time t is given by $\exp(\Omega t)$, we see that the eigenvalue of maximal real part $\mu(\Omega)$ determines the nature of the MBT: if $\mu(\Omega) < 0$, then on the average, the population size tends to zero when time increases, and the MBT is subcritical; if $\mu(\Omega) = 0$, then the population size is bounded and nonzero on the average, and the MBT is critical; and finally, if $\mu(\Omega) > 0$, then the population size grows without bounds on the average, and the MBT is supercritical.

We can give a physical interpretation to the inverse $(-\Omega)^{-1}$ when it is well defined, that is in the subcritical case, since we have then

$$\begin{aligned} [(-\Omega)^{-1}]_{ij} &= \int_0^\infty [e^{\Omega t}]_{ij} dt \\ &= \int_0^\infty \mathbb{E}[Z_j(t) \mid \varphi_0 = i] dt \\ &= \int_0^\infty \mathbb{E} \left[\sum_{n \geq 0} n \mathbf{1}_{\{Z_j(t)=n\}} \mid \varphi_0 = i \right] dt \\ &= \mathbb{E} \left[\sum_{n \geq 0} \int_0^\infty n \mathbf{1}_{\{Z_j(t)=n\}} dt \mid \varphi_0 = i \right]. \end{aligned}$$

If we define the total *cumulated* amount of time the process is in phase j as the sum of the lengths of intervals where $Z_j(\cdot) > 0$, weighted by Z_j , then the entry (i, j) of $(-\Omega)^{-1}$ may be interpreted as the expectation of that sum, given that the process starts with a first individual in phase i .

Conditional population size given extinction

We end the section by looking at the *conditional* distribution of the population size, given that extinction occurs. Recall that E denotes the total extinction event. The probability generating function of the conditional population size is defined as

$$F_e(\mathbf{s}, t) = \sum_{\mathbf{k} \geq \mathbf{0}} \mathbb{P}[\mathbf{Z}(t) = \mathbf{k} \mid E, \varphi_0] \mathbf{s}^{\mathbf{k}}.$$

Define

$$\Phi = \text{diag}(\mathbf{q}). \quad (5.17)$$

The inverse of Φ exists, provided $q_i \neq 0$ for all i (which follows from Assumption (1.2.2)). The following result was already stated by Athreya and Ney in the Galton-Watson case, see [6, Chapter I.12, Theorem 3].

Proposition 5.2.8. *The conditional distribution of the population size given extinction is given by*

$$\mathbf{F}_e(\mathbf{s}, t) = \Phi^{-1} \mathbf{F}(\Phi \mathbf{s}, t). \quad (5.18)$$

Proof. The i th entry of $\mathbf{F}_e(\mathbf{s}, t)$ is given by

$$\begin{aligned} (\mathbf{F}_e)_i(\mathbf{s}, t) &= \sum_{\mathbf{k} \geq \mathbf{0}} \mathbb{P}[\mathbf{Z}(t) = \mathbf{k} \mid E, \varphi_0 = i] \mathbf{s}^{\mathbf{k}} \\ &= \sum_{\mathbf{k} \geq \mathbf{0}} \frac{\mathbb{P}[\mathbf{Z}(t) = \mathbf{k} \cap E \mid \varphi_0 = i]}{\mathbb{P}[E \mid \varphi_0 = i]} \mathbf{s}^{\mathbf{k}} \\ &= \sum_{\mathbf{k} \geq \mathbf{0}} \frac{\mathbb{P}[\mathbf{Z}(t) = \mathbf{k} \mid \varphi_0 = i] \mathbb{P}[E \mid \mathbf{Z}(t) = \mathbf{k}]}{q_i} \mathbf{s}^{\mathbf{k}}, \end{aligned}$$

by the Markov property. Since $\mathbb{P}[E \mid \mathbf{Z}(t) = \mathbf{k}] = \mathbf{q}^{\mathbf{k}}$ by independence between individuals, we get

$$(\mathbf{F}_e)_i(\mathbf{s}, t) = \sum_{\mathbf{k} \geq \mathbf{0}} \frac{\mathbb{P}[\mathbf{Z}(t) = \mathbf{k} \mid \varphi_0 = i]}{q_i} \mathbf{q}^{\mathbf{k}} \mathbf{s}^{\mathbf{k}},$$

which, in matrix form, is $\mathbf{F}_e(\mathbf{s}, t) = \Phi^{-1} \mathbf{F}(\Phi \mathbf{s}, t)$. \square

It results from (5.18) with $\mathbf{s} = \mathbf{1}$ that $\mathbf{q} = \mathbf{F}(\mathbf{q}, t)$ for all $t \geq 0$, so that \mathbf{q} is a fixed point of the generating function $\mathbf{F}(\mathbf{s}, t)$.

Let us define the matrix

$$\Theta = D_0 + B(\mathbf{q} \oplus \mathbf{q}), \quad (5.19)$$

which is equal to the matrix Ω defined in (5.6) when $\mathbf{q} = \mathbf{1}$, that is in the subcritical and critical cases. It will actually play a role similar to Ω when we condition on the extinction event.

Corollary 5.2.9. *The matrix of conditional mean population size at time t , given that extinction occurs, is given by*

$$M_e^{(1)}(t) = \Phi^{-1} e^{\Theta t} \Phi.$$

Proof. The conditional mean is $M_e^{(1)}(t) = \frac{\partial}{\partial \mathbf{s}^T} \mathbf{F}_e(\mathbf{s}, t)|_{\mathbf{s}=\mathbf{1}}$ and by (5.18),

$$\frac{\partial}{\partial \mathbf{s}^T} \mathbf{F}_e(\mathbf{s}, t)|_{\mathbf{s}=\mathbf{1}} = \Phi^{-1} \frac{\partial}{\partial \mathbf{s}^T} \mathbf{F}(\Phi \mathbf{s}, t)|_{\mathbf{s}=\mathbf{1}} = \Phi^{-1} \frac{\partial}{\partial \mathbf{z}^T} \mathbf{F}(\mathbf{z}, t)|_{\mathbf{z}=\mathbf{q}} \Phi.$$

Let $U(t) = (\partial/\partial \mathbf{z}^T) \mathbf{F}(\mathbf{z}, t)|_{\mathbf{z}=\mathbf{q}}$. From (5.2), we see that it is solution of

$$U'(t) = D_0 U(t) + B[U(t) \otimes \mathbf{q} + \mathbf{q} \otimes U(t)],$$

with $U(0) = I$. Thus $U(t) = \exp(\Theta t)$, and the statement of the corollary follows. \square

The next result shows that, in the noncritical irreducible case, the inverse of Θ always exists.

Proposition 5.2.10. *If the MBT is noncritical and irreducible, the eigenvalues of Θ all have a strictly negative real part. In the critical case, Θ is singular.*

Proof. As we have seen in Section 1.5, there are several ways to interpret an MBT as a multitype branching process. Here, we apply the standard uniformization procedure to the MAP controlling the MBT.

Let $c \geq \max_j (-D_0)_{jj}$. After an exponential time with parameter c , a particle of type i may either die, or may remain in the same phase, or may change its phase, or, finally, may split and give birth to two new branches, with probabilities respectively given by the following matrices

$$\mathbf{d}^* = \frac{1}{c} \mathbf{d} \quad D_0^* = I + \frac{1}{c} D_0 \quad B^* = \frac{1}{c} B.$$

The generating function of the progeny of a particle of type i , after an exponential time with parameter c , is given by the i th entry of

$$\mathbf{G}^*(\mathbf{s}) = \mathbf{d}^* + D_0^* \mathbf{s} + B^*(\mathbf{s} \otimes \mathbf{s}).$$

Recall that in the proof of Theorem 2.3.1, we used the progeny generating function $\mathbf{G}(\mathbf{s}) = \boldsymbol{\theta} + \Psi(\mathbf{s} \otimes \mathbf{s})$ of another representation of the MBT to show that the eigenvalue of maximal real part of the matrix $(d/ds^T)\mathbf{G}(\mathbf{s})|_{\mathbf{s}=\mathbf{q}} = \Psi(\mathbf{q} \oplus \mathbf{q})$ is strictly less than 1 in the subcritical and supercritical cases, and is equal to 1 in the critical case.

By the same argument, in the noncritical case, the eigenvalue of maximal real part of the matrix

$$\frac{d}{ds^T} \mathbf{G}^*(\mathbf{s})|_{\mathbf{s}=\mathbf{q}} = D_0^* + B^*(\mathbf{q} \oplus \mathbf{q})$$

is strictly less than 1. Consequently, the eigenvalue of maximal real part of $\frac{1}{c}(D_0 + B(\mathbf{q} \oplus \mathbf{q}))$ is strictly less than 0, and since $1/c$ is a strictly positive constant, this implies that all the eigenvalues of the matrix $D_0 + B(\mathbf{q} \oplus \mathbf{q})$ have a strictly negative real part.

In the critical case, the matrix $D_0^* + B^*(\mathbf{q} \oplus \mathbf{q})$ has an eigenvalue equal to 1, resulting in one eigenvalue equal to 0 for Θ , which is thus singular. \square

Remark 5.2.11. Following the same argument than in Remark 5.2.7, in the noncritical case, we can give a probabilistic interpretation to the inverse $(-\Theta \Phi)^{-1} \Phi$: its (i, j) th entry represents the conditional mean total cumulated amount of time the process is in phase j , given that it starts with a first individual in phase i and that it will eventually become extinct.

5.3 Time until extinction

Our next measure of interest is the distribution of the time T_e until the MBT becomes extinct. We assume here that we are not in the critical case.

Time to extinction has been much investigated for the Galton-Watson branching process. To give a few references, Agresti [3] derives bounds for the distribution and for

the first moment of the time until extinction, and Lange, Boehnke and Carson [45] do the same for all factorial moments. In the simplest one-type Markovian case, the distribution of the time to extinction is the solution of an integral equation, or of a backward differential equation, and Wang [73] shows it is still possible to bound factorial moments. In the multitype Markovian subcritical case, Heinzmann [33] approximates the distribution exponentially with a controlled approximation error.

We denote by $\mathbf{F}(t) = \mathbb{P}[T_e \leq t | \varphi_0]$ the distribution function of T_e , given the initial phase, and we observe that the extinction probability \mathbf{q} is actually the limit of $\mathbf{F}(t)$ as t tends to infinity. It is clear that $T_e \leq t$ if and only if $\mathbf{Z}(t) = \mathbf{0}$, so that $\mathbf{F}(t) = \mathbf{F}(\mathbf{s}, t)|_{\mathbf{s}=\mathbf{0}}$.

Thus, taking $\mathbf{s} = \mathbf{0}$ in (5.2), we find that the distribution function $\mathbf{F}(t)$ satisfies the differential system

$$\frac{d}{dt}\mathbf{F}(t) = \mathbf{d} + D_0\mathbf{F}(t) + B(\mathbf{F}(t) \otimes \mathbf{F}(t)), \quad (5.20)$$

with $\mathbf{F}(0) = \mathbf{0}$.

This is a quadratic matrix differential equation which can not be solved explicitly when $n \geq 2$, but the same numerical tools as for the generating function $\mathbf{F}(\mathbf{s}, t)$ allow us to approximate the function at some discrete points.

If $\mathbf{q} < \mathbf{1}$, then T_e is infinite with a positive probability and its expectation is infinite. In order to investigate a meaningful quantity, we define \mathbf{M}_e as the conditional expectation of T_e , given the initial phase and given that extinction occurs:

$$\mathbf{M}_e = \Phi^{-1} \int_0^\infty [\mathbf{q} - \mathbf{F}(u)] du = \int_0^\infty [\mathbf{1} - \Phi^{-1}\mathbf{F}(u)] du$$

where Φ is given by (5.17).

To compute \mathbf{M}_e , we proceed as follows: we fix some time T^* such that

$$\|\mathbf{1} - \Phi^{-1}\mathbf{F}(T^*)\| < \epsilon \quad (5.21)$$

where ϵ is arbitrarily small, and we write that

$$\mathbf{M}_e = \int_0^{T^*} [\mathbf{1} - \Phi^{-1}\mathbf{F}(u)] du + \int_{T^*}^\infty [\mathbf{1} - \Phi^{-1}\mathbf{F}(u)] du. \quad (5.22)$$

The first integral may be approximated using the trapezoid rule: we choose a number k^* of intervals and write

$$\begin{aligned} \int_0^{T^*} [\mathbf{1} - \Phi^{-1}\mathbf{F}(u)] du &= h \left\{ \mathbf{1} - \Phi^{-1}[\mathbf{F}(0) + \mathbf{F}(T^*)] / 2 \right. \\ &\quad \left. + \sum_{i=1}^{k^*-1} [\mathbf{1} - \Phi^{-1}\mathbf{F}(ih)] \right\} + E, \end{aligned}$$

where $h = T^*/k^*$ and $E = T^*h^2\Phi^{-1}\mathbf{F}''(c)/12$ for some c in $(0, T^*)$ is the approximation error. In practice, we choose ϵ and h and compute $\mathbf{F}(ih)$ for successive values of i until $\mathbf{F}(k^*h)$ satisfies the inequality (5.21).

The second integral may be computed using a function $\tilde{\mathbf{F}}(t)$ which approximates $\mathbf{F}(t)$ for large values of t , that is, for values of t such that $\mathbf{F}(t) \approx \mathbf{q}$. This approximation is given by

$$\tilde{\mathbf{F}}(t) = [I - e^{\Theta t}] \mathbf{q}, \quad (5.23)$$

where Θ is defined in (5.19). It is obtained as follows. Define $\boldsymbol{\epsilon}(t) = \mathbf{q} - \mathbf{F}(t)$. The vector \mathbf{q} satisfies

$$\mathbf{0} = \mathbf{d} + D_0 \mathbf{q} + B(\mathbf{q} \otimes \mathbf{q}),$$

which is obtained by pre-multiplying both sides of (1.15) by D_0 . Subtracting this last equation from (5.20), we obtain

$$\begin{aligned} \boldsymbol{\epsilon}'(t) &= D_0 \boldsymbol{\epsilon}(t) + B[(\mathbf{q} \otimes \mathbf{q}) - (\mathbf{F}(t) \otimes \mathbf{F}(t))] \\ &= D_0 \boldsymbol{\epsilon}(t) + B[(\mathbf{q} - \mathbf{F}(t) \otimes \mathbf{q}) + (\mathbf{F}(t) \otimes \mathbf{q} - \mathbf{F}(t))] \\ &= D_0 \boldsymbol{\epsilon}(t) + B[(I \otimes \mathbf{q}) + (\mathbf{F}(t) \otimes I)] \boldsymbol{\epsilon}(t). \end{aligned}$$

Now, if t is large enough, then $\mathbf{F}(t)$ may be replaced by \mathbf{q} in the equation above and we obtain the approximate system $\tilde{\boldsymbol{\epsilon}}'(t) = \Theta \tilde{\boldsymbol{\epsilon}}(t)$, which leads to

$$\tilde{\boldsymbol{\epsilon}}(t) = e^{\Theta t} \mathbf{q},$$

since $\boldsymbol{\epsilon}(0) = \mathbf{q}$ by definition. This yields (5.23).

Thus, the second integral in (5.22) may be approximated by

$$\begin{aligned} \int_{T^*}^{\infty} [\mathbf{1} - \Phi^{-1} \tilde{\mathbf{F}}(u)] du &= \int_{k^* h}^{\infty} \Phi^{-1} e^{\Theta u} \mathbf{q} du \\ &= \Phi^{-1} [-\Theta]^{-1} e^{\Theta k^* h} \mathbf{q} \end{aligned} \quad (5.24)$$

which is well defined in the noncritical case by Proposition 5.2.10.

Notice that the expression $\Phi^{-1} e^{\Theta u} \mathbf{q}$ in (5.24) is nothing else than the conditional mean total population size at time u , given that extinction occurs, that is $M_e^{(1)}(u) \mathbf{1}$, as stated by Corollary 5.2.9. By the argument in Remark 5.2.11, the integral may thus be interpreted as the conditional expected total cumulative time the process still lives from time $k^* h$, given it eventually becomes extinct. This seems to be a reasonable estimation of the remaining mean time until extinction, since we expect that, close to extinction, the number of individuals still living in parallel must not be much bigger than one.

In summary, the mean time until extinction, given that extinction occurs, may be approximated by

$$\begin{aligned} \tilde{M}_e &= h \left\{ \mathbf{1} - \Phi^{-1} [\mathbf{F}(0) + \mathbf{F}(T^*)] \right\} / 2 \\ &\quad + \sum_{i=1}^{k^*-1} [\mathbf{1} - \Phi^{-1} \mathbf{F}(ih)] \left\} + \Phi^{-1} [-\Theta]^{-1} e^{\Theta T^*} \mathbf{q}. \end{aligned} \quad (5.25)$$

5.4 Total progeny size

Recall that in an MBT, the lifetime of an individual is governed by a transient MAP which controls when children are born and when death occurs. We analyze here the distribution of the total number $N(t)$ of individuals born until time t , irrespective of their status, and its limit as t goes to infinity.

The distribution of the total progeny of a Galton-Watson branching process has been studied by several authors, among whom we cite Dwass [18] who examines the total progeny until extinction, and Pakes [59] who investigates the total progeny until the n th generation, and asymptotic results when n tends to infinity.

The probability generating function $g(s)$ of the total progeny until extinction is easily shown to satisfy the functional equation $g(s) = sP(g(s))$, where recall that $P(\cdot)$ is the progeny generating function. In principle, one may invert $g(s)$ with the Lagrange inversion formula [16]. But the results provided for instance by Good [24] in the multitype case are hardly implementable, and we follow a different approach, making use of the specific features of MBTs.

Let $\mathbf{g}(k, t) = \mathbb{P}[N(t) = k | \varphi_0]$ denote the probability that a total of k individuals are born before time t , given the initial phase of the first individual.

Proposition 5.4.1. *The probabilities $\mathbf{g}(k, t)$ are recursively given by*

$$\mathbf{g}(0, t) = \mathbf{0} \quad (5.26)$$

$$\mathbf{g}(1, t) = e^{D_0 t} \mathbf{1} + \int_0^t e^{D_0 u} \mathbf{d} du, \quad (5.27)$$

$$\begin{aligned} \mathbf{g}(k, t) &= \int_0^t e^{D_0 u} B \\ &\quad \cdot \sum_{i=1}^{k-1} [\mathbf{g}(i, t-u) \otimes \mathbf{g}(k-i, t-u)] du. \end{aligned} \quad (5.28)$$

for $k \geq 2$, $t \geq 0$.

Proof. The first equation is justified by the fact that there is always at least one individual, the one at the origin of the process, in the total progeny. In order to justify (5.27), we note that at time t there is only one individual in total if either the one at the origin has not yet given birth or has died at some time $u \leq t$.

Finally, if at time t the total progeny is $k \geq 2$, it means that the first individual gives birth to a child at some time $u \leq t$ and that the sum of the total progenies in the independent families generated by the two individuals after the birth event equals k ; this proves (5.28). \square

We may express the probability generating function of $N(t)$, $\mathbf{G}(z, t) = \sum_{k \geq 0} \mathbf{g}(k, t) z^k$, as the solution of a differential equation, by using the recursive expressions in Propo-

sition 5.4.1 and taking derivatives with respect to t :

$$\frac{\partial}{\partial t} \mathbf{G}(z, t) = \mathbf{d}z + D_0 \mathbf{G}(z, t) + B(\mathbf{G}(z, t) \otimes \mathbf{G}(z, t)), \quad (5.29)$$

with $\mathbf{G}(z, 0) = z$. Note that $\mathbf{G}(\mathbf{1}, t) = \mathbf{1}$ for all finite t .

We might numerically solve (5.29) and take the inverse transform, as suggested for the generating function $\mathbf{F}(s, t)$ of the total population size at time t ; here, however, the distribution of the total progeny size is directly computable by (5.26)–(5.28).

Let $\mathbf{D}^{(k)}(t) = \partial^k \mathbf{G}(z, t) / (\partial z)^k |_{z=\mathbf{1}}$ denote the $n \times 1$ k th factorial moment vector of $N(t)$. These moments are recursively characterized as follows, the proof being by induction using standard scalar differentiation rules.

Proposition 5.4.2. *The vectors $\mathbf{D}^{(k)}(t)$ satisfy the following recurrence*

$$\begin{aligned} \frac{d}{dt} \mathbf{D}^{(1)}(t) &= \Omega \mathbf{D}^{(1)}(t) + \mathbf{d}, \\ \frac{d}{dt} \mathbf{D}^{(k)}(t) &= \Omega \mathbf{D}^{(k)}(t) + \sum_{i=1}^{k-1} \binom{k}{i} B[\mathbf{D}^{(i)}(t) \otimes \mathbf{D}^{(k-i)}(t)], \end{aligned} \quad (5.30)$$

for $k \geq 2$, with $\mathbf{D}^{(1)}(0) = \mathbf{1}$ and $\mathbf{D}^{(k)}(0) = \mathbf{0}$ for $k \geq 2$. □

One easily obtains an explicit expression for the first moment: the solution of (5.30), is given by

$$\mathbf{D}^{(1)}(t) = e^{\Omega t} \left(\int_0^t e^{-\Omega u} du \mathbf{d} + \mathbf{1} \right).$$

If the inverse of Ω exists, then this is equivalent to

$$\mathbf{D}^{(1)}(t) = [I - e^{\Omega t}] (-\Omega)^{-1} \mathbf{d} + e^{\Omega t} \mathbf{1}.$$

Higher moments may not be written explicitly, but they may easily be computed numerically. The second factorial moment is, for instance, given by

$$\mathbf{D}^{(2)}(t) = e^{\Omega t} \left(\int_0^t e^{-\Omega u} 2 B(\mathbf{D}^{(1)}(u) \otimes \mathbf{D}^{(1)}(u)) du \right).$$

We now turn our attention to the asymptotic distribution of $N(t)$ when t tends to infinity. Define $\mathbf{g}(k) = \lim_{t \rightarrow \infty} \mathbf{g}(k, t)$. We easily obtain from (5.26–5.28) that

$$\begin{aligned} \mathbf{g}(0) &= \mathbf{0} \\ \mathbf{g}(1) &= \boldsymbol{\theta} \\ \mathbf{g}(k) &= \Psi \sum_{i=1}^{k-1} [\mathbf{g}(i) \otimes \mathbf{g}(k-i)], \end{aligned}$$

for $k \geq 2$. The generating function $\mathbf{G}(z) = \sum_{k \geq 0} \mathbf{g}(k) z^k$ is such that $\mathbf{G}(1) = \mathbf{q}$ and, for every z , it satisfies the functional fixed point equation

$$\mathbf{G}(z) = \boldsymbol{\theta}z + \Psi(\mathbf{G}(z) \otimes \mathbf{G}(z)), \quad (5.31)$$

which has the same structure as the extinction equation (1.15).

Equation (5.31) has the following interpretation. We condition on the first observable event: either the first individual dies before giving birth, which occurs with probability $\boldsymbol{\theta}$, and $N(\infty) = 1$, or it gives birth with probability Ψ , and the total progeny is the sum of the total progenies in the subtrees generated by the child and by the parent after the birth, both evolving independently.

The derivatives $\mathbf{D}^{(k)} = d^k \mathbf{G}(z)/(dz)^k|_{z=1}$ for $k \geq 1$ are here equal to the factorial moment vectors of the total progeny $N(\infty)$ on the paths where extinction occurs. By differentiating (5.31), it is easy to show that, provided that the MBT is noncritical,

$$\begin{aligned} \mathbf{D}^{(1)} &= (-\Theta)^{-1} \mathbf{d}, \\ \mathbf{D}^{(k)} &= (-\Theta)^{-1} \sum_{i=1}^{k-1} \binom{k}{i} B(\mathbf{D}^{(i)} \otimes \mathbf{D}^{(k-i)}) \end{aligned} \quad (5.32)$$

for $k \geq 2$, where Θ is defined in (5.19).

Here, the moments may be expressed explicitly. For instance, the second factorial moment is given by

$$\mathbf{D}^{(2)} = 2(-\Theta)^{-1} B[(-\Theta)^{-1} \mathbf{d} \otimes (-\Theta)^{-1} \mathbf{d}]$$

but such expressions rapidly become very cumbersome.

It is more natural to consider the conditional distribution of $N(\infty)$ given that extinction occurs. It suffices to multiply by Φ^{-1} the expressions obtained so far, where Φ is defined in (5.17). We obtain, for instance, that the conditional mean total progeny size, given that extinction occurs, is

$$\mathbf{D}_e^{(1)} = \Phi^{-1} (-\Theta)^{-1} \mathbf{d} = -(\Theta \Phi)^{-1} \mathbf{d}, \quad (5.33)$$

and the conditional standard deviation as

$$\sigma_{D_e} = \left[\Phi^{-1} \mathbf{D}^{(2)} + \text{diag}(\mathbf{D}_e^{(1)}) (\mathbf{1} - \mathbf{D}_e^{(1)}) \right]^{1/2}. \quad (5.34)$$

5.5 Application in demography

We now apply the results presented in the previous sections to our demographic application.

Family size

We first look at the mean total size at time t of the family generated by a woman born at time 0. From (5.13), it is given by $m(t) = \boldsymbol{\alpha} e^{\Omega t} \mathbf{1}$, where recall that $\boldsymbol{\alpha} = [1, \mathbf{0}]$ is the initial probability vector.

We plot $m(t)$ as a function of t on Figure 5.1 for seven countries. We see how fast the female Congolese family grows compared to the other countries. Some families reach a maximum size after about sixty years, and then eventually tend to extinction. Notice that after 250 years, the curves of Turkey and of South Africa intersect, and that before 70 years, the mean family sizes in Turkey and in Morocco are quite the same, after what they completely diverge. Observe also how the Turkish family size, which is nearly critical, grows slowly.

On Figure 5.2 we show the standard deviation of the family size for three countries: Congo (supercritical), Turkey (supercritical - nearly critical) and Japan (subcritical). We can compare it with the mean family size.

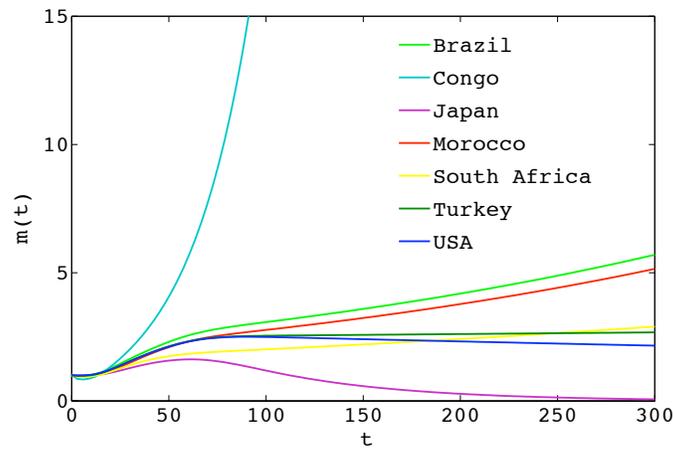


Figure 5.1: Mean family size generated by a new-born woman as a function of time

Remark 5.5.1. The standard deviation of the family size involves the computation of the second factorial moment $M^{(2)}(t) = X(t) (I_{n^2} + I_{(n,n)})$ where $X(t)$ satisfies the Lyapunov equation (5.15). The numerical solution of this equation requires the matrix $[(\Omega \oplus \Omega)^T \otimes I_n] - (I_{n^2} \otimes \Omega)$ to be well-conditioned, which was not the case for Turkey and Japan. Another way to compute $X(t)$ is to return to its definition

$$X(t) = \int_0^t e^{\Omega(t-u)} B (e^{\Omega u} \otimes e^{\Omega u}) du,$$

and to numerically evaluate it using for instance the trapezoid rule.

Time until extinction

We plot on Figure 5.3 the distribution of the time until extinction of the family generated by a new-born woman, that is the first component of $F(t)$. We observe that when time goes to infinity, the curves do tend to the extinction probability presented in Section 3.4. We remark a big difference in the shape of the curves for Congo and for

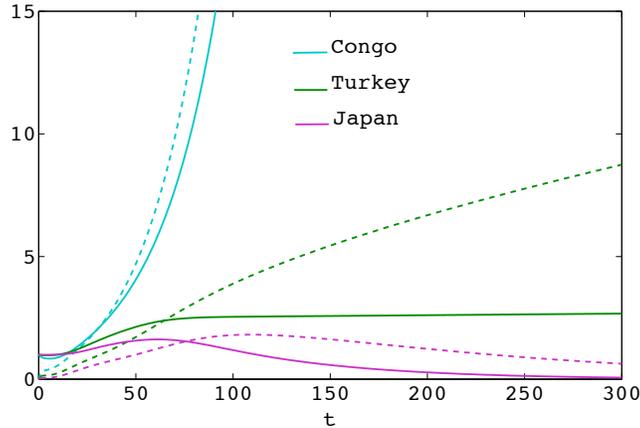


Figure 5.2: Mean (plain line) and standard deviation (dashed line) of the family size generated by a new-born woman as a function of time, for three countries

South Africa compared to other countries, especially in the way they increase in the first years. We interpret it again by an infant mortality effect; it reflects also the fact that if a Congolese family eventually becomes extinct, it happens quite quickly, before it has the time to grow. So it seems that if the first mother and her young daughters survive, then the family has a high probability to be maintained, which explains why the curve of Congo is already almost constant after 100 years only.

Recall that the conditional mean time until extinction is approximated by (5.25). We present the first entry of \tilde{M}_e in Table 5.1 for $h = 10^{-2}$ and $\epsilon = 5 \cdot 10^{-2}$. A priori we are surprised by the high values for the USA and for Turkey. The reason is that these countries are just at the limit between almost sure extinction and possible explosion (the USA being subcritical and Turkey being supercritical). Exactly critical populations eventually become extinct with probability one, while their mean population size is always one, and Θ is singular. Here, Θ has a maximal eigenvalue very close to zero: $\mu(\Theta) = -7.37 \cdot 10^{-4}$ for the USA, and $\mu(\Theta) = -2.48 \cdot 10^{-4}$ for Turkey. Since the inverse of Θ appears in the approximation \tilde{M}_e , this explains the large values obtained.

We see again that for Congo, if a family does not explode, then it becomes extinct very quickly.

Country	\tilde{M}_{e_1}	Country	\tilde{M}_{e_1}	Country	\tilde{M}_{e_1}
Congo	28.9	Belgium	170.1	South Africa	499.1
Japan	123.9	Morocco	317.7	USA	2280.6
China	133.2	Brazil	349.2	Turkey	8428.8

Table 5.1: Conditional mean time until extinction of the female family generated by a new-born woman, given that extinction occurs.

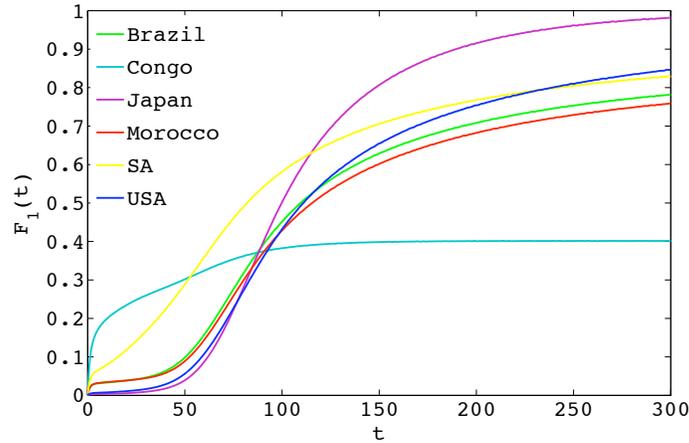


Figure 5.3: Distribution function of the time until extinction of the family generated by a first new-born woman

Total progeny size

The conditional mean total family size vector $D_e^{(1)}$ given extinction is given by (5.33), and the standard deviation σ_{D_e} by (5.34).

We give in Table 5.2 the first entry of $D_e^{(1)}$ and σ_{D_e} , that is, the conditional mean total family size generated by a new-born woman and its standard deviation, given that extinction occurs.

We observe that the standard deviation is quite large for some countries (Brazil, South Africa, USA and Turkey), which reflects a large variability in the distribution. The USA and Turkey, again, show a different behavior from the other countries, the inverse of Θ appearing in $D_e^{(1)}$ and σ_{D_e} . The whole vector $D_e^{(1)}$ is shown on Figure 5.4 for six countries.

Country	$D_{e_1}^{(1)}$	$(\sigma_{D_e})_1$	Country	$D_{e_1}^{(1)}$	$(\sigma_{D_e})_1$
Congo	1.58	1.56	Brazil	11.74	42.93
Japan	2.57	3.5	South Africa	19.1	95.28
China	3.95	7.8	USA	45.47	336.14
Belgium	4.75	10.2	Turkey	136.88	1806.4
Morocco	10.33	35.14			

Table 5.2: Conditional mean total size of the family generated by a new-born woman and its standard deviation, given that extinction occurs.

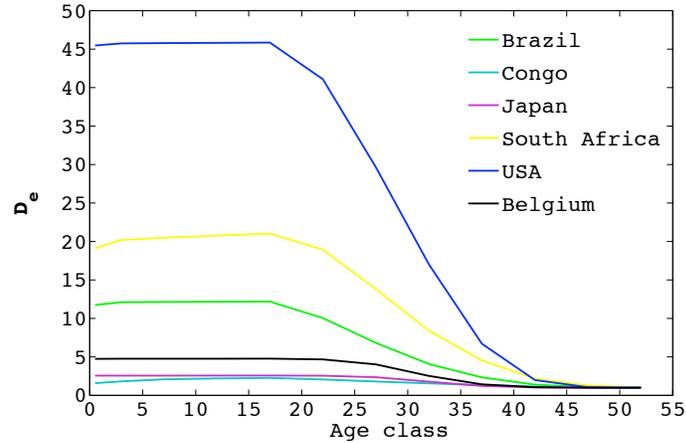


Figure 5.4: Conditional mean total size of the family generated by a first woman as a function of her age class, given that extinction occurs

Comparing the three models

Recall from Section 1.4 that we can actually consider three models in our demographic application, called the *raw*, the *smooth*, and the *gap* models, which respectively correspond to an MBT with $n = 22$, $n = 101$ and $n = 136$ phases. The previous results are those obtained with the raw model.

We compare on Figure 5.5 the mean Belgian family size in finite time for the three models. With the smooth and the gap models, we see more clearly the beginning of the life of the first daughter after about twenty years, followed by a second hump at the beginning of the life of the first grand-daughter after about 60 years.

Adding the intermediate phases to take care of the after-birth gap periods makes the total number of daughters of a woman decrease; it is reflected by the size of the family she generates, and is a natural effect since it induces a reduction in the total fertility time. This result also appears in Table 5.3, where we compare the mean total progeny size of a new-born Belgian woman for the three models.

Model	n	$D_1^{(1)}$
Raw	22	4.7
Smooth	101	4.1
Gap	136	3.6

Table 5.3: Mean total size of the family generated by a new-born woman in Belgium.

Let us now look at countries whose criticality changes when passing from the raw model to the gap model (see Section 3.4). In particular, recall that South Africa goes from supercritical to subcritical, Turkey from supercritical - nearly critical, to

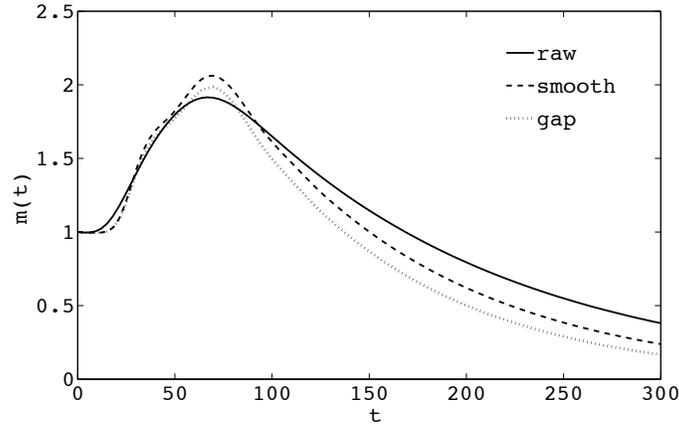


Figure 5.5: Comparison of the mean Belgian family size at a given time with $n = 22$, $n = 101$, and $n = 136$.

subcritical, and the USA from subcritical - nearly critical, to subcritical. We plot on Figure 5.6 the mean South African family size as a function of the time, for the raw and for the gap models. Here, we see that the difference between the two models is important. For the three countries, we finally report in Table 5.4 the conditional mean time until extinction and the conditional mean total progeny size, given extinction, for the two models. Again, the differences are significant, which shows that the results are highly sensitive to the data.

Country	\tilde{M}_{e_1}		$D_{e_1}^{(1)}$	
	Raw	Gap	Raw	Gap
South Africa	499.08	914.73	19.1	31.52
USA	2280.6	301	45.47	9.73
Turkey	8428.8	332.6	136.88	11.25

Table 5.4: Conditional expected time until extinction and mean total size of the family generated by a new-born woman, given that extinction occurs

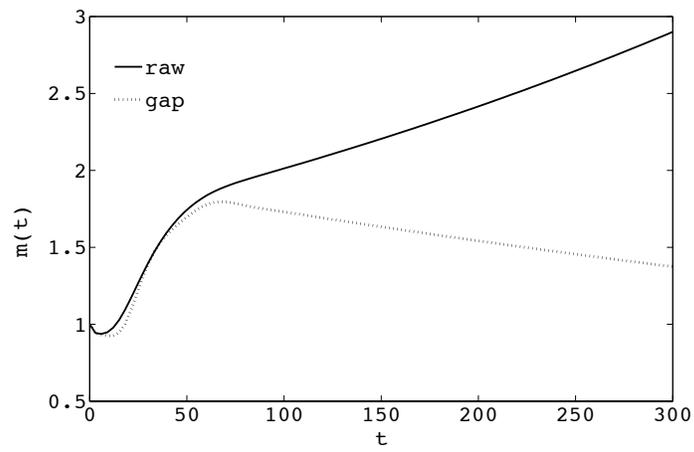


Figure 5.6: Comparison of the mean South African family size at a given time with the raw and the gap models.

CHAPTER 6

Structured Markov chain approach

In this chapter, we show the correspondence between MBTs and quasi-birth-and-death processes, and between GMTs and M/G/1-type Markov chains. We then adapt numerical techniques of level-dependent structured Markov chains to Markovian trees.

When the usual fixed point extinction equation does not hold anymore, the structured Markov chain approach allows to compute the extinction probability of a Markovian tree. This is illustrated in Hautphenne, Leibnitz and Rémiche [31], as well as in Chapters 7 and 8. We introduce a linear algorithm, which has a physical interpretation in terms of Markov chains, and which is used on several occasions in the chapter.

Then, we use the structured Markov chain approach to compute transient measures in a Markovian tree. The distribution of the maximal population size before extinction may be obtained with the linear algorithm used to compute the extinction probability. The mean time until extinction or until the population reaches k individuals may be calculated by adapting numerical tools for first passage times to lower and to upper levels in structured Markov chains.

We do emphasize that the techniques presented in this chapter must be confined to Markovian trees with a small number of phases in order to be numerically efficient.

6.1 Structured Markov chains

A structured Markov chain is a two-dimensional Markov chain whose generator has a particular block-structure which may be exploited from a numerical point of view; see for instance Bini, Latouche and Meini [10]. Structured Markov chains have many applications in queueing theory and in stochastic modelling, and they include M/G/1- and G/M/1-type Markov chains, quasi-birth-and-death (QBD) processes, skip-free queues

and tree-like stochastic processes.

The MBT as a level-dependent QBD process

A QBD process is a two-dimensional Markovian process $\{(X(t), \varphi(t)) : t \in \mathbb{R}^+\}$, where $X(t)$ is called the *level* at time t , and $\varphi(t)$ is called the *phase* at time t . Here, the level space will always be \mathbb{N} , and the phase space at level k is finite and will be denoted by $L(k)$.

The specificity of this process is that the only permitted transitions from the state (k, i) , $k \in \mathbb{N}$, $i \in L(k)$, are within the same level k , or towards the previous level $k - 1$, or the next level $k + 1$. When the transition rates between the phases depend on the level, we say that the QBD is *level-dependent*.

The infinitesimal generator of a level-dependent QBD is as follows

$$Q = \begin{bmatrix} A_0^{(0)} & A_1^{(0)} & 0 & 0 & \dots \\ A_{-1}^{(1)} & A_0^{(1)} & A_1^{(1)} & 0 & \dots \\ 0 & A_{-1}^{(2)} & A_0^{(2)} & A_1^{(2)} & \dots \\ 0 & 0 & A_{-1}^{(3)} & A_0^{(3)} & \ddots \\ \vdots & \vdots & \vdots & \ddots & \ddots \end{bmatrix}, \quad (6.1)$$

where the (i, j) th entry of the block matrix $A_\ell^{(k)}$ is the transition rate from phase i in level k to phase j in level $k + \ell$. Level-independent QBD processes have been extensively studied, see for instance Latouche and Ramaswami [47], and references therein.

A first representation of an MBT as a level-dependent QBD goes as follows: the level $X(t)$ is defined as the total population size in the MBT at time t , that is $X(t) = \mathbf{Z}(t) \mathbf{1}$. If $X(t) = k \geq 1$, then the phase is the k -tuple $\varphi(t) = (\phi_1(t), \phi_2(t), \dots, \phi_k(t))$ describing the phase of each individual MAP, enumerated from left to right in the tree. The phase space at level k is thus

$$L(k) = \{(S_1, S_2, \dots, S_k) : 1 \leq S_j \leq n \text{ for } 1 \leq j \leq k\},$$

and is of cardinality $|L(k)| = n^k$.

In many situations, it is of numerical importance to reduce the phase space cardinality when it is possible. Here the cardinality increases exponentially with the level.

There exists another representation of the MBT as a level-dependent QBD where the phase space cardinality growth is polynomial of order $n - 1$ (linear when $n = 2$): the level is defined as above, as the total population size at time t , but the phase is the n -uple $\varphi(t) = (Z_1(t), Z_2(t), \dots, Z_n(t))$ describing the number of individuals in each phase at time t .

The phase space at level k is now

$$L(k) = \{(S_1, S_2, \dots, S_n) : S_1 + S_2 + \dots + S_n = k \text{ with } S_j \geq 0 \text{ for } 1 \leq j \leq n\}, \quad (6.2)$$

and is of cardinality $|L(k)| = \binom{k+n-1}{n-1}$. We order the phases in the lexicographic manner. For example, if $n = 2$, then the phase space of level 3 is given by

$$L(3) = \{(0, 3), (1, 2), (2, 1), (3, 0)\}.$$

Notice that with both representations, we have $A_0^{(0)} = A_1^{(0)} = 0$, since the level 0 is absorbing.

The GMT as a level-dependent M/G/1-type Markov chain

A level-dependent M/G/1-type Markov chain is defined exactly like a level-dependent QBD process, except that here, transitions are permitted from level k to any higher level $k + m$, $m \geq 1$, as well as to level k and to level $k - 1$. The generator takes the form

$$Q = \begin{bmatrix} A_0^{(0)} & A_1^{(0)} & A_2^{(0)} & A_3^{(0)} & A_4^{(0)} & A_5^{(0)} & \dots \\ A_{-1}^{(1)} & A_0^{(1)} & A_1^{(1)} & A_2^{(1)} & A_3^{(1)} & A_4^{(1)} & \dots \\ 0 & A_{-1}^{(2)} & A_0^{(2)} & A_1^{(2)} & A_2^{(2)} & A_3^{(2)} & \dots \\ 0 & 0 & A_{-1}^{(3)} & A_0^{(3)} & A_1^{(3)} & A_2^{(3)} & \ddots \\ \vdots & \vdots & \vdots & \vdots & \vdots & \ddots & \ddots \end{bmatrix}. \quad (6.3)$$

The two representations of a GMT as a level-dependent M/G/1-type Markov chain are exactly the same as the ones of an MBT as a level-dependent QBD. Again, as level 0 is absorbing, we have $A_\ell^{(0)} = 0$ for all $\ell \geq 0$.

From now on, we shall use the *second* representation for MBTs and GMTs, since the phase space is smaller.

6.2 Extinction probability

Let G_k , $k \geq 1$ be an infinite sequence of matrices which are defined as follows: $(G_k)_{ij}$ is the probability that a structured Markov chain reaches level $k - 1$ for the first time in phase j , given that it starts in phase i of level k , that is

$$(G_k)_{ij} = P[\gamma(k-1) < \infty, \varphi(\gamma(k-1)) = j | X(0) = k, \varphi(0) = i],$$

where $\gamma(k) = \inf\{t \geq 0 : X(t) = k\}$ is the first passage time to level k , $k \geq 0$.

If a Markovian tree starts with one individual in phase i at time 0, then it means that the corresponding Markov chain starts in state $(1, e_i)$, and the extinction probability q_i of the Markovian tree is equal to the probability $(\mathbf{G}_1)_i$ that the Markov chain eventually reaches level 0, starting from the state $(1, e_i)$. Notice that here \mathbf{G}_1 is a vector since the level 0 contains one phase only.

In a level-dependent QBD process, the matrices G_k satisfy the infinite system of matrix equations

$$G_k = (A_0^{(k)})^{-1} A_{-1}^{(k)} + (A_0^{(k)})^{-1} A_1^{(k)} G_{k+1} G_k, \quad k \geq 1. \quad (6.4)$$

Indeed, starting from level k , the QBD may directly move to level $k - 1$ at the next level change, with probability $(A_0^{(k)})^{-1} A_{-1}^{(k)}$, or it may move up to level $k + 1$ with probability $(A_0^{(k)})^{-1} A_1^{(k)}$. Upon arrival in level $k + 1$, it eventually returns to level k with probability G_{k+1} and then to level $k - 1$ with probability G_k .

A way to obtain the vector \mathbf{G}_1 is to compute the vectors $\mathbf{G}_1(M)$ of probability that the QBD eventually reaches level 0, starting from level 1, *without going over level M*, for $M \geq 1$. Letting M tend to infinity removes the restriction, and $\lim_{M \rightarrow \infty} \mathbf{G}_1(M) = \mathbf{G}_1$.

More generally, we define for $M \geq 1$, $1 \leq k \leq M$, the matrices

$$G_k(M) = \mathbf{P}[\gamma(k-1) < \gamma(M+1), \varphi(\gamma(k-1)) | X(0) = k, \varphi(0)].$$

We can then write

$$G_M(M) = (-A_0^{(M)})^{-1} A_{-1}^{(M)}, \quad (6.5)$$

since, starting from level M , the probability to reach level $M-1$ before going over level M , is the probability to directly move to level $M-1$ when leaving level M ; and for $M-1 \geq k \geq 1$,

$$G_k(M) = (-A_0^{(k)})^{-1} A_{-1}^{(k)} + (-A_0^{(k)})^{-1} A_1^{(k)} G_{k+1}(M) G_k(M),$$

since, starting from level k , the process may directly move to level $k-1$, or go up to level $k+1$, and finally move back to level k , and then to level $k-1$, both without going over level M . This last equation may be rewritten as

$$G_k(M) = \left[I - (-A_0^{(k)})^{-1} A_1^{(k)} G_{k+1}(M) \right]^{-1} (-A_0^{(k)})^{-1} A_{-1}^{(k)}. \quad (6.6)$$

Therefore, starting from (6.5), we obtain $\mathbf{G}_1(M)$ after M steps.

Equation (6.6) is similar to the M th step of the linear algorithm U , which computes the matrix G for level-*independent* QBDs (Latouche and Ramaswami [47, Chapter 8]).

The drawback of this method is that for each M , we need to iterate through the M steps (6.5–6.6) to finally get $\mathbf{G}_1(M)$, without being able to make use of any previous computation from the stage $M-1$. To remedy to this point, we can instead compute the matrices

$$F_M = \mathbf{P}[\gamma(M+1) < \gamma(0), \varphi(\gamma(M+1)) | X(0) = 1, \varphi(0)], \quad M \geq 1, \quad (6.7)$$

giving the probability to reach level $M+1$ before level 0, starting from level 1, so that $\mathbf{G}_1(M) = \mathbf{1} - F_M \mathbf{1}$, and $\mathbf{G}_1 = \mathbf{1} - \lim_{M \rightarrow \infty} F_M \mathbf{1}$. The advantage is that we can write F_M as the product

$$F_M = L_1 L_2 \cdots L_M,$$

where $(L_i)_{j\ell}$ is the probability that the process reaches level $i+1$ for the first time in phase ℓ , *before* reaching level 0, given that it starts in phase j of level i , that is

$$L_i = \mathbf{P}[\gamma(i+1) < \gamma(0), \varphi(\gamma(i+1)) | X(0) = i, \varphi(0)], \quad i \geq 1.$$

The matrices L_i may be recursively computed as

$$L_1 = (-A_0^{(1)})^{-1} A_1^{(1)}, \quad (6.8)$$

and for $i \geq 2$, $L_i = (-A_0^{(i)})^{-1} A_1^{(i)} + (-A_0^{(i)})^{-1} A_{-1}^{(i)} L_{i-1} L_i$, which can be rewritten as

$$L_i = \left[I - (-A_0^{(i)})^{-1} A_{-1}^{(i)} L_{i-1} \right]^{-1} (-A_0^{(i)})^{-1} A_1^{(i)}. \quad (6.9)$$

The justification of equations (6.8–6.9) is very similar to that of equations (6.5–6.6).

Therefore, for each M , we have $F_M = F_{M-1} L_M$, so that we just need to compute a new matrix L_M using the matrix L_{M-1} from the previous stage, via Equation (6.9).

Therefore, we can write $\mathbf{G}_1(1) = (-A_0^{(1)})^{-1} A_{-1}^{(1)}$, and for $M \geq 2$,

$$\mathbf{G}_1(M) = \mathbf{G}_1(M-1) + F_{M-1}(\mathbf{1} - L_M \mathbf{1}), \quad (6.10)$$

which highlights the probability mass added at each stage.

This method is not found as such in the literature, although the idea is close to that of Lemma 11.2.2 in [47, Chapter 11] related to first passage times in a level-independent QBD. For further reference, we shall call this linear procedure the *algorithm L*.

We have examined other algorithms for which we do not provide the details here, as they are less efficient than the algorithm *L*. Quadratic algorithms developed for level-independent QBDs may be adapted to the level-dependent case, and used to compute \mathbf{G}_1 . For instance, Ramaswami and Taylor [62] adapted the *Logarithmic-Reduction algorithm* of Latouche and Ramaswami [47, Chapter 8]; in a similar manner, we have investigated the generalization of the *Cyclic-Reduction algorithm* developed by Bini, Latouche and Meini [10] to the level-dependent case.

Finally, the linear algorithm *U* [47] may be adapted to M/G/1-type Markov chains, and thus used to compute the extinction probability of a GMT. Bini, Latouche and Meini [10] also propose a version of the cyclic-reduction algorithm adapted to M/G/1-type processes in the level-independent case; again, we investigated this algorithm in the level-dependent case.

Recall from the previous section that the size of the block matrices in the generator of a level-dependent Markov chain increases polynomially with the level and the number of phases. It may thus be costly to use one of the algorithms discussed above to compute the extinction probability of a Markovian tree. However, if the number of phases in the Markovian tree is not too large, it is fully feasible to use those techniques.

Indeed, there are some situations where the extinction probability of a Markovian tree may not be expressed as the minimal nonnegative solution of the fixed point extinction equation. For example in Hautphenne, Leibnitz and Remiche [31], we model the spread of a file in a peer-to-peer network with a population-size-dependent MBT. In that case, the structured Markov chain approach is the only one we could use to compute the extinction probability of the MBT.

Other examples are given in the next two chapters, where MBTs evolve under external influences, which removes the independence assumption between individuals. The extinction equation (1.15) does not hold anymore, and one technique to compute the extinction probability is to use the structured Markov chain approach.

6.3 Maximum population size

Let M be the maximum population size of an MBT. We investigate its distribution, given the initial phase of the MBT, and its conditional distribution, given extinction

of the MBT.

The cumulative distribution of M is studied for the discrete one-type Galton-Watson process by Bishir [11], and Adke [2]. Lindvall [51], and Nagaev and Vakhtel [55] analyze the tail behaviour of the distribution of M , for the same process. Pakes [61] determines bounds for $E[M_m]$ in the critical case, where M_m is the maximum generation size among the first m generations. Topchii and Vatutin [70] study asymptotics for $E[M_m]$.

Let us look at the cumulative distribution $\mathbf{v}(m) = P[M \leq m | \varphi_0]$ of the maximal MBT size, given its initial phase. We know that $\mathbf{v}(1) = \boldsymbol{\theta}$ and $\mathbf{v}(\infty) = \mathbf{q}$. The usual approach of conditioning on the first observable event in the tree fails in this case, and we only obtain lower and upper bounds for the distribution:

$$\boldsymbol{\theta} + \Psi \sum_{i=1}^{m-1} \mathbf{v}(i) \otimes \mathbf{v}(m-i) \leq \mathbf{v}(m) \leq \mathbf{q}, \quad m \geq 2.$$

The first inequality results from the fact that it is possible that the maximum size of the MBT is at most m , with a left and a right subtree of maximum sizes m at different times.

It is actually essential to keep track of the population composition in each phase, each time a birth or a death event occurs. This leads us to the structured Markov chain approach.

The probability that the MBT eventually becomes extinct without growing up to more than m individuals is given by the vector $\mathbf{v}(m) = \mathbf{G}_1(m)$ defined in the previous section, and may thus be computed with the algorithm L .

The conditional cumulative distribution of the maximum population size in the MBT, given its initial phase and that extinction occurs, is thus

$$\mathbf{v}_e(m) = P[M \leq m | \varphi_0, E] = \Phi^{-1} \mathbf{G}_1(m), \quad (6.11)$$

where Φ is defined in (5.17).

As mentioned in the previous section, the same numerical technique may be applied in the GMT case, provided we generalize the algorithm L to M/G/1-type Markov chains.

This method is costly when the number n of phases in the Markovian tree is large, but is still more effective than the one proposed by Bishir [11], which requires the inversion of matrices of size $\sum_{k=1}^m \binom{k+n-1}{n-1}$ when computing $\mathbf{v}(m)$.

Example 6.3.1. Let us apply the algorithm L to an MBT with $n = 3$ phases. The birth rates matrix B is such that $B_{i,jk} = (D_1)_{ik} (P_1)_{ij}$ with

$$D_1 = \begin{bmatrix} 15 & 0 & 0 \\ 0 & 4 & 0 \\ 0 & 0 & 1 \end{bmatrix}, \quad P_1 = \begin{bmatrix} 0.95 & 0.05 & 0 \\ 0.01 & 0.94 & 0.05 \\ 0 & 0.02 & 0.98 \end{bmatrix}$$

and

$$D_0 = \begin{bmatrix} -23.2 & 0.1 & 0.1 \\ 0.1 & -8.6 & 0.5 \\ 0 & 2 & -15 \end{bmatrix}, \quad \mathbf{d} = \begin{bmatrix} 8 \\ 4 \\ 12 \end{bmatrix}.$$

In this MBT, the first phase is very fertile, while the second phase has equal birth and death rates, and the third phase has a very high death rate compared to its birth rate. Both the second and third phases may eventually change into the first phase via the matrix D_0 or produce a child in the first phase via the matrix P_1 , which makes the whole MBT supercritical, with extinction probability vector

$$\mathbf{q} = \begin{bmatrix} 0.57 \\ 0.94 \\ 0.99 \end{bmatrix}.$$

The conditional cumulative distribution $v_e(m)$ is plotted on Figure 6.1, for $0 \leq m \leq 10$. We see that, given extinction, the maximum population size is very low if we start in the third phase. Starting in the first phase, which leads to a quite high survival probability ($1 - q_1 = 0.43$), extinction must happen before the process grows very much.

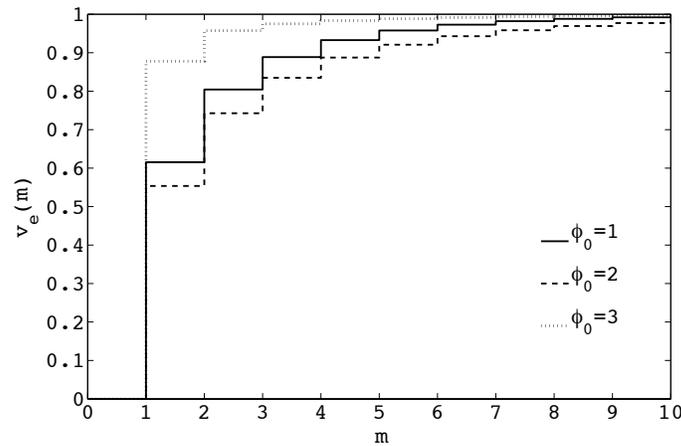


Figure 6.1: Conditional cumulative distribution of the maximum population size in an MBT, given its extinction

6.4 Time until extinction

The time until extinction of an MBT may be seen as the first passage time from level 1 to level 0 in the corresponding level-dependent QBD. We adapt here an algorithmic procedure described in Gaver, Jacobs and Latouche [22], which computes the distribution of the first passage time to lower levels in a level-dependent QBD with a *finite* number of levels.

As the QBD associated to an MBT has an *infinite* number of levels, we need to truncate it at some level M . In this manner, we are computing the mean time until the

extinction of the MBT, given its initial phase, on the paths where extinction occurs before the process reaches $M + 1$ individuals, that is

$$\mathbf{d}_{M+1}^{(1)} = \mathbb{E}[\gamma(0) \mathbf{1}_{\{\gamma(0) < \gamma(M+1)\}} | X(0) = 1, \varphi(0)].$$

Letting M grow to infinity provides us with the mean time until extinction, on the paths where extinction occurs in a finite time.

The truncated QBD may be seen as a Markovian process with two absorbing states, corresponding to levels 0 and $M + 1$. More generally, we define

$$\mathbf{d}_{M+1}^{(k)} = \mathbb{E}[\gamma(k-1) \mathbf{1}_{\{\gamma(0) < \gamma(M+1)\}} | X(0) = k, \varphi(0)],$$

for $1 \leq k \leq M$; $\mathbf{d}_{M+1}^{(k)}$ is thus the expected passage time from level k to level $k - 1$, on the paths where absorption occurs in level 0 rather than in level $M + 1$.

Define C_k for $1 \leq k \leq M$, as the generator of the restriction S_k of the QBD observed only during those intervals of time spent at level k , before the QBD moves down for the first time to level $k - 1$ or to level $M + 1$. We clearly have

$$C_M = A_0^{(M)}$$

since both level $M - 1$ and level $M + 1$ are taboo. Then, for $M - 1 \geq k \geq 1$,

$$C_k = A_0^{(k)} + A_1^{(k)} (-C_{k+1})^{-1} A_{-1}^{(k+1)}.$$

Indeed, a transition of the subprocess S_k occurs from level k to itself either in one step, with the rate recorded by $A_0^{(k)}$, or by first going up to level $k + 1$ and spending some time in levels $k + 1, k + 2, \dots, M$, before going back to level k , with the rate recorded by $A_1^{(k)} (-C_{k+1})^{-1} A_{-1}^{(k+1)}$. The inverse $(-C_{k+1})^{-1}$ gives the expected amount of time spent at level $k + 1$ before the first visit to level k or to level $M + 1$.

Finally, we define the probabilities that, starting from level k , the QBD eventually gets absorbed in level 0 rather than in level $M + 1$, for $1 \leq k \leq M$, as

$$\mathbf{x}_k = \prod_{k \geq j \geq 1} (-C_j)^{-1} A_{-1}^{(j)}.$$

Now, we can write

$$\mathbf{d}_{M+1}^{(M)} = (-C_M)^{-1} \mathbf{x}_M, \tag{6.12}$$

since the the expected passage time from level M to level $M - 1$, on the paths where absorption occurs in level 0 rather than in level $M + 1$, is given by the expected amount of time spent at level M before the first visit to level $M - 1$ or to level $M + 1$, times the probability that starting from level M , the process gets absorbed in level 0 rather than in level $M + 1$. And for $M - 1 \geq k \geq 1$,

$$\mathbf{d}_{M+1}^{(k)} = (-C_k)^{-1} (\mathbf{x}_k + A_1^{(k)} \mathbf{d}_{M+1}^{(k+1)}). \tag{6.13}$$

Indeed, keep in mind that we consider paths where absorption occurs in level 0 rather than in level $M + 1$. Then, the first term $(-C_k)^{-1} \mathbf{x}_k$ is the expected time in level

k before reaching level $k - 1$. The second term $(-C_k)^{-1} A_1^{(k)} \mathbf{d}_{M+1}^{(k+1)}$ is the expected number of times the process moves from level k to level $k + 1$ before its first visit to level $k - 1$, times the expected passage time from level $k + 1$ to level k .

Equations (6.12) and (6.13) provide us with a numerical procedure to compute $\mathbf{d}_{M+1}^{(1)}$ for one fixed M . The drawback, when using that scheme as it is, lies in the fact that the first step (6.12) already requires the computation of all the matrices C_k for $1 \leq k \leq M$, since we need \mathbf{x}_M . It would be more efficient to compute one matrix C_k at a time, at each step of the algorithm. In order to do that, let us display the whole expression for $\mathbf{d}_{M+1}^{(1)}$:

$$\mathbf{d}_{M+1}^{(1)} = (-C_1)^{-1} \sum_{k=1}^M \left(\prod_{1 \leq j \leq k-1} A_1^{(j)} (-C_{j+1})^{-1} \right) \left(\prod_{k \geq j \geq 1} (-C_j)^{-1} A_{-1}^{(j)} \right), \quad (6.14)$$

where an empty product is equal to the identity matrix.

In practice, we work at fixed M , and we exploit the structure of (6.14): indeed, we see that the M terms have common factors that should be computed only once. In order to do so, we go from $k = M$ down to $k = 1$ in the sum, and we construct the terms little by little, from the interior, with the idea that a part of the sum from $k = M$ to $k = \ell$ is easily expressed when we know the partial sum from $k = M$ to $k = \ell + 1$.

This is described by Algorithm 6.4.1, in which the approximation Y at the end of the loop for a given i is actually

$$Y(i) = \sum_{k=i}^M \left(\prod_{i-1 \leq j \leq k-1} A_1^{(j)} (-C_{j+1})^{-1} \right) \left(\prod_{k \geq j \geq i} (-C_j)^{-1} A_{-1}^{(j)} \right),$$

with the convention that $A_1^{(0)} = I$; when $i = 1$, we do obtain (6.14).

We thus run Algorithm 6.4.1 for successive values of M until it converges to $\mathbf{d}_\infty^{(1)}$, that is, the mean time until extinction on the paths where extinction occurs in finite time. The conditional mean time until extinction, *given* that extinction occurs, is then given by

$$\mathbf{d}_e^{(1)} = \Phi^{-1} \mathbf{d}_\infty^{(1)}.$$

In contrast to the method described in Section 5.3 where we evaluate the conditional mean time until extinction by numerically computing an integral, the technique presented here does not require to numerically solve any differential equation, which can produce some errors, and furthermore, we do not need to fix any error ε and step size h , the solution being somewhat sensitive to the choice of these parameters. The structured Markov chain approach is actually very efficient for small values of the number n of phases in the MBT.

This method may be generalized to the GMT case, by adapting the ideas of Latouche, Jacob and Gaver [46], who develop algorithms to compute the distribution of the first passage time to lower levels, in a *finite* level-dependent G/M/1-type Markov chain.

Algorithm 6.4.1 Algorithm to compute the vector $\mathbf{d}_{M+1}^{(1)}$

```

i := M
C := A0(i)
L := A1(i-1) (-C)-1
R := (-C)-1 A-1(i)
Y := L R
for i = M - 1 to 2 do
  C := A0(i) + A1(i) (-C)-1 A-1(i+1)
  L := A1(i-1) (-C)-1
  R := (-C)-1 A-1(i)
  Y := L R + L Y R
end for
i := 1
C := A0(i) + A1(i) (-C)-1 A-1(i+1)
L := (-C)-1
R := (-C)-1 A-1(i)
 $\mathbf{d}_{M+1}^{(1)}$  := L R + L Y R

```

Example 6.4.1. We consider an MBT with $n = 2$ phases. The birth rates matrix B is such that $B_{i,jk} = (D_1)_{ik} (P_1)_{ij}$ with

$$D_1 = \begin{bmatrix} 15 & 0 \\ 0 & 10 \end{bmatrix}, \quad P_1 = I$$

and

$$D_0 = \begin{bmatrix} -15.5 - p & 0.5 \\ 0.5 & -25.5 \end{bmatrix}, \quad \mathbf{d} = \begin{bmatrix} p \\ 15 \end{bmatrix}.$$

The parameter p controls the criticality of the MBT; we take the two values $p = 35$ (subcritical) and $p = 5$ (supercritical), in which case the extinction probability is given by

$$\mathbf{q} = \begin{bmatrix} 0.36 \\ 0.95 \end{bmatrix}.$$

We plot on Figure 6.2 the expected passage time $\mathbf{d}_{M+1}^{(1)}$ from level 1 to level 0, on the paths where absorption occurs in level 0 rather than in level $M + 1$, as a function of M , for $1 \leq M \leq 20$.

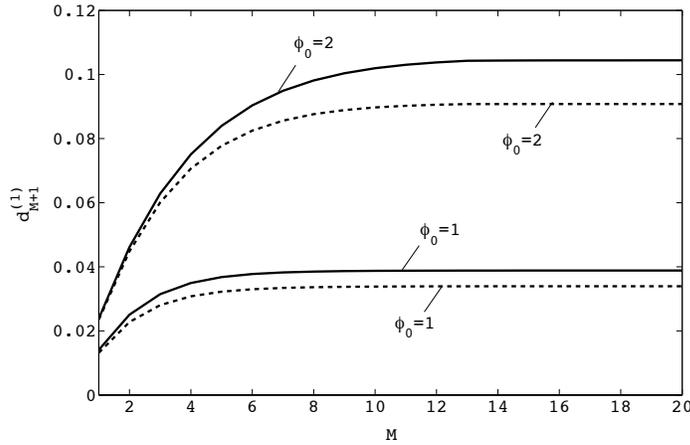
We compare in Table 6.1 the conditional mean time until extinction obtained via (5.25) by the method described in Section 5.3 with some step $h = 5 \cdot 10^{-3}$ and error $\varepsilon = 10^{-3}$, and with the structured Markov chain approach.

6.5 Time to reach k individuals

To the best of our knowledge, there does not seem to be much literature on the question of the time needed for a branching process to reach a given population size.

Criticality	φ_0	\tilde{M}_e	$d_e^{(1)}$
Subcritical ($p = 35$)	1	0.0388	0.0388
	2	0.1054	0.1044
Supercritical ($p = 5$)	1	0.0931	0.0932
	2	0.0961	0.0958

Table 6.1: Conditional mean time until extinction, given that extinction occurs.

Figure 6.2: Mean time until extinction on the paths where the MBT does not go over M individuals, for the subcritical case (plain line) and the supercritical case (dashed line).

The time until the population reaches k individuals for the first time in the MBT corresponds to the first passage time to level k in the associated level-dependent QBD.

We shall compute the mean time until the MBT reaches $k \geq 2$ individuals, given its initial phase, on the paths where it does not become extinct before reaching that population size. Expressed in terms of QBD, this expected time is given by

$$s_0^{1 \rightarrow k} = E[\gamma(k) \mathbf{1}_{\{\gamma(k) < \gamma(0)\}} | X(0) = 1, \varphi(0)].$$

Observe that

$$\begin{aligned} & E[\gamma(k) \mathbf{1}_{\{\gamma(k) < \gamma(0)\}} | X(0) = 1, \varphi(0)] \\ &= E[\min[\gamma(0), \gamma(k)] | X(0) = 1, \varphi(0)] \\ &\quad - E[\gamma(0) \mathbf{1}_{\{\gamma(0) < \gamma(k)\}} | X(0) = 1, \varphi(0)]. \end{aligned}$$

If we define $\ell_{0,k}^{(1)} = E[\min[\gamma(0), \gamma(k)] | X(0) = 1, \varphi(0)]$ as the expected time until the process reaches for the first time either level 0 or level k , starting from level 1, then we

have

$$\mathbf{s}_0^{1 \rightarrow k} = \boldsymbol{\ell}_{0,k}^{(1)} - \mathbf{d}_k^{(1)}, \quad (6.15)$$

where $\mathbf{d}_k^{(1)}$ is calculated in the previous section. It thus remains for us to compute $\boldsymbol{\ell}_{0,k}^{(1)}$ for $k \geq 2$. More generally, we define for $1 \leq i \leq k-1$,

$$\boldsymbol{\ell}_{i-1,k}^{(i)} = \mathbb{E}[\min[\gamma(i-1), \gamma(k)] \mid X(0) = i, \varphi(0)],$$

which is the expected time until the process reaches for the first time either level $i-1$ or level k , starting from level i . With the definition of the matrices C_i , for $1 \leq i \leq k-1$, given in Section 6.4 taking $M = k-1$, we have

$$\boldsymbol{\ell}_{k-2,k}^{(k-1)} = (-A_0^{(k-1)})^{-1} \mathbf{1}$$

and for $k-2 \geq i \geq 1$,

$$\boldsymbol{\ell}_{i-1,k}^{(i)} = (-C_i)^{-1} [\mathbf{1} + A_1^{(i)} \boldsymbol{\ell}_{i,k}^{(i+1)}].$$

Indeed, the first term $(-C_i)^{-1} \mathbf{1}$ is the expected time spent in level i before the first visit to level $i-1$ or to level k , and the second term $(-C_i)^{-1} A_1^{(i)} \boldsymbol{\ell}_{i,k}^{(i+1)}$ is the expected number of times the process moves from level i to level $i+1$ before its first visit to level $i-1$ or to level k , times the expected passage time from level $i+1$ to level i or level k .

It thus suffices to combine the iterative computation of the vectors $\boldsymbol{\ell}_{i-1,k}^{(i)}$ for $k-1 \geq i \geq 1$ and the numerical scheme for $\mathbf{d}_k^{(1)}$ described by Algorithm 6.4.1 with $M+1 = k$, to obtain Algorithm 6.5.1, which computes $\mathbf{s}_0^{1 \rightarrow k}$ via (6.15).

Recall from Section 6.2 that the probability that the MBT reaches k individuals in a finite time, before a possible extinction, is equal to $F_{k-1} \mathbf{1} = \mathbf{1} - \mathbf{G}_1(k-1)$, where $\mathbf{G}_1(k-1)$ is the probability for an MBT to eventually become extinct without going up to k individuals. Let $\Upsilon_k = \text{diag}(F_{k-1} \mathbf{1})$. The conditional expected time for the MBT to reach for the first time k individuals, given it occurs before extinction is thus given by

$$\mathbf{s}^{1 \rightarrow k} = \Upsilon_k^{-1} \mathbf{s}_0^{1 \rightarrow k}.$$

We can again generalize the method to the GMT case, for instance by adapting the ideas of Latouche, Jacob and Gaver [46], who develop algorithms to compute the distribution of the first passage time to upper levels, in a finite level-dependent G/M/1-type Markov chain.

Example 6.5.1. Let us take again the MBT of Example 6.4.1 with the same parameter values.

We first compute the vector $\mathbf{s}_0^{1 \rightarrow k}$ for $2 \leq k \leq 35$, and we depict the graphs on Figure 6.3. In the subcritical case, we see that $\lim_{k \rightarrow \infty} \mathbf{s}_0^{1 \rightarrow k} = \mathbf{0}$, since $\lim_{k \rightarrow \infty} \mathbb{1}_{\{\gamma(k) < \gamma(0)\}} = 0$; in the supercritical case, $\lim_{k \rightarrow \infty} \mathbf{s}_0^{1 \rightarrow k} = \infty$.

Then, for the supercritical case, we plot the vector $\mathbf{s}^{1 \rightarrow k}$ on Figure 6.4. Again, the curves grow to infinity since their limit records the mean time for a population to reach an infinite size, given its survival.

Algorithm 6.5.1 Algorithm to compute the vectors $\mathbf{d}_k^{(1)}$, $\ell_{0,k}^{(1)}$ and $\mathbf{s}_0^{1 \rightarrow k}$

```

i = k - 1
C :=  $A_0^{(i)}$ 
L :=  $A_1^{(i-1)} (-C)^{-1}$ 
R :=  $(-C)^{-1} A_{-1}^{(i)}$ 
Y := L R
Z := L 1
for i = k - 2 to 2 do
  C :=  $A_0^{(i)} + A_1^{(i)} (-C)^{-1} A_{-1}^{(i+1)}$ 
  L :=  $A_1^{(i-1)} (-C)^{-1}$ 
  R :=  $(-C)^{-1} A_{-1}^{(i)}$ 
  Y := L R + L Y R
  Z := L 1 + L Z
end for
i = 1
C :=  $A_0^{(i)} + A_1^{(i)} (-C)^{-1} A_{-1}^{(i+1)}$ 
L :=  $(-C)^{-1}$ 
R :=  $(-C)^{-1} A_{-1}^{(i)}$ 
 $\mathbf{d}_k^{(1)}$  := L R + L Y R
 $\ell_{0,k}^{(1)}$  := L 1 + L Z
 $\mathbf{s}_0^{1 \rightarrow k}$  =  $\ell_{0,k}^{(1)} - \mathbf{d}_{k-1}^{(1)}$ 

```

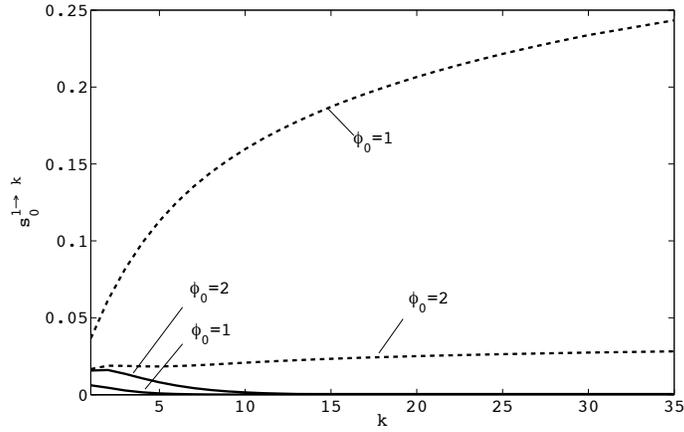


Figure 6.3: Mean time for the MBT to reach for the first time k individuals, on the paths where it happens before extinction, in the subcritical case $p = 35$ (plain line) and in the supercritical case $p = 5$ (dashed line).

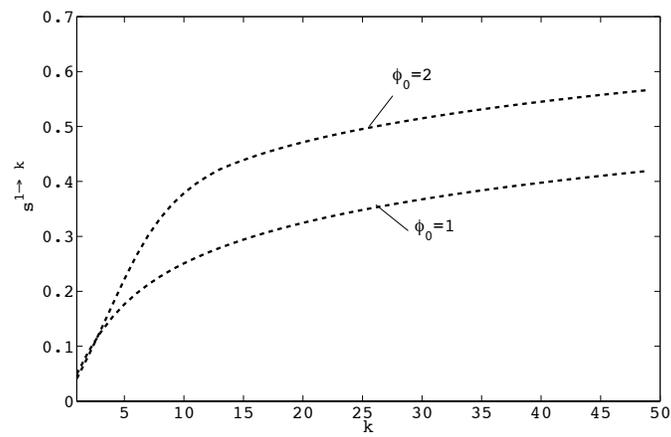


Figure 6.4: Conditional mean time until the MBT reaches for the first time k individuals, given that extinction does not happen before, in the supercritical case.

CHAPTER 7

Random environments

In the preceding chapters, we assumed that the parameters d , D_0 and B controlling the lifetime of individuals in a population stay constant over time. In reality, this assumption does not always hold, as many external phenomena may influence the behaviour of individuals.

For instance, weather conditions may have an impact on the reproduction of some plants or animals; or an economic crisis may create a decrease in the fertility rates of humans. We may then wonder how such external causes influence the probability that the population eventually becomes extinct.

In this chapter, we study the MBT evolving under the influence of an external Markovian random environment which controls the individuals' parameters over time. The major difference with the preceding chapters is that in this context, individuals do not behave independently of each others anymore, and some approaches previously used are not applicable anymore.

For instance, the extinction probability may no longer be computed as the minimal nonnegative solution of a fixed point equation, and the distribution of the time until extinction is no longer solution of an ordinary differential equation. The simple extinction criteria do not hold anymore either.

We carry out the analysis of the extinction probability in two ways: first, through the computation of transient measures for the MBT under random environment, and second by the structured Markov chain approach.

Using the forward Kolmogorov approach, we start by characterizing the population size distribution as the solution of a system of partial differential equations, from which we extract formulas for the factorial moments, as in Chapter 5. We do the same for the distribution of the total progeny until any given time.

The distribution of the time until extinction is obtained from the one of the pop-

ulation size, and the extinction probability is defined as its asymptotic limit. A first natural way to evaluate these quantities is to numerically solve the system of partial differential equations of the population size distribution, using tools from numerical analysis. We present two methods, called the finite difference and the semi-Lagrangian methods, that we apply to an exponential MBT. The corresponding algorithms do not have any physical interpretation.

Then, we use a probabilistic approach in which we compute the population size distribution by imposing constraints on the random environment. This provides us with a superlinear iterative integral scheme to compute the distribution of the time until extinction of an MBT and its extinction probability. A second integral equation also allows us to obtain the distribution of the number of environmental changes before extinction.

Finally, we use the structured Markov chain approach to compute the extinction probability. We end the chapter by a comparison between the various numerical approaches.

The lack of real data on external random environments in human demography, as well as the limitation of our methods to MBTs with a small number of phases, oblige us to provide only artificial illustrations of our results.

We will use the terminology *standard* MBT in the next two chapters, to refer to the MBT previously studied which does not undergo any external influence.

7.1 Definition

Consider an irreducible positive recurrent Markovian process $\{\xi(t) : t \in \mathbb{R}^+\}$ on m (finite) states, and with infinitesimal generator Q . Let $\boldsymbol{\pi}$ be its stationary distribution, that is the unique solution of $\boldsymbol{\pi}Q = \mathbf{0}$, $\boldsymbol{\pi}\mathbf{1} = 1$.

Suppose that at time 0, the Markovian process $\xi(t)$ is in a state determined by the vector $\boldsymbol{\pi}$, and that it evolves independently of an MBT, started in a given phase. The choice of the particular initial distribution $\boldsymbol{\pi}$ is justified by its physical interpretation: it corresponds to the distribution of the process $\xi(t)$ if we assume that it started a very long time before the birth of the first individual in the MBT. In addition, it simplifies some expressions.

Let $\mathcal{P} = \{(\mathbf{d}^{(i)}, D_0^{(i)}, B^{(i)}), i = 1, \dots, m\}$ be a set of 3-uples of MBT parameters. The states of the Markovian process control the parameters of the MBT over time. We associate to each state i of $\xi(t)$ the 3-uple $(\mathbf{d}^{(i)}, D_0^{(i)}, B^{(i)})$ of parameters such that, when $\xi(t) = i$, the MBT evolves with the death rates vector $\mathbf{d}^{(i)}$, the birth rates matrix $B^{(i)}$, and the transition rates matrix $D_0^{(i)}$. We say that the MBT evolves *under the Markovian random environment* (MRE in short) $(\xi(t), \mathcal{P})$.

An example of evolution path of an MBT under MRE is depicted on Figure 7.1. The different types of lines on the MBT picture indicates that the parameters of the MBT change as a function of the current state of the Markovian process.

Between two epochs of state changes in the Markovian environmental process, the individuals in the MBT behave independently of each others; and *conditionally* given

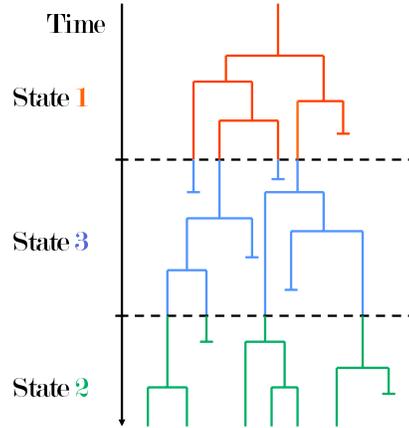


Figure 7.1: Example of path of an MBT under a Markovian random environment

the whole sequences of environmental states and sojourn time in each state, the individuals evolve independently too.

However, unconditionally, the individuals of the MBT do not evolve independently of each other anymore. Indeed, the histories of the trees generated by two individuals are linked by the fact that their parameters of evolution will change exactly at the same epochs. This loss of independence makes for instance the extinction equation (1.15) and the backward equation (5.2) not valid anymore.

In the literature on branching processes in random environment, most of the results are conditional, given the whole environmental sequence. We have chosen to work unconditionally, following another approach which requires to start the analysis with the transient measures of an MBT under MRE.

7.2 Transient features

Population size

Suppose there are n phases in the MBT, and m states in the MRE. Let $\tilde{\mathbf{Z}}(t) = [\tilde{Z}_1(t), \tilde{Z}_2(t), \dots, \tilde{Z}_n(t)]^T$ denote the population size at time t , in each phase of the MBT under MRE. We define the $n \times m$ probability generating function $\tilde{F}(\mathbf{s}, t)$ of $\tilde{\mathbf{Z}}(t)$, given the initial phase of the MBT, *jointly* with the state of the MRE at time t , as

$$\tilde{F}_{ij}(\mathbf{s}, t) = \sum_{\mathbf{k} \geq \mathbf{0}} \mathbb{P}[\tilde{\mathbf{Z}}(t) = \mathbf{k}, \xi(t) = j | \varphi_0 = i] \mathbf{s}^{\mathbf{k}} \quad 1 \leq i \leq n, 1 \leq j \leq m.$$

Consequently, $\tilde{F}(\mathbf{1}, t) = (\mathbf{1} \otimes \boldsymbol{\pi})$, since $\mathbb{P}[\xi(t) = j] = (\boldsymbol{\pi} e^{\mathbf{Q}t})_j = \pi_j$, for all $t \geq 0$.

Throughout the chapter, we use the following notation

$$\mathcal{D}[v^{(1)} \dots v^{(m)}] = \begin{bmatrix} v^{(1)} & & & \\ & v^{(2)} & & \\ & & \ddots & \\ & & & v^{(m)} \end{bmatrix},$$

where the $v^{(i)}$'s are either all scalars, all vectors, or all matrices of the same dimension.

We now give the forward Kolmogorov partial differential system of equations for the distribution $\tilde{F}(\mathbf{s}, t)$. The proof is omitted as it follows the same lines as the first part of the proof of Theorem 5.2.1; the only difference is that here, we establish the forward Kolmogorov equations for the joint process $(\tilde{\mathbf{Z}}(t), \xi(t))$, and the generating function is defined on the first dimension $\tilde{\mathbf{Z}}(t)$ only.

Theorem 7.2.1. *The forward Kolmogorov system of equations for the generating function $\tilde{F}(\mathbf{s}, t)$ of an MBT under MRE is*

$$\begin{aligned} \frac{\partial}{\partial t} \tilde{F}(\mathbf{s}, t) - \frac{\partial}{\partial \mathbf{s}^T} \tilde{F}(\mathbf{s}, t) \cdot A(\mathbf{s}) &= \tilde{F}(\mathbf{s}, t) \cdot Q, \\ \tilde{F}(\mathbf{s}, 0) &= \mathbf{s} \cdot \boldsymbol{\pi}, \end{aligned} \quad (7.1)$$

where the $mn \times m$ matrix $A(\mathbf{s}) = \mathcal{D}[\mathbf{a}^{(1)}(\mathbf{s}) \dots \mathbf{a}^{(m)}(\mathbf{s})]$, and $\mathbf{a}^{(i)}(\mathbf{s}) = \mathbf{d}^{(i)} + D_0^{(i)} \mathbf{s} + B^{(i)}(\mathbf{s} \otimes \mathbf{s})$, $i = 1, \dots, m$. \square

The difference with the forward Kolmogorov equation (5.1) for the standard MBT lies in the right-hand side of the matrix equation, which makes (7.1) non homogeneous anymore.

Remark 7.2.2. The *backward* Kolmogorov equation here involves different generating functions, conditioned on starting with more than one individual at time 0. Because of the loss of independence between the individuals, these generating functions cannot be decomposed as a product of factors reduced to $\tilde{F}(\mathbf{s}, t)$. The backward equation will thus not be of any help to us in this chapter.

We derive the factorial moments of the population size from (7.1). Recall the matrix derivative rules from Section 5.1, and define the $n \times mn^k$ matrix

$$\tilde{M}^{(k)}(t) = \frac{\partial^k}{(\partial \mathbf{s}^T)^k} \tilde{F}(\mathbf{s}, t) |_{\mathbf{s}=\mathbf{1}}, \quad (7.2)$$

as the k th factorial moment of $\tilde{\mathbf{Z}}(t)$ jointly with $\xi(t)$. The k th factorial moment $\tilde{m}^{(k)}(t)$ of $\tilde{\mathbf{Z}}(t)$ is an $n \times n^k$ matrix given by

$$\tilde{m}^{(k)}(t) = \tilde{M}^{(k)}(t) (\mathbf{1}_m \otimes I_{n^k}). \quad (7.3)$$

The following matrices, respectively of sizes $mn \times mn$ and $mn \times mn^2$, appear in the formulas for the factorial moments

$$\Omega^* = \mathcal{D}[\Omega^{(1)} \dots \Omega^{(m)}],$$

where $\Omega^{(i)} = D_0^{(i)} + B^{(i)} (\mathbf{1} \oplus \mathbf{1})$, and

$$\Gamma = \mathcal{D} [B^{(1)} (I_{n^2} + I_{(n,n)}) \cdots B^{(m)} (I_{n^2} + I_{(n,n)})].$$

The following proposition is to be compared to Proposition 5.2.4 in the standard MBT case. Next, we specify the two first moments. Again, the proofs are not given here since they are very similar to the standard case.

Proposition 7.2.3. *The matrices $\tilde{M}^{(k)}(t)$, for $k \geq 1$, are solutions of the following recursive system of differential equations, with initial conditions $\tilde{M}^{(1)}(0) = (\boldsymbol{\pi} \otimes I_n)$ and $\tilde{M}^{(k)}(0) = 0$ for $k \geq 2$:*

$$\begin{aligned} \frac{d}{dt} \tilde{M}^{(k)}(t) &= \tilde{M}^{(k)}(t) [(\Omega^* \otimes I_{n^{k-1}}) A(k) + (Q \otimes I_{n^k})] \\ &\quad + \tilde{M}^{(k-1)}(t) (\Gamma \otimes I_{n^{k-2}}) C(k), \end{aligned} \quad (7.4)$$

where the $mn^k \times mn^k$ coefficient matrices $A(k)$ and $C(k)$ are defined as

$$\begin{aligned} A(1) &= I_{mn} \\ C(1) &= 0_{mn} \\ A(k) &= I_{(n^{k-1}, mn)} (I_{(m, n^{k-1})} \otimes I_n) + (A(k-1) \otimes I_n), \quad k \geq 2 \\ C(k) &= I_{(n^{k-2}, mn^2)} (I_{(mn, n^{k-2})} \otimes I_n) (A(k-1) \otimes I_n) \\ &\quad + (C(k-1) \otimes I_n), \quad k \geq 2. \end{aligned}$$

□

Corollary 7.2.4. *The first two moments of the population size in an MBT under MRE are given by*

$$\begin{aligned} \tilde{m}^{(1)}(t) &= (\boldsymbol{\pi} \otimes I_n) e^{\tilde{A}t} (\mathbf{1}_m \otimes I_n) \\ \tilde{m}^{(2)}(t) &= (\boldsymbol{\pi} \otimes I_n) X(t) (\mathbf{1}_m \otimes I_{n^2}), \end{aligned} \quad (7.5)$$

where $X(t)$ is the solution of the Lyapunov equation

$$X(t) \tilde{B} - \tilde{A} X(t) + e^{\tilde{A}t} \Gamma - \Gamma e^{\tilde{B}t} = 0,$$

with

$$\tilde{A} = [\Omega^* + (Q \otimes I_n)], \quad (7.6)$$

and

$$\tilde{B} = (\Omega^* \otimes I_n) [I_{(n, mn)} (I_{(m, n)} \otimes I_n) + I_{mn^2}] + (Q \otimes I_{n^2}).$$

□

Extinction probability and time until extinction

Let $\tilde{\mathbf{q}}$ denote the extinction probability vector of the MBT under MRE, given the phase of the initial individual. It is defined by

$$\tilde{\mathbf{q}} = \lim_{t \rightarrow \infty} \tilde{\mathbf{F}}(t), \quad (7.7)$$

where $\tilde{\mathbf{F}}(t) = \tilde{F}(\mathbf{0}, t) \mathbf{1}$ is the distribution function of the time until extinction of the MBT under MRE.

Recall that in the standard case, the extinction equation $\mathbf{s} = \boldsymbol{\theta} + \Psi(\mathbf{s} \otimes \mathbf{s})$ relies on the assumption of independence between individuals, which does not hold anymore here. We can thus not characterize the extinction probability $\tilde{\mathbf{q}}$ as the minimal nonnegative solution of a simple fixed point equation.

Moreover, in a standard MBT, recall that the mean population size is given by $M^{(1)}(t) = e^{\Omega t}$, and the eigenvalue of maximal real part of Ω determines the criticality of the MBT (see Remark 5.2.7). Here, the usual almost sure extinction criteria do not hold anymore either.

Let us have a look at the mean population size given by (7.5). Recall that $\mu(\tilde{\mathcal{A}})$ denotes the eigenvalue of maximal real part of the matrix $\tilde{\mathcal{A}}$. When $t \rightarrow \infty$, we are led to three cases

$$\tilde{m}^{(1)}(\infty) = \begin{cases} \infty & \text{if } \mu(\tilde{\mathcal{A}}) > 0 \\ C & \text{if } \mu(\tilde{\mathcal{A}}) = 0 \\ 0 & \text{if } \mu(\tilde{\mathcal{A}}) < 0 \end{cases},$$

such that $0 < C < \infty$. It is still true that $\mu(\tilde{\mathcal{A}}) \leq 0$ implies the almost sure extinction of the process, but $\mu(\tilde{\mathcal{A}}) > 0$ does *not* necessarily imply that $\tilde{\mathbf{q}} < \mathbf{1}$; an MBT under MRE may eventually become extinct with probability one at the same time as its population explodes on the average, as we shall show on one example in Remark 7.3.3. The condition $\mu(\tilde{\mathcal{A}}) \leq 0$ is thus a *sufficient* but not necessary condition for almost sure extinction. Extinction criteria for an MBT under MRE are discussed in the next section.

The tools developed in Chapters 2 and 3 to evaluate the extinction probability may not be used in the present context. We thus propose other methods to numerically compute $\tilde{\mathbf{q}}$. The most direct method is to numerically solve the partial differential equation (7.1) for large values of t , at $\mathbf{s} = \mathbf{0}$, as suggested by (7.7). This is the object of Section 7.4.

However, we like to emphasize numerical methods which have a probabilistic interpretation in terms of the branching processes. We thus develop two other approaches to compute $\tilde{\mathbf{q}}$, using the MBT dynamic itself, and we give their physical interpretation in terms of the tree: we investigate iterative integral equations in Section 7.5, and we use the structured Markov chain approach in Section 7.6.

The numerical methods of Sections 7.4 and 7.5 may also be used to evaluate the distribution function $\tilde{\mathbf{F}}(t)$ of the time until extinction at any given time $t \geq 0$.

Total progeny size

The total progeny size in an MBT under MRE until time t is denoted by $\tilde{N}(t)$. In order to characterize the distribution of $\tilde{N}(t)$, given the initial phase of the MBT, we need to keep track of the current population size $\tilde{Z}(t)$ alongside the total progeny $\tilde{N}(t)$, because the rate of change of $\tilde{N}(t)$ depends on $\tilde{Z}(t)$.

The approach we use here differs from the one used in the standard case in Section 5.4, which was based on the independence assumption. We determine the forward Kolmogorov equations for the joint distribution of $(\tilde{Z}(t), \tilde{N}(t))$.

The joint probability generating function $\tilde{G}(\mathbf{s}, z, t)$ is an $n \times m$ matrix defined as

$$\tilde{G}_{ij}(\mathbf{s}, z, t) = \sum_{\mathbf{k} \geq \mathbf{0}} \sum_{\ell \geq \mathbf{k} \cdot \mathbf{1}} \mathbb{P}[(\tilde{Z}(t), \tilde{N}(t)) = (\mathbf{k}, \ell), \xi(t) = j | \varphi_0 = i] \mathbf{s}^{\mathbf{k}} z^{\ell}.$$

Proposition 7.2.5. *The forward Kolmogorov system of equations for the generating function $\tilde{G}(\mathbf{s}, z, t)$ of an MBT under MRE is*

$$\begin{aligned} \frac{\partial}{\partial t} \tilde{G}(\mathbf{s}, z, t) - \frac{\partial}{\partial \mathbf{s}^T} \tilde{G}(\mathbf{s}, z, t) \cdot A(\mathbf{s}, z) &= \tilde{G}(\mathbf{s}, z, t) \cdot Q, \\ \tilde{G}(\mathbf{s}, z, 0) &= z \mathbf{s} \cdot \boldsymbol{\pi}, \end{aligned} \quad (7.8)$$

where the $mn \times m$ matrix $A(\mathbf{s}, z) = \mathcal{D}[\mathbf{a}^{(1)}(\mathbf{s}, z) \cdots \mathbf{a}^{(m)}(\mathbf{s}, z)]$, and $\mathbf{a}^{(i)}(\mathbf{s}, z) = \mathbf{d}^{(i)} + D_0^{(i)} \mathbf{s} + z B^{(i)}(\mathbf{s} \otimes \mathbf{s})$, $i = 1, \dots, m$. \square

The proof is omitted since it is essentially the same as that for the population size generating function $\tilde{F}(\mathbf{s}, t)$.

We use the following notations for the $n \times 1$ factorial moments of $\tilde{N}(t)$

$$\tilde{\mathbf{m}}_k(t) = \frac{\partial^k}{(\partial z)^k} \tilde{G}(\mathbf{s}, z, t) |_{\mathbf{s}=\mathbf{1}, z=1} \cdot \mathbf{1}_m, \quad k \geq 1; \quad (7.9)$$

we shall also need the following factorial moments of size $n \times n$

$$\tilde{M}_0^{(1)}(t) = \tilde{M}^{(1)}(t), \quad \tilde{M}_k^{(1)}(t) = \frac{\partial^k}{(\partial z)^k} \frac{\partial}{\partial \mathbf{s}^T} \tilde{G}(\mathbf{s}, z, t) |_{\mathbf{s}=\mathbf{1}, z=1}, \quad (7.10)$$

for $k \geq 1$.

We easily derive a formula for the factorial moments $\tilde{\mathbf{m}}_k(t)$ from the partial differential equation (7.8).

Proposition 7.2.6. *The vectors $\tilde{\mathbf{m}}_k(t)$ ($k \geq 1$) are solutions of the following matrix differential equations, with initial conditions $\tilde{\mathbf{m}}_1(0) = \mathbf{1}_n$ and $\tilde{\mathbf{m}}_k(0) = \mathbf{0}_n$ for $k \geq 2$:*

$$\frac{d}{dt} \tilde{\mathbf{m}}_k(t) = k \tilde{M}_{k-1}^{(1)}(t) \mathcal{D}[B^{(1)} \mathbf{1}_{n^2} \cdots B^{(m)} \mathbf{1}_{n^2}] \mathbf{1}_m.$$

\square

We might as well obtain a recursive expression for the matrices $\tilde{M}_{k-1}^{(1)}(t)$ by successive derivatives of (7.8), but it would be quite involved and not very enlightening. Instead, we focus on the first moment $\tilde{\mathbf{m}}_1(t)$ of the total progeny until time t .

Recall from (7.3) and Corollary 7.2.4 that $\tilde{M}^{(1)}(u) = (\boldsymbol{\pi} \otimes I_n) e^{\tilde{\mathcal{A}}u}$, where $\tilde{\mathcal{A}}$ is given by (7.6). We have

$$\begin{aligned}\tilde{\mathbf{m}}_1(t) &= \mathbf{1} + \int_0^t \tilde{M}^{(1)}(u) du \mathcal{D}[B^{(1)} \mathbf{1}_{n^2} \cdots B^{(m)} \mathbf{1}_{n^2}] \mathbf{1}_m \\ &= \mathbf{1} + (\boldsymbol{\pi} \otimes I_n) \int_0^t e^{\tilde{\mathcal{A}}u} du \mathcal{D}[B^{(1)} \mathbf{1}_{n^2} \cdots B^{(m)} \mathbf{1}_{n^2}] \mathbf{1}_m.\end{aligned}$$

If $\tilde{\mathcal{A}}$ is nonsingular, then we obtain

$$\tilde{\mathbf{m}}_1(t) = \mathbf{1} + (\boldsymbol{\pi} \otimes I_n) (-\tilde{\mathcal{A}})^{-1} \left(I - e^{\tilde{\mathcal{A}}t} \right) \mathcal{D}[B^{(1)} \mathbf{1}_{n^2} \cdots B^{(m)} \mathbf{1}_{n^2}] \mathbf{1}_m.$$

When $t \rightarrow \infty$, we are led to two cases for the mean total progeny size

$$\tilde{\mathbf{m}}_1(\infty) = \begin{cases} \infty & \text{if } \mu(\tilde{\mathcal{A}}) > 0 \\ \mathbf{1} + (\boldsymbol{\pi} \otimes I_n) (-\tilde{\mathcal{A}})^{-1} \mathcal{D}[B^{(1)} \mathbf{1}_{n^2} \cdots B^{(m)} \mathbf{1}_{n^2}] \mathbf{1}_m & \text{if } \mu(\tilde{\mathcal{A}}) < 0 \end{cases}.$$

Recall that the first case does not exclude an almost sure extinction of the process. In the case $\mu(\tilde{\mathcal{A}}) < 0$, by some algebraic manipulations using the fact that $B^{(i)} \mathbf{1} = -D_0^{(i)} \mathbf{1} - \mathbf{d}^{(i)}$, we can rewrite the mean total progeny vector as

$$\tilde{\mathbf{m}}_1(\infty) = (\boldsymbol{\pi} \otimes I_n) (-\tilde{\mathcal{A}})^{-1} \mathcal{D}[\mathbf{d}^{(1)} \cdots \mathbf{d}^{(m)}] \mathbf{1}_m. \quad (7.11)$$

Mean behaviour

Despite their differences, we can construct a standard MBT which *on the average* behaves like an MBT under MRE, in the sense that the mean population sizes at any given time and the mean total progeny sizes coincide.

Suppose that the MBT under MRE has n phases and that the environment is defined on m states. Then, the corresponding standard MBT has mn phases, which are the pairs (i, j) , for $1 \leq i \leq m$, $1 \leq j \leq n$. It is exactly as if each individual had *its own* random environment, and thus all individuals behave independently of each others. Then, an individual is in the state (i, j) if the random environment which controls its life is in state i , and the individual itself is in the “physical” phase j .

We shall introduce a notation to decompose the birth rates matrix B of an MBT with entries $B_{i,jk}$, $i, j, k = 1, 2, \dots, n$: let the $n \times n$ block matrix $B(j)$ be defined as $[B(j)]_{ik} = B_{i,jk}$. Consequently, we can write $B = [B(1), \dots, B(n)]$.

The parameters of the “equivalent” standard MBT are

$$\begin{aligned}\mathbf{d}' &= \mathcal{D}[\mathbf{d}^{(1)} \cdots \mathbf{d}^{(m)}] \mathbf{1}_m, \\ D'_0 &= \mathcal{D}[D_0^{(1)} \cdots D_0^{(m)}] + (Q \otimes I_n),\end{aligned}$$

and, since the environmental state does not change at the time of a birth, the only nonzero entries in B' are the entries

$$B'_{(\ell,i),(\ell,j)(\ell,k)} = B_{i,jk}^{(\ell)}.$$

We can thus write $B' = \mathcal{D}[\mathcal{B}^{(1)} \cdots \mathcal{B}^{(m)}]$ where $\mathcal{B}^{(i)}$ is an $n \times n^2 m$ matrix defined by

$$\mathcal{B}^{(i)} = [0_{n \times n(i-1)} B^{(i)}(1) 0_{n \times n(m-1)} B^{(i)}(2) 0_{n \times n(m-1)} \cdots B^{(i)}(n) 0_{n \times n(m-i)}], \quad (7.12)$$

where the 0 blocks have the size indicated by their subscript.

As a result, the matrix $\Omega' = D'_0 + B'(\mathbf{1} \oplus \mathbf{1})$ of the standard MBT coincides with the matrix $\tilde{\mathcal{A}}$ defined in (7.6). The matrix of mean population size at time t in the standard MBT is $M^{(1)}(t) = e^{\tilde{\mathcal{A}}t}$ by (5.13), and the mean total progeny size vector in the subcritical case is $\mathbf{D}^{(1)} = (-\tilde{\mathcal{A}})^{-1} \mathcal{D}[d^{(1)} \cdots d^{(m)}] \mathbf{1}_{mn}$ by (5.32). If we only care about the physical phase of the individuals, we do obtain (7.5) and (7.11) respectively.

It would be interesting to investigate if the mean of other transient measures, such as the mean time until extinction, or the mean time to reach k individuals, are the same in the MBT under MRE and in the standard MBT with parameters \mathbf{d}' , D'_0 and B' .

Illustrations

Example 7.2.7. Let us illustrate this section with an example of MBT with $n = 3$ phases. This is a highly simplified version of the demographic application, and we assume that it evolves under a MRE with $m = 2$ states.

In order to simplify the discussion, we suppose here that the lifetime of an individual is made up of three phases: the first one represents childhood and has a mean length of 15 years, the second one represents the only fertile period and has a mean length of 35 years, and the last one lasts 33 years on average.

In the first state of the MRE, the rates are those of a subcritical country comparable to Belgium

$$\mathbf{d}^{(1)} = \begin{bmatrix} 4 \cdot 10^{-4} \\ 8 \cdot 10^{-4} \\ 3 \cdot 10^{-2} \end{bmatrix}, D_0^{(1)} = \begin{bmatrix} * & 1/15 & \\ & * & 1/35 \\ & & * \end{bmatrix}, B_{2,12}^{(1)} = 2.5 \cdot 10^{-2},$$

the other entries of $B^{(1)}$ being zero.

The second state of the environment positively influences the growth of the population; there, the MBT evolves with parameters $\mathbf{d}^{(2)}$, $D_0^{(2)}$, and $B^{(2)}$, where the infant mortality is reduced by a factor 0.75, that is $d_1^{(2)} = 4 \cdot 10^{-4}(1 - 0.75)$, and the fertility rate is parameterized by a factor $p \geq 0$: $B_{2,12}^{(2)} = 2.5 \cdot 10^{-2}(1 + p)$.

The generator of the MRE is given by

$$Q = \begin{bmatrix} -\kappa/2 & \kappa/2 \\ \kappa & -\kappa \end{bmatrix},$$

so that the stationary distribution of the MRE is $\boldsymbol{\pi} = [2/3, 1/3]$, independently of the value of κ .

We represent on Figure 7.2 the mean total family size as a function of time, if the process starts with one individual in phase 1 in the stationary state of the MRE. We choose $\kappa = 1/5$, and three different values for the parameter p , leading to sensibly

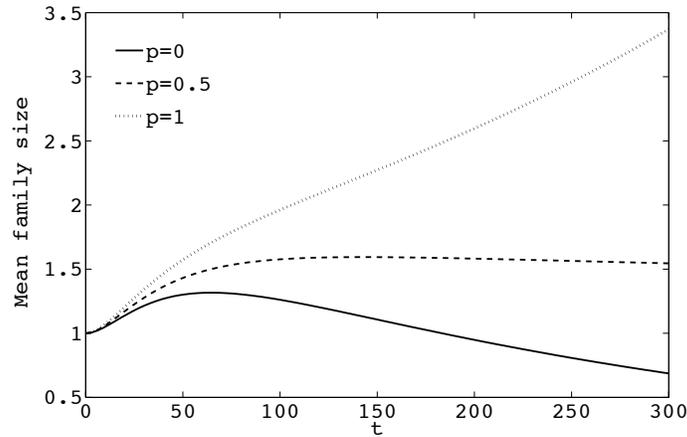


Figure 7.2: Mean family size of an MBT under MRE with $\kappa = 1/5$, and three different values of the parameter p .

different behaviours. Indeed, we observe that for $p = 1$, the expected population size explodes, for $p = 0.5$, it decreases slowly, and for $p = 0$, it decreases rapidly.

Next, we fix $p = 1$ and we let κ vary between 10^{-6} and 10^2 ; our objective is to measure how the speed of environmental changes affects the system dynamics, keeping constant the proportion of time spent in each environmental state.

We show on Figure 7.3 the mean total progeny size after 100 years as a function of the logarithm of κ , if the process starts with one child at time 0. Six curves are represented: lines 1 and 2 represent the total progeny size if the MBT always evolves with parameters $d^{(i)}, D_0^{(i)},$ and $B^{(i)}$, for $i = 1$ and 2 respectively; the curves 3 and 4 show the evolution of the total progeny size if the MRE starts in state 1 and 2 of the environment respectively; the curve 5 represents the situation where the initial state of the environment is chosen with its stationary distribution π , and finally, the curve 6 represents the total progeny size in a standard MBT evolving with the average parameters $\mathbf{d} = \pi_1 \mathbf{d}^{(1)} + \pi_2 \mathbf{d}^{(2)}, D_0 = \pi_1 D_0^{(1)} + \pi_2 D_0^{(2)},$ and $B = \pi_1 B^{(1)} + \pi_2 B^{(2)}$.

We observe that if κ is large, then the environment changes rapidly, and the system behaves like a standard MBT with the average parameters. On the other hand, if κ is small, then the environment stays for long periods in the same state, which influences the behaviour of the system: for $\kappa < 10^{-2}$, we can expect that the first environmental change occurs on the average after 100 years, so that the system is almost completely decomposed into two different processes corresponding to each environmental state.

7.3 Extinction criteria

Extinction criteria have been widely investigated in the literature on branching processes in random environments. These criteria depend both on the type of branching

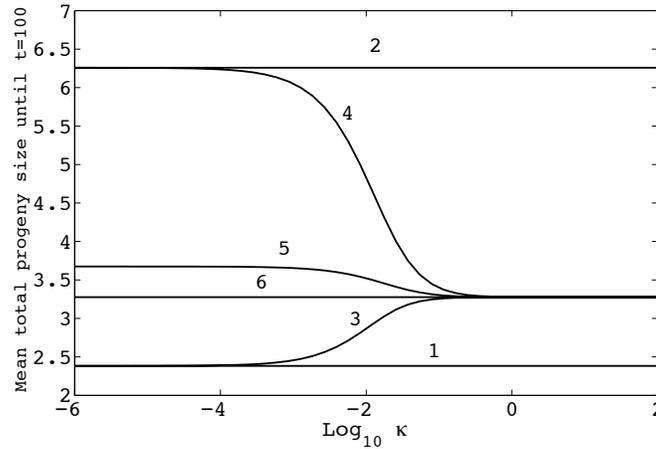


Figure 7.3: Mean total progeny size after $t = 100$ years in an MBT under MRE with $p = 1$, as a function of the parameter κ .

process and of random environment which are considered. Indeed, we distinguish between discrete-time or continuous-time, one-type or multitype branching processes, and independent identically distributed (i.i.d.) or stationary ergodic random environments. In our case, we deal with the continuous-time stationary ergodic case.

Recall from Section 1.5 that an MBT may be seen as a multitype branching process, where the *types* correspond to the *phases* of the MBT. In this section we do not make any difference between the two terminologies. We successively consider the one-type and the multitype cases.

When $n = 1$, the MBT is exponential with parameters $d^{(i)} = \mu^{(i)}$, $B^{(i)} = \lambda^{(i)}$, and $D_0^{(i)} = -\mu^{(i)} - \lambda^{(i)}$, $i = 1, 2, \dots, m$. Then, $\Omega^{(i)} = \omega^{(i)} = \lambda^{(i)} - \mu^{(i)}$.

If the initial distribution of the Markovian environmental process is its stationary distribution π , this immediately implies that the Markovian environmental process is stationary and ergodic (Karlin and Taylor [37, Chapter 9]). We can then follow for instance Cogburn and Torrez [15] to conclude with the following criterion

Corollary 7.3.1. *The extinction probability of an exponential MBT under MRE with stationary distribution π is equal to one if and only if*

$$\sum_{i=1}^m \pi_i \omega^{(i)} \leq 0.$$

□

This result may also be derived from the extinction criteria for a *discrete-time* branching process in random environment. Recall that in the standard case, the average

number $m(k)$ of offsprings per individual in the k th generation is actually independent of k ($m = m(k)$), and determines the criticality of the process: it eventually becomes extinct with probability one if and only if $m \leq 1$.

For a branching process in random environment, the mean progenies $\{m(k)\}_{k \geq 0}$ constitute a random sequence, and if the random environment is i.i.d. or stationary ergodic, so is that sequence. The value $E[\log m(0)]$ now decides the criticality of a population. Indeed, the asymptotic growth rate of a population is given by

$$\lim_{k \rightarrow \infty} [m(0)m(1) \cdots m(k-1)]^{\frac{1}{k}}.$$

We have

$$[m(0)m(1) \cdots m(k-1)]^{\frac{1}{k}} = e^{\frac{1}{k}(\log m(0) + \log m(1) + \cdots + \log m(k-1))},$$

and by the Law of Large Numbers for the stationary ergodic sequence $\{\log m(k)\}$,

$$\lim_{k \rightarrow \infty} \frac{1}{k}(\log m(0) + \log m(1) + \cdots + \log m(k-1)) = E[\log m(0)].$$

The asymptotic growth rate is thus $\exp(E[\log m(0)])$, and the branching process is subcritical if $E[\log m(0)] < 0$, critical if $E[\log m(0)] = 0$, or supercritical if $E[\log m(0)] > 0$.

In the i.i.d case, Smith and Wilkinson [64] show that $E[\log m(0)] \leq 0$ is a necessary and sufficient condition for the almost sure extinction of the discrete-time branching process in random environment. Athreya and Karlin [5] show that this criterion still holds in the stationary and ergodic case, provided $E[\log m(0)]^+ < \infty$ and $E[\log m(0)]^- < \infty$.

In order to use this criterion, we need to discretize the continuous-time exponential MBT under MRE. One way to proceed is to uniformize the Markovian environmental process $\xi(t)$ (see for instance [47, Page 57]).

Let $c = \max_{1 \leq i \leq m} |Q_{ii}|$; take a Poisson process of rate c and denote by $0 = t_0, t_1, t_2, \dots$ the epochs of events in that process, and by $\tau_i = t_i - t_{i-1}$ ($i \geq 1$) the intervals of time between events. The τ_i 's are i.i.d. and follow an exponential law with parameter c .

Define the discrete-time Markov chain $\{\bar{\xi}_k : k \in \mathbb{N}\}$ with transition matrix $K = (1/c)Q + I$, and the discrete-time branching process $\bar{Z}_k = \bar{Z}(t_k)$. The stationary distribution π of K is the same as that of the continuous-time Markovian process $\xi(t)$. The Markov chain $\bar{\xi}_k$ with initial distribution π is thus stationary and ergodic.

Conditionally given $\bar{\xi}_k$ and τ_{k+1} , the mean progeny of an individual from generation k in the discrete-time branching process is $m(k) = \exp(\omega^{(\bar{\xi}_k)} \tau_{k+1})$. Therefore, $m(k)$ is random through two components, namely the state of the Markov chain at time k , and the time interval τ_{k+1} . The random environment is thus twofold and characterized by $(\bar{\xi}_k, \tau_{k+1})$, $k \geq 0$, which is still a stationary ergodic sequence.

If we apply the result mentioned above, we find that the extinction of an exponential MBT under MRE is certain if and only if

$$0 \geq E[\log m(0)] = \sum_{j=1}^m \pi_j E[\log \exp(\omega^{(j)} \tau_1)] = \sum_{j=1}^m \pi_j \omega^{(j)} E[\tau_1],$$

which is equivalent to $0 \geq \sum_{j=1}^m \pi_j \omega^{(j)}$, and we prove in this way the statement of Corollary 7.3.1.

Let us now investigate the almost sure extinction criteria in the multitype case, that is for an MBT with $n \geq 2$ phases. We return again to extinction criteria for discrete-time branching processes in random environment.

We now denote by $A(k)$ the mean progeny matrix of an individual from generation k . The asymptotic growth rate of a population is then determined by

$$\lim_{k \rightarrow \infty} \|A(0)A(1) \cdots A(k-1)\|^{\frac{1}{k}} = \lim_{k \rightarrow \infty} e^{\frac{1}{k} \log \|A(0)A(1) \cdots A(k-1)\|}.$$

If the sequence $\{A(k)\}_{k \geq 0}$ is stationary ergodic, then

$$\lim_{k \rightarrow \infty} k^{-1} \log \|A(0)A(1) \cdots A(k-1)\|$$

exists with probability one, and

$$\begin{aligned} & \lim_{k \rightarrow \infty} k^{-1} \log \|A(0)A(1) \cdots A(k-1)\| \\ &= \lim_{k \rightarrow \infty} \mathbb{E}(k^{-1} \log \|A(0)A(1) \cdots A(k-1)\|) = \eta \end{aligned}$$

with probability one for any matrix norm, where η is a constant (Kingman, [41]).

We use again the uniformization technique to discretize the MBT, and we define the discrete-time multitype branching process $\bar{\mathbf{Z}}_k = \tilde{\mathbf{Z}}(t_k)$. Conditionally given $\bar{\xi}_k$ and τ_{k+1} , the mean progeny matrix of an individual from generation k in this process is $A(k) = \exp(\Omega^{(\bar{\xi}_k)} \tau_{k+1})$.

We now refer to Tanny [67], who proves that the extinction of a discrete-time multitype branching process in a stationary ergodic random environment is certain if and only if $\eta \leq 0$, under the following regularity assumptions

- (i) $\mathbb{E}(\log^+ \|A(0)\|) < \infty$;
- (ii) there exist integers $K > 0$, $1 \leq \ell \leq n$ such that

$$\mathbb{P} \left[\min_{1 \leq i, j \leq n} (A(0)A(1) \cdots A(K-1))_{ij} > 0 \right] = 1$$

and

$$\mathbb{E}[\log(1 - \mathbb{P}[(\bar{\mathbf{Z}}_K)_\ell = 0 \mid \bar{\mathbf{Z}}_0 = \mathbf{e}_\ell, \bar{\xi}])] < \infty,$$

where $\bar{\xi} = \{(\bar{\xi}_k, \tau_{k+1})\}_{k \geq 0}$ is an environmental sequence;

- (iii) the multitype branching process in random environment is *strongly regular*, that is there exists a positive integer K such that

$$\mathbb{P} \left[\min_i \mathbb{P}(\bar{\mathbf{Z}}_K \mathbf{1} > 1 \mid \bar{\mathbf{Z}}_0 = \mathbf{e}_i, \bar{\xi}) > 0 \right] > 0.$$

We can assume that conditions (i)–(iii) are satisfied for the discrete-time process \bar{Z}_k . Indeed, (i) roughly supposes a finite mean progeny, (ii) corresponds to an irreducibility assumption for the process \bar{Z}_k , and (iii) asks that, given the environmental sequence, the process \bar{Z}_k must be able to grow from each initial type. We then have the following result

Corollary 7.3.2. *Under conditions (i)–(iii), the extinction of an MBT under MRE is almost sure if and only if*

$$\lim_{k \rightarrow \infty} \frac{1}{k} E \log \| e^{\Omega^{(\bar{\epsilon}_0)} \tau_1} e^{\Omega^{(\bar{\epsilon}_1)} \tau_2} \dots e^{\Omega^{(\bar{\epsilon}_{k-1})} \tau_k} \| \leq 0, \quad (7.13)$$

where τ_k is exponentially distributed with parameter c for $k \geq 1$. \square

In this case, the difficulty lies in computing the limit in (7.13). Notice that the random matrices $e^{\Omega^{(\bar{\epsilon}_k)} \tau_{k+1}}$ do not necessarily commute. So far, we have not been able to simplify the expression of the limit. One way to determine its value is to run simulations.

Remark 7.3.3. Recall from Section 7.1 that the condition $\mu(\tilde{\mathcal{A}}) \leq 0$ is a sufficient but not necessary condition for the almost sure extinction of the process. In the case $n = 1$, $\tilde{\mathcal{A}} = \text{diag}[\omega^{(i)}] + Q$, and we can find examples where

$$\sum_{i=1}^m \pi_i \omega^{(i)} \leq 0 < \mu(\tilde{\mathcal{A}})$$

so that extinction is almost sure, and the mean size of the exponential MBT grows to infinity at the same time. Take for instance

$$Q = \begin{bmatrix} -5 & 5 \\ 3 & -3 \end{bmatrix}$$

so that $\boldsymbol{\pi} = [0.375, 0.625]$, and $\lambda^{(1)} = 8$, $\mu^{(1)} = 4$, $\lambda^{(2)} = 2$, $\mu^{(2)} = 12$, so that $\omega^{(1)} = 4$ and $\omega^{(2)} = -10$. We have then $\sum_{i=1}^m \pi_i \omega^{(i)} = -4.75$ and $\mu(\tilde{\mathcal{A}}) = 0.1414$.

We now turn to numerical methods to compute the extinction probability vector $\tilde{\boldsymbol{q}}$. This is the object of the next three sections.

7.4 Numerical partial differential equations

In this section, we investigate numerical methods inspired from well-known techniques in numerical analysis to solve the partial differential system (7.1) for the population size generating function $\tilde{F}(\mathbf{s}, t)$. This is the fruit of a collaboration with Pauline Lafitte from the University of Lille 1.

The aim here is to give the reader an insight of methods other than probabilistic ones to efficiently compute the distribution of the time until extinction and the extinction probability of an MBT under MRE.

We focus on the one-phase case, the multiphase case being still a work in progress.

In the one-phase case, the generating function $\tilde{\mathbf{F}}(s, t)$ is a $1 \times m$ vector, where recall that m is the number of states of the Markovian environmental process. The partial differential system becomes

$$\frac{\partial}{\partial t} \tilde{\mathbf{F}}(s, t) - \frac{\partial}{\partial s} \tilde{\mathbf{F}}(s, t) \cdot A(s) = \tilde{\mathbf{F}}(s, t) \cdot Q, \quad (7.14)$$

$$\tilde{\mathbf{F}}(s, 0) = s \boldsymbol{\pi}, \quad (7.15)$$

where the $m \times m$ matrix $A(s) = \mathcal{D}[a^{(1)}(s) \cdots a^{(m)}(s)]$, and $a^{(i)}(s) = \mu^{(i)} - (\lambda^{(i)} + \mu^{(i)})s + \lambda^{(i)}s^2$, for $i = 1, \dots, m$. This is a *hyperbolic* system of partial differential equations with *variable coefficients* $A(s)$ and *source terms* $\tilde{\mathbf{F}}(s, t) \cdot Q$ (see Leveque [50]).

We define a grid of points in the two-dimensional plane (s, t) , for $-1 \leq s \leq 1$ and $t \geq 0$, that approximates our domain and at which we shall evaluate $\tilde{\mathbf{F}}(s, t)$. Let $\Delta s = 2/J$, where J is an even positive integer representing the total number of space steps, and let Δt be another positive number which denotes the time step.

The grid is defined by the points $(s_k, t^n) = (-1 + k \Delta s, n \Delta t)$, where k and n are integers such that $0 \leq k \leq J$ and $n \geq 0$. The particular value $s = 0$ corresponds to the point s_k with $k = J/2$. We use the notation $\tilde{\mathbf{F}}_k^n$ for a numerical approximation of $\tilde{\mathbf{F}}(s_k, t^n)$.

We would like to compute the successive approximations of the distribution of the time until extinction $\tilde{\mathbf{F}}(0, t^n) \mathbf{1}$ for $n \geq 0$, that is, $\tilde{q}^n = \tilde{\mathbf{F}}_{J/2}^n \mathbf{1}$, and its limit $\tilde{q} = \tilde{q}^\infty$, giving the extinction probability. In practice, we iterate \tilde{q}^n for $n \geq 0$ with one of the methods proposed below, until some time step t^{n^*} such that $|\tilde{q}^{n^*} - \tilde{q}^{n^*-1}| < \epsilon$ for a fixed error ϵ .

Numerical methods are usually developed for homogeneous partial differential equations. In order to numerically solve a non-homogeneous system such as (7.14), a standard approach is to use a *fractional step* method, in which we alternate between solving the associated homogeneous partial differential system

$$\frac{\partial}{\partial t} \tilde{\mathbf{F}}(s, t) - \frac{\partial}{\partial s} \tilde{\mathbf{F}}(s, t) \cdot A(s) = 0, \quad (7.16)$$

and solving the ordinary differential system involving the source term

$$\frac{\partial}{\partial t} \tilde{\mathbf{F}}(s, t) = \tilde{\mathbf{F}}(s, t) \cdot Q, \quad (7.17)$$

see [50, Chapter 17].

The time step is then split into $t^n \rightarrow t^{n+\frac{1}{2}}$ and $t^{n+\frac{1}{2}} \rightarrow t^{n+1}$, respectively corresponding to the treatment of parts (7.16) and (7.17). We thus start by computing $\tilde{\mathbf{F}}(s, t^{\frac{1}{2}})$ from (7.16) with the initial condition (7.15); then, we compute $\tilde{\mathbf{F}}(s, t^1)$ from (7.17) with the initial condition $\tilde{\mathbf{F}}(s, t^{\frac{1}{2}})$ obtained at the previous stage. Next, we

calculate $\tilde{\mathbf{F}}(s, t^{1+\frac{1}{2}})$ from (7.16) with the initial condition $\tilde{\mathbf{F}}(s, t^1)$, and then $\tilde{\mathbf{F}}(s, t^2)$ from (7.17) with the initial condition $\tilde{\mathbf{F}}(s, t^{1+\frac{1}{2}})$, and so on.

The first system (7.16) is solved using a numerical scheme for homogeneous partial differential equations; in this section, we present two techniques, the *finite difference* methods, and the *semi-Lagrangian* method.

The second system (7.17) is usually solved using a numerical scheme for ordinary differential equations, such as the forward Euler method. Here, the differential system can be solved explicitly, so that no numerical scheme is actually required.

Notice that splitting the equation in this manner introduces some error of order Δt , no matter how well we approximate the subproblems at each step.

The resulting method is summarized in Algorithm 7.4.1, where the intermediate stage $\tilde{\mathbf{F}}_k^{n+\frac{1}{2}}$ depends on the numerical technique used to solve the homogeneous part (7.16), and is specified through the discussion.

The finite difference methods

The basic idea of finite difference methods is to replace derivatives by finite differences, which can be done in many ways. The homogeneous system (7.16) may be solved using any of the following schemes of order $O(\Delta t) + O(\Delta s)$, see for instance Thomas [69]:

- the *forward-time forward-space* scheme if $A(s_k) > 0$:

$$\tilde{\mathbf{F}}_k^{n+1} = \tilde{\mathbf{F}}_k^n + \frac{\Delta t}{\Delta s} (\tilde{\mathbf{F}}_{k+1}^n - \tilde{\mathbf{F}}_k^n) A(s_k) \quad (7.18)$$

- the *forward-time backward-space* scheme if $A(s_k) < 0$:

$$\tilde{\mathbf{F}}_k^{n+1} = \tilde{\mathbf{F}}_k^n + \frac{\Delta t}{\Delta s} (\tilde{\mathbf{F}}_k^n - \tilde{\mathbf{F}}_{k-1}^n) A(s_k). \quad (7.19)$$

In order for a finite difference scheme to converge when Δs and Δt tend to 0, the space and time steps must be related by a condition needed to have the stability of the method [50, Chapter 4]. This necessary condition is called the Courant-Friedrichs-Lewy (CFL) condition, and is as follows: for a scheme to be stable, ν must be smaller than 1, where

$$\nu = \frac{\Delta t}{\Delta s} \max_{-1 \leq s \leq 1} \max_{1 \leq i \leq m} |\lambda_i(s)|,$$

and the $\lambda_i(s)$ ($1 \leq i \leq m$) are the eigenvalues of $A(s)$. In other words, by the diagonal structure of $A(s)$, one must have

$$\max_{1 \leq i \leq m} |a^{(i)}(s_k)| \Delta t \leq \Delta s$$

for all values of s_k in the domain of computation.

In practice, we thus choose Δs as small as possible (taking a large number J of space steps), and we take

$$\Delta t = \Delta s / \max_{i,k} |a^{(i)}(s_k)|. \quad (7.20)$$

Algorithm 7.4.1 Algorithm to compute the extinction probability \tilde{q} of an exponential MBT under MRE.

```

 $\tilde{\mathbf{F}}_k^0 := s_k \boldsymbol{\pi}, \quad 0 \leq k \leq J$ 
 $\tilde{q}^0 := \tilde{\mathbf{F}}_{J/2}^0 \mathbf{1}$ 
for  $n = 0$  to  $n^* - 1$  do
   $\tilde{\mathbf{F}}_k^{n+\frac{1}{2}} := (7.21), \text{ or } (7.25)$ 
   $\tilde{\mathbf{F}}_k^{n+1} := \tilde{\mathbf{F}}_k^{n+\frac{1}{2}} e^{Q\Delta t}, \quad 1 \leq k \leq J - 1$ 
   $\tilde{\mathbf{F}}_0^{n+1} := \tilde{\mathbf{F}}_1^{n+1}$ 
   $\tilde{\mathbf{F}}_J^{n+1} := \boldsymbol{\pi}$ 
   $\tilde{q}^{n+1} := \tilde{\mathbf{F}}_{J/2}^{n+1} \mathbf{1}.$ 
end for
 $\tilde{q} := \tilde{q}^{n^*}$ 

```

We can combine (7.18) and (7.19) in one unique scheme including a discussion on the sign of $A(s_k)$. For that purpose, define the function $\text{sign}(x)$ which is equal to -1 if $x < 0$, to 0 if $x = 0$, and to $+1$ if $x > 0$. Then, for any matrix A , $\text{sign}(A) = (\text{sign}(A_{ij}))$. We obtain the numerical scheme described by Algorithm 7.4.1 with

$$\begin{aligned} \tilde{\mathbf{F}}_k^{n+\frac{1}{2}} := \tilde{\mathbf{F}}_k^n + \frac{1}{2} \frac{\Delta t}{\Delta s} & \left[(\tilde{\mathbf{F}}_{k+1}^n - \tilde{\mathbf{F}}_k^n) \cdot |\text{sign}[-A(s_k)] - I| \cdot A(s_k) \right. \\ & \left. + (\tilde{\mathbf{F}}_k^n - \tilde{\mathbf{F}}_{k-1}^n) \cdot |\text{sign}[-A(s_k)] + I| \cdot A(s_k) \right]. \end{aligned} \quad (7.21)$$

From now on, we call this scheme the *upwind* scheme.

Remark 7.4.1. In the multiphase case $n \geq 2$, we need to define a grid in a space of dimension $n + 1$ (n dimensions for the space variable, and one dimension for the time variable). The generalization of the finite difference methods is more difficult to carry out, the notions of *forward-* and *backward-space* being more complex than in the one-phase case.

The semi-Lagrangian method

First, notice that, thanks to the diagonal structure of the matrix $A(s)$, the homogeneous system (7.16) is decomposed into m independent scalar partial differential equations, one for each entry of the vector function $\tilde{\mathbf{F}}(s, t)$:

$$\frac{\partial}{\partial t} \tilde{F}_i(s, t) - \frac{\partial}{\partial s} \tilde{F}_i(s, t) \cdot a^{(i)}(s) = 0, \quad 1 \leq i \leq m. \quad (7.22)$$

Each unknown function $\tilde{F}_i(s, t)$ is actually constant along a particular curve including the point (s, t) , parameterized by $(X_i(\tau; s, t), \tau)$ and satisfying the ordinary differential equation

$$\frac{\partial}{\partial \tau} X_i(\tau; s, t) = -a^{(i)}(X_i(\tau; s, t)), \quad (7.23)$$

with $X_i(t; s, t) = s$. Indeed, if $\tilde{F}_i(s, t)$ satisfies (7.22), then for all (s_0, t_0) ,

$$\begin{aligned} \frac{\partial}{\partial \tau} \tilde{F}_i(X_i(\tau; s_0, t_0), \tau) &= \frac{\partial}{\partial s} \tilde{F}_i(X_i(\tau; s_0, t_0), \tau) \frac{\partial}{\partial \tau} X_i(\tau; s_0, t_0) \\ &\quad + \frac{\partial}{\partial t} \tilde{F}_i(X_i(\tau; s_0, t_0), \tau) \\ &= -\frac{\partial}{\partial s} \tilde{F}_i(X_i(\tau; s_0, t_0), \tau) a^{(i)}(X_i(\tau; s_0, t_0)) \\ &\quad + \frac{\partial}{\partial t} \tilde{F}_i(X_i(\tau; s_0, t_0), \tau) \\ &= 0. \end{aligned}$$

Such a curve is called a *characteristic curve*, see [53].

We may thus write $\tilde{F}_i(s, t) = \tilde{F}_i(X_i(\tau; s, t), \tau)$ for all $\tau \geq 0$. In particular, if we know the characteristic curves $X_i(\tau; s, t)$, then the solution of (7.22) with the initial condition $\tilde{F}_i(s, 0) = s \pi_i$ is given by

$$\tilde{F}_i(s, t) = \tilde{F}_i(X_i(\tau; s, t), \tau) = \tilde{F}_i(X_i(0; s, t), 0) = X_i(0; s, t) \pi_i.$$

It turns out that in the exponential MBT case, (7.23) is a Riccati differential equation that may be solved explicitly, and we obtain

$$X_i(\tau; s, t) = 1 + \frac{(\mu^{(i)} - \lambda^{(i)})(s - 1)}{\lambda^{(i)}(s - 1) + (\mu^{(i)} - \lambda^{(i)}s) \exp[(\mu^{(i)} - \lambda^{(i)})(t - \tau)]}$$

if $\lambda^{(i)} \neq \mu^{(i)}$, and

$$X_i(\tau; s, t) = 1 + \frac{(s - 1)}{1 - \lambda^{(i)}(t - \tau)(s - 1)}$$

if $\lambda^{(i)} = \mu^{(i)}$. Notice that, since the functions $a^{(i)}(\cdot)$ do not depend on the time variable, the functions $X_i(\tau; s, t)$ actually only depend on the difference $t - \tau$, so that, in particular, $X_i(\tau; s, t) = X_i(0; s, t - \tau)$.

We use the idea described above to construct a scheme which computes $\tilde{F}_i(s, t)$ along the characteristic curves. Suppose that we know some approximations $(\tilde{F}_i)_k^n$ of $\tilde{F}_i(s, t)$ at a fixed time t^n , for each space value s , that is for all $0 \leq k \leq J$. We can then write for the next time step, for $0 \leq k \leq J$,

$$\begin{aligned} (\tilde{F}_i)_k^{n+1} &= \tilde{F}_i(s_k, t^{n+1}) \\ &= \tilde{F}_i(X_i(\tau; s_k, t^{n+1}), \tau) \quad \text{for all } \tau \geq 0 \\ &= \tilde{F}_i(X_i(t^n; s_k, t^{n+1}), t^n) \\ &= \tilde{F}_i(X_i(0; s_k, \Delta t), t^n) \\ &= (\tilde{F}_i)_{[X_i(0; s_k, \Delta t)]}^n, \end{aligned}$$

where the function

$$[v] := \arg \min_j |v - s_j| \tag{7.24}$$

returns the index of the closest space grid point to the value v . A piecewise constant interpolation is thus implicitly assumed, since we set

$$\tilde{F}_i(X_i(0; s_k, \Delta t), t^n) = \tilde{F}_i(s_{[X_i(0; s_k, \Delta t)]}, t^n).$$

The resulting scheme

$$(\tilde{F}_i)_k^{n+1} = (\tilde{F}_i)_{[X_i(0; s_k, \Delta t)]}^n, \quad 1 \leq i \leq m, \quad 0 \leq k \leq J$$

is called the *semi-Lagrangian* method, see for instance Falcone and Ferretti [19, 20] and Strain [66]. Using this method to solve the homogeneous part (7.16), we thus obtain Algorithm 7.4.1 with

$$\tilde{\mathbf{F}}_k^{n+\frac{1}{2}} = \left[(\tilde{F}_1)_{[X_1(0; s_k, \Delta t)]}^n, (\tilde{F}_2)_{[X_2(0; s_k, \Delta t)]}^n, \dots, (\tilde{F}_m)_{[X_m(0; s_k, \Delta t)]}^n \right]. \quad (7.25)$$

Unlike with the finite difference methods, the CFL condition is not required for the convergence of the semi-Lagrangian scheme applied to the homogeneous equation (7.16).

However, there are difficulties: on the one hand, Falcone and Ferretti [19] show that the upper bound of the L^∞ -norm of the error between the approximation and the exact value grows proportionally with the number of timesteps used and the impact of the interpolation error. Therefore, the time step Δt must actually not be chosen too small, as we are interested in the solution for large values of time.

On the other hand, recall that the splitting in the fractional step method introduces some errors that depend on the time step Δt , so that Δt must not be taken too large either.

The difficulty encountered when using this method thus lies in the optimal choice of the time step Δt ; so far, no theoretical rule exists.

Numerical examples

Let us apply the two methods on two examples of exponential MBT under MRE. In the first example, the system is subcritical, in the second one it is supercritical.

Example 7.4.2. Take the subcritical MBT under MRE discussed in Remark 7.3.3 whose mean population size explodes as the time goes to infinity; recall that the parameters are $\lambda^{(1)} = 8$, $\mu^{(1)} = 4$, $\lambda^{(2)} = 2$, $\mu^{(2)} = 12$, and

$$Q = \begin{bmatrix} -5 & 5 \\ 3 & -3 \end{bmatrix},$$

so that $\boldsymbol{\pi} = [0.375, 0.625]$.

The curve denoted A on Figure 7.4 represents the approximations \tilde{q}^n obtained with the upwind scheme for $J = 5 \cdot 10^2$ and $\Delta t = 1.43 \cdot 10^{-4}$ given by (7.20). The results obtained with the semi-Lagrangian method for $J = 7 \cdot 10^5$ and $\Delta t = 0.1$ perfectly coincide and are not depicted.

As discussed above, the optimal choice of the time step Δt in the semi-Lagrangian method is not well-defined yet. We show on Figure 7.5 the approximations of the

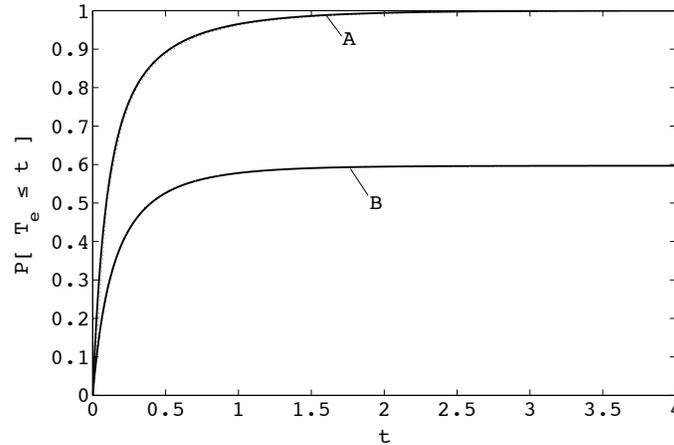


Figure 7.4: Distribution of the time until extinction of two exponential MBTs. The curve A corresponds to a subcritical MBT, and the curve B to a supercritical MBT

extinction probability computed with this method, as a function of the time step. This clearly illustrates that the time step must not be too small, and, as expected, not too large either. We heuristically see that the optimal time step is $\Delta t \approx 0.1$.

Example 7.4.3. Take now a supercritical MBT under MRE with parameters $\lambda^{(1)} = 8$, $\mu^{(1)} = 4$, $\lambda^{(2)} = 2$, $\mu^{(2)} = 8$, and

$$Q = \begin{bmatrix} -1 & 1 \\ 10 & -10 \end{bmatrix},$$

so that $\pi = [0.9091, 0.0909]$. The curve B plotted on Figure 7.4 represents the approximations \tilde{q}^n obtained with the upwind scheme for $J = 3 \cdot 10^3$ and $\Delta t = 2.78 \cdot 10^{-5}$ provided by (7.20). The semi-Lagrangian method for $J = 7 \cdot 10^5$ and $\Delta t = 0.05$ again produces the same curve. The extinction probability obtained with the upwind method is $\tilde{q} = 0.5968$, and with the semi-Lagrangian method, we get $\tilde{q} = 0.5965$.

7.5 Integral equations approach

We propose now two recursive integral equations for the generating function of the population size, which have a probabilistic interpretation. They may be used to develop other numerical methods to compute the extinction probability of an MBT under MRE.

We compute the extinction probability in a context where we impose constraints on the number of environmental changes, in the same manner as, in Chapter 2, we computed the extinction probability by setting constraints on the shape of the tree.

Both integral equations are interesting because the first one also provides us with the distribution of the time until extinction, while the second one allows us to compute

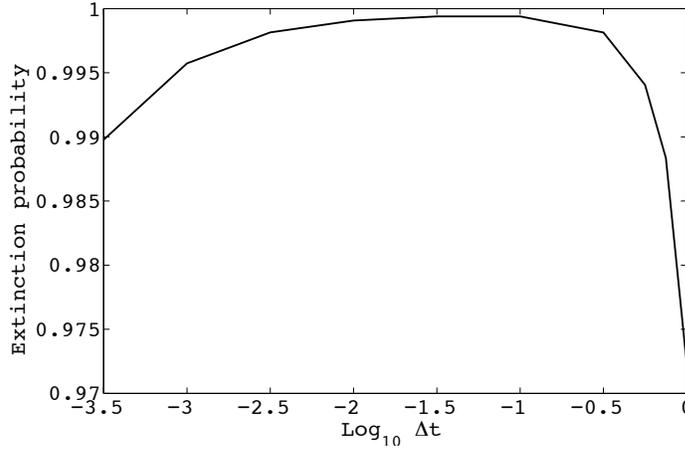


Figure 7.5: Approximations of \tilde{q} using the semi-Lagrangian method as a function of the time step Δt .

the distribution of the total number of environmental changes before extinction, given extinction occurs.

First, let $N(t)$ denote the number of transitions occurring in the Markov environmental process during the time interval $[0, t[$. The probability generating function of the population size at time t in the MBT under MRE on the paths with at most n environmental transitions is defined as

$$(\tilde{F}_n)_{ij}(\mathbf{s}, t) = \sum_{\mathbf{k} \geq \mathbf{0}} P[\tilde{\mathbf{Z}}(t) = \mathbf{k}, \xi(t) = j, N(t) \leq n \mid \varphi_0 = i] \mathbf{s}^{\mathbf{k}}.$$

Recall that $\boldsymbol{\pi}$ is the initial probability vector of the environmental process. For $1 \leq j \leq m$, let $\mathbf{F}^{(j)}(\mathbf{s}, t)$ denote the $n \times 1$ probability generating function of the population size at time t in the standard MBT evolving with parameters $\mathbf{d}^{(j)}$, $D_0^{(j)}$, and $B^{(j)}$, which is supposed to be known (see Section 5.2). We then have

$$(\tilde{F}_0)_{ij}(\mathbf{s}, t) = F_i^{(j)}(\mathbf{s}, t) \pi_j e^{Q_{jj} t};$$

indeed, with probability $\pi_j e^{Q_{jj} t}$, $\xi(0) = j$ and no environmental transition occurred before time t ; in that case, the population size at time t is that of a standard MBT evolving with parameters $\mathbf{d}^{(j)}$, $D_0^{(j)}$, and $B^{(j)}$.

For $n \geq 1$, the generating function $\tilde{F}_n(\mathbf{s}, t)$ satisfies the integral recursive equation

$$\begin{aligned} (\tilde{F}_n)_{ij}(\mathbf{s}, t) &= (\tilde{F}_0)_{ij}(\mathbf{s}, t) \\ &+ \int_0^t \sum_{k \neq j} (\tilde{F}_{n-1})_{ik} \left(\mathbf{F}^{(j)}(\mathbf{s}, t-u), u \right) Q_{kj} e^{Q_{jj}(t-u)} du. \end{aligned} \quad (7.26)$$

This is obtained by decomposing on the time of the *last* environmental transition before time t . Indeed, either at time t , no environmental transition has occurred yet, which is

recorded by the first term $(\tilde{F}_0)_{ij}(\mathbf{s}, t)$. Or at some time u in $(0, t)$, the environmental process makes a transition from k to j , which happens with probability $Q_{kj} du$, and then it makes no further transition in (u, t) with probability $e^{Q_{jj}(t-u)}$. At time u , there was at most $n-1$ environmental changes, which is recorded by $\tilde{F}_{n-1}(\cdot, u)$, and in (u, t) , the individuals evolve independently with parameters $\mathbf{d}^{(j)}$, $D_0^{(j)}$, and $B^{(j)}$, which is recorded by $\mathbf{F}^{(j)}(\mathbf{s}, t-u)$.

Taking the limit for $n \rightarrow \infty$ in (7.26), we obtain the implicit solution

$$\tilde{F}_{ij}(\mathbf{s}, t) = F_i^{(j)}(\mathbf{s}, t) \pi_j e^{Q_{jj}t} + \int_0^t \sum_{k \neq j} \tilde{F}_{ik}(\mathbf{F}^{(j)}(\mathbf{s}, t-u), u) Q_{kj} e^{Q_{jj}(t-u)} du$$

of the partial differential equation (7.1) with initial condition $\tilde{F}_{ij}(\mathbf{s}, 0) = s_i \pi_j$.

Let $\tilde{\mathbf{q}}_n(t) = \tilde{F}_n(\mathbf{0}, t) \mathbf{1}$ be the probability that, at time t , the MBT under MRE is extinct, and that at most n environmental transitions have occurred. The distribution $\tilde{\mathbf{F}}(t) = \mathbb{P}[T_e \leq t \mid \varphi_0]$ of the time until extinction is obtained as $\tilde{\mathbf{F}}(t) = \lim_{n \rightarrow \infty} \tilde{\mathbf{q}}_n(t)$, and the extinction probability is then given by $\tilde{\mathbf{q}} = \lim_{t \rightarrow \infty} \tilde{\mathbf{F}}(t)$.

In order to study the convergence properties of $\tilde{F}_n(\mathbf{s}, t)$ to $\tilde{F}(\mathbf{s}, t)$, we define the norm of the approximation error at time t as

$$\tilde{e}_n(t) = \sup_{0 \leq s \leq 1} \|\tilde{F}_n(\mathbf{s}, t) - \tilde{F}(\mathbf{s}, t)\|, \quad n \geq 0, \quad (7.27)$$

where $\|\cdot\|$ denotes any matrix norm.

We have

$$\sup_{0 \leq s \leq 1} \left\| \tilde{F}_n(\mathbf{F}^{(j)}(\mathbf{s}, t-u), u) - \tilde{F}(\mathbf{F}^{(j)}(\mathbf{s}, t-u), u) \right\| \leq \tilde{e}_n(t), \quad (7.28)$$

independently of j . Using for instance the L^∞ -norm and setting $\Lambda = \text{diag}(Q)$, we can thus write $\tilde{e}_0(t) \leq 2$ for all $t \geq 0$, and using (7.26) and (7.28) for $n \geq 1$,

$$\tilde{e}_n(t) \leq \int_0^t \tilde{e}_{n-1}(u) \|Q - \Lambda\| \|e^{\Lambda(t-u)}\| du.$$

Define $-q_0 = \max_j Q_{jj}$. We have $\|e^{\Lambda(t-u)}\|_\infty = e^{-q_0(t-u)}$, and we get

$$\tilde{e}_n(t) \leq \|Q - \Lambda\| \int_0^t \tilde{e}_{n-1}(u) e^{-q_0(t-u)} du.$$

We then show by induction on n that

$$\tilde{e}_n(t) \leq 2 \left(\frac{\|Q - \Lambda\|}{q_0} \right)^n e^{-q_0 t} \left[e^{q_0 t} - \sum_{i=0}^{n-1} \frac{(q_0 t)^i}{i!} \right], \quad n \geq 1.$$

The factor in square brackets is the remainder of the Taylor expansion of $e^{q_0 t}$, and thus by the Taylor-Lagrange formula, we have for $n \geq 1$

$$\tilde{e}_n(t) \leq 2 \frac{(\|Q - \Lambda\|t)^n}{n!} e^{-q_0(t-\zeta)},$$

where $0 < \zeta < t$.

The *root-convergence factor*, or *R-factor*, is defined as

$$\tilde{R}(t) = \limsup_{n \rightarrow \infty} \tilde{e}_n(t)^{\frac{1}{n}}. \quad (7.29)$$

Using the Stirling formula $n! \sim \sqrt{2\pi n}(n/e)^n$, we get $\tilde{R}(t) = 0$ for all $t \geq 0$, which indicates that the convergence of the sequence $\tilde{F}_n(\mathbf{s}, t)$ is *R-superlinear* (Ortega and Rheinboldt [58]).

In practice, we choose some errors ϵ_1 and ϵ_2 , we compute the time T such that the probability of extinction after time T of any of the standard MBTs with parameters $(\mathbf{d}^{(j)}, D_0^{(j)}, B^{(j)})$ ($j = 1, \dots, m$) is smaller than ϵ_1 , that is

$$T = \max_{1 \leq j \leq m} T_j \quad \text{with} \quad T_j = \inf \left\{ t \geq 0 : \|\mathbf{q}^{(j)} - \mathbf{F}^{(j)}(\mathbf{0}, t)\| < \epsilon_1 \right\},$$

and we compute $\tilde{\mathbf{q}}_n(t)$ for $0 \leq t \leq T$, for successive values of n , until some n^* such that $\|\tilde{\mathbf{q}}_{n^*}(T) - \tilde{\mathbf{q}}_{n^*-1}(T)\|_\infty < \epsilon_2$. We then have the following approximations

$$\begin{aligned} \tilde{\mathbf{F}}(t) &\approx \tilde{\mathbf{q}}_{n^*}(t) \quad 0 \leq t \leq T, \\ \tilde{\mathbf{q}} &\approx \tilde{\mathbf{q}}_{n^*}(T). \end{aligned}$$

Another approach is based on examining the process at the times $\{\theta_n\}_{n \geq 1}$ of the successive environmental transitions. The probability generating function of the population size at the time of the n th environmental transition is defined as

$$(\tilde{\varphi}_n)_{ij}(\mathbf{s}) = \sum_{\mathbf{k} \geq \mathbf{0}} \text{P}[\tilde{\mathbf{Z}}(\theta_n) = \mathbf{k}, \xi(\theta_n^+) = j \mid \varphi_0 = i] \mathbf{s}^{\mathbf{k}}.$$

We have $(\tilde{\varphi}_0)_{ij}(\mathbf{s}) = \tilde{F}_{ij}(\mathbf{s}, 0) = s_i \pi_j$, and for $n \geq 1$, the generating function $\tilde{\varphi}_n(\mathbf{s})$ satisfies the integral recursive equation

$$(\tilde{\varphi}_n)_{ij}(\mathbf{s}) = \int_0^\infty \sum_{k \neq j} (\tilde{\varphi}_{n-1})_{ik} \left(\mathbf{F}^{(k)}(\mathbf{s}, u) \right) e^{Q_{kk} u} Q_{kj} du. \quad (7.30)$$

This integral equation is obtained by conditioning on the time interval $u = \theta_n - \theta_{n-1}$ between the $(n-1)$ th and the n th environmental transition. Indeed, the population at the n th environmental transition is made up of the descendants of individuals living at the $(n-1)$ th environmental transition, which evolve independently with parameters $\mathbf{d}^{(k)}, D_0^{(k)}$, and $B^{(k)}$ during a time interval u exponentially distributed with parameter $-Q_{kk}$, if the state of the environmental process at time θ_{n-1}^+ is k .

The probability that the process eventually becomes extinct with at most n environmental transitions is equivalent to the probability that the process gets extinct before the $(n+1)$ th transition, and is given by $\tilde{\mathbf{q}}_n = \tilde{\varphi}_{n+1}(\mathbf{0}) \mathbf{1}$, $n \geq 0$. The extinction probability is then given by $\tilde{\mathbf{q}} = \lim_{n \rightarrow \infty} \tilde{\mathbf{q}}_n$.

By its probabilistic interpretation, the convergence of the sequence is ensured, but the convergence rate is not easily obtained. Define the approximation error by $\tilde{e}_n =$

$\sup_{0 \leq s \leq 1} \|\tilde{\varphi}_n(\mathbf{s}) - \tilde{\varphi}_\infty(\mathbf{s})\|$, where $\tilde{\varphi}_\infty(\mathbf{s}) = \tilde{\mathbf{q}} \cdot \boldsymbol{\pi}$ for $\mathbf{s} < \mathbf{1}$ (and $\tilde{\varphi}_n(\mathbf{1}) = \mathbf{1} \cdot \boldsymbol{\pi}$ for all $n \geq 0$). One shows that

$$\tilde{e}_n \leq \frac{\|Q - \Lambda\|}{q_0} \tilde{e}_{n-1},$$

for $n \geq 1$, which is unfortunately not useful here since $\|Q - \Lambda\|_\infty / q_0 \geq 1$, and we can generally not tell much about other norms.

In practice, we fix some errors ϵ_1 and ϵ_2 . The upper bound in the integral (7.30) is replaced by T^* such that

$$T^* = \inf \left\{ u \geq 0 : \max_j \left(\sum_{k \neq j} e^{Q_{kk} u} Q_{kj} \right) < \epsilon_1 \right\}.$$

We then compute $\tilde{\mathbf{q}}_n$ until some n^* such that $\|\tilde{\mathbf{q}}_{n^*} - \tilde{\mathbf{q}}_{n^*-1}\|_\infty < \epsilon_2$, and we obtain

$$\tilde{\mathbf{q}} \approx \tilde{\mathbf{q}}_{n^*}.$$

Once we know the sequence $\tilde{\mathbf{q}}_n$ and its limit $\tilde{\mathbf{q}}$, we can compute the conditional cumulated distribution of the total number of environmental transitions before extinction, given that extinction occurs. Recall that E denotes the extinction event. Then,

$$\mathbb{P}[N(T_e) \leq n \mid E, \varphi_0 = i] = \frac{(\tilde{q}_n)_i}{\tilde{q}_i}.$$

Numerical examples

In order to evaluate the functions $\tilde{F}_n(\mathbf{s}, t)$ for $0 \leq t \leq T$ and $\tilde{\varphi}_n(\mathbf{s})$ at $\mathbf{s} = \mathbf{0}$, we divide the space hypercube $[0, 1]^n$ and the time interval $[0, T]$ in cells, which form a grid in the $(n + 1)$ -dimensional space, and we numerically compute these functions at each grid point, in the same spirit as for the numerical resolution of partial differential equations in the previous section. We use the trapezoid rule to evaluate the integrals in (7.26) and (7.30).

Example 7.5.1. Take the supercritical MBT with $n = 1$ phase evolving under a MRE with $m = 2$ states from Example 7.4.3. On Figure 7.6, we show the successive approximations of the extinction probability when the initial state of the environment is chosen with its stationary distribution $\boldsymbol{\pi} = [0.9091, 0.0909]$. The plain curve is obtained with the first integral equation approach, that is $\tilde{\mathbf{q}}_n(T) = \tilde{F}_n(0, T) \mathbf{1}$. The waves in the curve clearly show the changes of dynamics when passing from one state of the environment to the other one. The dashed curve is computed with the second integral equation approach, that is $\tilde{\mathbf{q}}_n = \tilde{\varphi}_{n+1}(\mathbf{0}) \mathbf{1}$. The conditional mean number of environmental changes before extinction, given that extinction occurs, is $\mathbb{E}[N(T_e) \mid E] = 0.69$.

7.6 Structured Markov chain approach

Recall from Section 6.1 that a standard MBT may be seen as a level-dependent QBD $\{(X(t), \boldsymbol{\varphi}(t)) : t \in \mathbb{R}^+\}$, where the level $X(t)$ is the total number of individuals living at time t , and the phase $\boldsymbol{\varphi}(t) = \mathbf{Z}(t)$ is the population in each phase at time t .

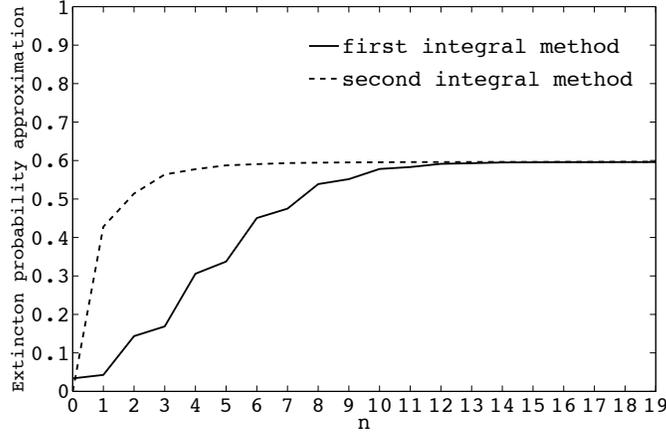


Figure 7.6: Approximations of the extinction probability using the two integral equation approaches.

An MBT under MRE may likewise be represented by a level-dependent QBD $\{(\tilde{X}(t), \tilde{\varphi}(t)) : t \in \mathbb{R}^+\}$, where the level $\tilde{X}(t)$ is still the total number of individuals living at time t , and $\tilde{\varphi}(t) = (\xi(t), \tilde{Z}(t))$, the first entry being the state of the Markovian environmental process at time t , and $\tilde{Z}(t)$ being the population in each phase at time t .

The phase space at level k is thus

$$\tilde{L}(k) = \{(i, S_1, S_2, \dots, S_n) : S_1 + S_2 + \dots + S_n = k, S_j \geq 0, 1 \leq j \leq n, 1 \leq i \leq m\}, \quad (7.31)$$

and it is of cardinality $|\tilde{L}(k)| = m \binom{k+n-1}{n-1}$.

The generator of this level-dependent QBD is

$$\tilde{Q} = \begin{bmatrix} Q & 0 & 0 & 0 & 0 & \dots \\ \tilde{A}_{-1}^{(1)} & \tilde{A}_0^{(1)} & \tilde{A}_1^{(1)} & 0 & 0 & \dots \\ 0 & \tilde{A}_{-1}^{(2)} & \tilde{A}_0^{(2)} & \tilde{A}_1^{(2)} & 0 & \dots \\ 0 & 0 & \tilde{A}_{-1}^{(3)} & \tilde{A}_0^{(3)} & \tilde{A}_1^{(3)} & \dots \\ & & \vdots & & & \ddots \end{bmatrix}.$$

The block matrices $\tilde{A}_{-1}^{(k)}$, $\tilde{A}_0^{(k)}$ and $\tilde{A}_1^{(k)}$ ($k \geq 1$) are constructed as follows. Let $A_{-1}^{(k)(i)}$, $A_0^{(k)(i)}$, and $A_1^{(k)(i)}$ be the block matrices of the level-dependent QBD associated with the standard MBT with parameters $\mathbf{d}^{(i)}$, $D_0^{(i)}$ and $B^{(i)}$, for $i = 1, 2, \dots, m$. Then, for $k \geq 1$,

$$\begin{aligned} \tilde{A}_{-1}^{(k)} &= \mathcal{D}[A_{-1}^{(k)(1)} \dots A_{-1}^{(k)(m)}] \\ \tilde{A}_0^{(k)} &= \mathcal{D}[A_0^{(k)(1)} \dots A_0^{(k)(m)}] + (Q \otimes I) \\ \tilde{A}_1^{(k)} &= \mathcal{D}[A_1^{(k)(1)} \dots A_1^{(k)(m)}], \end{aligned} \quad (7.32)$$

where the identity matrix appearing in (7.32) is of size $\binom{k+n-1}{n-1} \times \binom{k+n-1}{n-1}$.

If the random environment starts with the initial distribution $\boldsymbol{\pi}$, then the extinction probability of the MBT under MRE is given by

$$\tilde{q} = (\boldsymbol{\pi} \otimes I_n) G_1 \mathbf{1}_m,$$

where G_1 is the $mn \times m$ matrix of first passage probabilities from level 1 to level 0 defined in Section 6.2, that we compute for instance with the algorithm L presented in that section.

Remark 7.6.1. The structured Markov chain approach also allows to compute some additional measures about MBTs under MRE, such as the maximum number of individuals, the mean time until extinction, and the mean time to reach k individuals; we refer to Sections 6.3 to 6.5.

Numerical examples

We illustrate the use of the structured Markov chain approach to compute the extinction probability of an MBT under MRE on three examples.

Example 7.6.2. Take the supercritical exponential MBT under MRE with $m = 2$ from Example 7.4.3. We use the algorithm L to compute $\tilde{q} = \boldsymbol{\pi} G_1 \mathbf{1}$. As stopping criterion, we ask that the difference between two successive approximations is less than 10^{-7} . The algorithm converges with $M = 579$ iterations and $\tilde{q} = 0.5965$, which is in accord with the results obtained by the upwind and the semi-Lagrangian methods in Section 7.4.

Example 7.6.3. Consider a second example with $n = m = 2$, and the following parameters

$$\mathbf{d}^{(1)} = \begin{bmatrix} 6 \\ 8 \end{bmatrix}, D_0^{(1)} = \begin{bmatrix} -18 & 5 \\ 3 & -16 \end{bmatrix}, B^{(1)} = \begin{bmatrix} 0 & 0 & 2.1 & 4.9 \\ 0 & 0 & 2.5 & 2.5 \end{bmatrix},$$

$$\mathbf{d}^{(2)} = \begin{bmatrix} 20 \\ 1 \end{bmatrix}, D_0^{(2)} = \begin{bmatrix} -120.5 & 0.5 \\ 0.5 & -2.5 \end{bmatrix}, B^{(2)} = \begin{bmatrix} 100 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}.$$

The change of parameters from one state of the environment to the other one are rather significant. In the first state of the environment, the MBT is subcritical. In the second state, the MBT is supercritical, the first phase has now a very high birth rate, and the second phase has low birth and death rates. The transition rates between the two phases is also lower. The corresponding extinction probability is $\mathbf{q}^{(2)} = [0.2023, 0.571]^T$.

The generator of the Markovian random environment is

$$Q = \begin{bmatrix} -10 & 10 \\ \kappa & -\kappa \end{bmatrix},$$

and depends on one parameter κ . The objective here is to measure how the mean sojourn time in the second state influences the global extinction probability of the MBT.

We show on Figure 7.7 the extinction probability \tilde{q} obtained using the algorithm L , as a function of κ which varies between 0 and 250. We stopped after $M = 60$ iterations, because the picture has become obvious enough; the L^∞ -norm between two successive approximations is then of order 10^{-4} . We see that when $\kappa = 0$, the environmental process stays indefinitely in state 2, and thus $\tilde{q} = \mathbf{q}^{(2)}$; when κ increases, the length of the visit to state 2 decreases, and the extinction probability \tilde{q} converges to $\mathbf{q}^{(1)} = \mathbf{1}$.

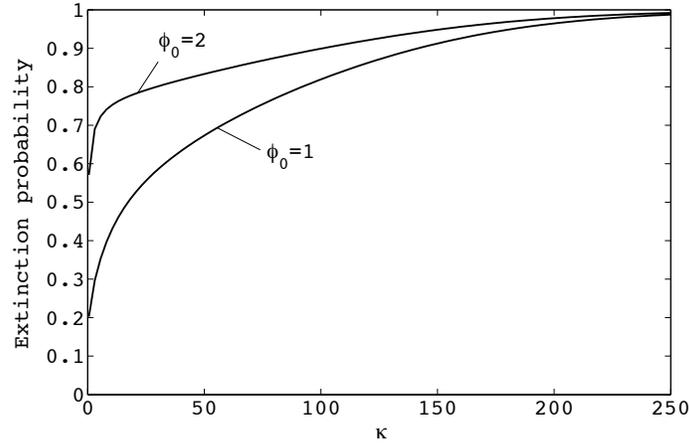


Figure 7.7: Extinction probability of the MBT under MRE as a function of the parameter κ .

Example 7.6.4. Let us return to the MBT from Example 7.2.7 which models the evolution of a feminine family under the influence of a MRE with two states.

Our interest here is in the extinction probability of this family. The third phase which has a fertility rate equal to zero is thus not useful anymore, and we can bring the last two phases together, thereby obtaining the following parameters corresponding to the first environmental state

$$\mathbf{d}^{(1)} = \begin{bmatrix} 4 \cdot 10^{-4} \\ 1.5 \cdot 10^{-2} \end{bmatrix}, D_0^{(1)} = \begin{bmatrix} * & 1/15 \\ & * \end{bmatrix}, B_{2,12}^{(1)} = 0.012,$$

the other entries of the matrix $B^{(1)}$ being zero.

For the second environmental state, $D_0^{(2)} = D_0^{(1)}$, $B_{2,12}^{(2)} = 0.012(1 + p)$, for $p \geq 0$, and

$$\mathbf{d}^{(2)} = \begin{bmatrix} 4 \cdot 10^{-4} (1 - 0.75) \\ 1.5 \cdot 10^{-2} \end{bmatrix}.$$

The MRE is characterized by the following generator

$$Q = \begin{bmatrix} -1/10 & 1/10 \\ \kappa & -\kappa \end{bmatrix}.$$

Thus the mean time spent in the first state of the environment is set at ten years, and the mean time spent in the second state of the environment is given by $1/\kappa$.

We first take $\kappa = 1/5$, and we compute the probability that the family generated by a first child eventually becomes extinct with a maximal size M , as a function of M , for four values of p ; this is shown on Figure 7.8.

Then, we plot on Figure 7.9 the evolution of the extinction probability of the family generated by a first child as a function of the parameter $0 \leq p \leq 3$, for three values of the parameter κ . We stopped the iterations at $M = 60$ again. As expected, the greater the value of p , and the longer the time interval spent in the state 2 of the environmental process, the lower the extinction probability of the system.

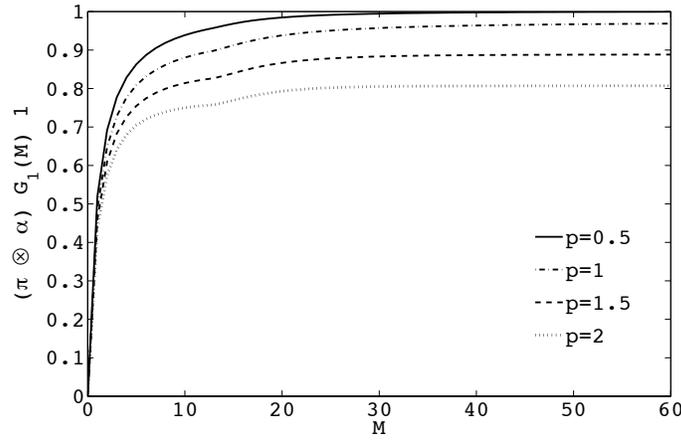


Figure 7.8: Probability that the process eventually becomes extinct with a maximal population size M , as a function of M , for four values of p .

7.7 Comparison of the methods

The three types of numerical methods proposed in the previous sections to evaluate the extinction probability of an MBT under MRE are rather difficult to compare since they are based on completely different approaches. We summarize below their principal characteristics.

Upwind method

- It is developed for $n = 1$, and seems rather involved to generalize to $n \geq 2$.
- The input is the number J of space steps. The time step is given by the CFL condition.
- The k th step provides an approximation of $\tilde{F}(s, t^k)$ for $s \in [-1, 1]$.
- No probabilistic interpretation can be given to the algorithm.

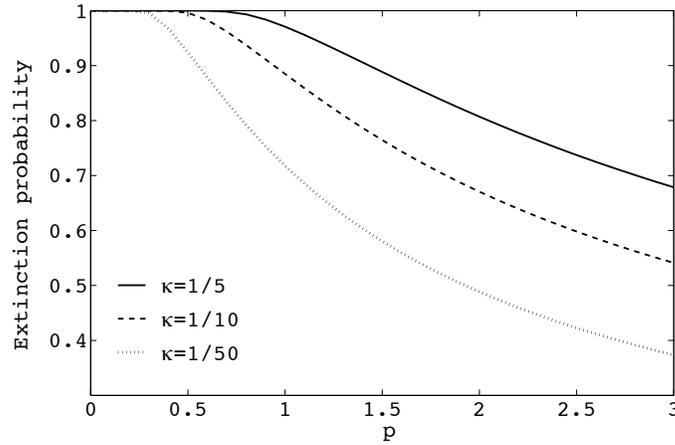


Figure 7.9: Extinction probability of the MBT under MRE as a function of the parameter p , for three values of κ .

- The numerical complexity of each iteration is $(m^2 + 10m)J$.

Semi-Lagrangian method

- It is developed for $n = 1$ and might be generalized to $n \geq 2$ rather easily.
- The input is the number J of space steps. However, the time step is not well-defined. Finally, one needs to know the characteristic curves.
- The k th step provides an approximation of $\tilde{F}(s, t^k)$ for $s \in [-1, 1]$.
- No probabilistic interpretation can be given to the algorithm.
- The numerical complexity of each iteration is $(m^2 + m)J$.

First integral equation approach

- It is developed for $n \geq 1$.
- The input is the number J of space steps per dimension, and the number N of time steps. It assumes the knowledge of the functions $F^{(i)}(\mathbf{s}, t)$ for $i = 1, \dots, m$.
- The k th step gives an approximation of $\tilde{F}_k(\mathbf{s}, t)$ for $\mathbf{s} \in [0, 1]^n$ and $0 \leq t \leq T$, where T is estimated with some fixed error ε .
- There is a probabilistic interpretation to the algorithm.
- The dominant term of the numerical complexity of each iteration is $m(m-1)n(N-2)(N-1)J^n$.

Second integral equation approach

- It is developed for $n \geq 1$.
- The input is the number J of space steps per dimension, and the number N of time steps for the numerical computation of the integral, of which the upper bound is evaluated with some error ε . It assumes the knowledge of the functions $F^{(i)}(\mathbf{s}, t)$ for $i = 1, \dots, m$.
- The k th step gives an approximation of $\tilde{\varphi}_k(\mathbf{s})$ for $\mathbf{s} \in [0, 1]^n$.
- There is a probabilistic interpretation to the algorithm.
- The dominant term of the numerical complexity of each iteration is $m(m - 1)n(3N + 1)J^n$.

Structured Markov chain approach

- It is developed for $n \geq 1$.
- It assumes the knowledge of the generator \tilde{Q} .
- The k th step computes $G_1(k)$.
- There is a probabilistic interpretation to the algorithm.
- The numerical complexity increases with the iterations. The dominant terms of the numerical complexity at the k th iteration are $2f_{n,m}(k)^3 + 2f_{n,m}(k)^2 f_{n,m}(k + 1)$, with $f_{n,m}(k) = m \binom{k+n-1}{n-1}$.

We end by comparing in Table 7.1 the CPU time needed to evaluate the extinction probability \tilde{q} of the supercritical MBT from Example 7.4.3 with the five methods; we stopped the iterations as soon as the difference between two successive approximations became less than 10^{-7} (in L^∞ -norm). For the two integral equation methods, the CPU time is decomposed in two parts: the first term corresponds to the time needed to evaluate the functions $F^{(i)}(\mathbf{s}, t)$ at each space and time points for $i = 1, \dots, m$, and the second term corresponds to the iteration itself.

Method	Input	CPU time
Upwind	$J = 3 \cdot 10^3$	272.16
Semi-Lagrangian	$J = 7 \cdot 10^5, \Delta t = 5 \cdot 10^{-2}$	14.87
First integral	$J = 189, N = 700, \varepsilon = 10^{-5}$	18.45 + 3941.14
Second integral	$J = 750, N = 7 \cdot 10^5, \varepsilon = 10^{-15}$	3904.39 + 404.47
Structured Markov chain	—	0.71

Table 7.1: Comparison of the CPU time (in seconds) for the five methods.

CHAPTER 8

Catastrophes

A population may undergo external catastrophes killing a random number of individuals; some examples are earthquakes, floods, wars, or epidemics. We may thus ask how these disasters increase the extinction probability of the population.

This last chapter is devoted to the analysis of MBTs with constant parameters which undergo catastrophes occurring at the event epochs of a Markovian arrival process. We assume that the impact of a catastrophe on an individual depends on the phase of the individual.

As for an MBT under random environment, the individuals do not behave independently of each others anymore. The analysis of both types of external influences is very similar, and we thus keep exactly the same structure as in the previous chapter, as well as the same notations with a change of accents, replacing tildes by hats.

The different approaches to compute transient features and the extinction probability of an MBT undergoing catastrophes are the same as those described in the previous chapter, and are thus generally neither justified, nor detailed anymore.

We emphasize the main differences with the random environments. These lie for example in the form of the source term in the partial differential system satisfied by the population size distribution, in the extinction criteria that we derive from those in the random environment case, and in the structured Markov chain approach.

8.1 Definition

Consider an irreducible MAP $\{(M(t), \phi_c(t)), t \in \mathbb{R}^+\}$ with m phases and transition rates matrices A_0 and A_1 (see Section 1.3).

Suppose that the MAP evolves independently of an MBT with n phases and pa-

rameters \mathbf{d} , D_0 , and B . It is reasonable to assume that the external MAP started far in the past; we thus take for initial distribution vector $\boldsymbol{\alpha}$ its stationary distribution, that is, the unique solution of $\boldsymbol{\alpha} A = \mathbf{0}$, $\boldsymbol{\alpha} \mathbf{1} = 1$, where $A = A_0 + A_1$; this simplifies matters in a few places.

We associate with each observable event in the external MAP a phenomenon called a *catastrophe* which kills a random number of living individuals in the MBT: an individual in phase i at the catastrophe epoch survives with probability δ_i , or is killed with the complementary probability $\varepsilon_i = 1 - \delta_i$. We gather these probabilities in the vectors $\boldsymbol{\delta}$ and $\boldsymbol{\varepsilon}$ and we set $\Delta = \text{diag}(\boldsymbol{\delta})$.

An illustration of a catastrophe process affecting an MBT is shown in Figure 8.1.

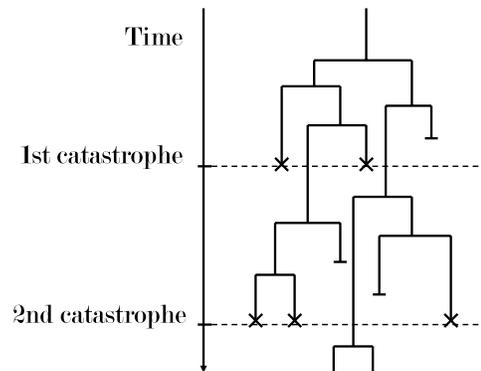


Figure 8.1: Example of path of an MBT undergoing a catastrophe process

A particular case is when $m = 1$: catastrophes then occur following a Poisson process with parameter β , that is $\boldsymbol{\alpha} = \mathbf{1}$, $A_0 = -\beta$ and $A_1 = \beta$. We refer to that case as the $\text{Poisson}(\beta)$ catastrophe case; it will sometimes be more convenient to work with this simpler case.

Like in an MBT under MRE, unless we condition on the sequence of catastrophe instants, the individuals in an MBT with catastrophes do not behave independently of each other, because different lines of descendants experience catastrophes exactly at the same epochs. However, between two catastrophes events, individuals evolve independently.

8.2 Transient features

Population size

Suppose there are n phases in the MBT, and m states in the MAP controlling the catastrophes arrivals. Let $\hat{\mathbf{Z}}(t) = [\hat{Z}_1(t), \hat{Z}_2(t), \dots, \hat{Z}_n(t)]^T$ denote the population size vector at time t of the MBT with catastrophes. We define the $n \times m$ generating

function $\hat{F}(\mathbf{s}, t)$ of $\hat{\mathbf{Z}}(t)$, given the initial phase of the MBT, jointly with the state of the catastrophic MAP at time t , as

$$\hat{F}_{ij}(\mathbf{s}, t) = \sum_{\mathbf{k} \geq \mathbf{0}} \mathbb{P}[\hat{\mathbf{Z}}(t) = \mathbf{k}, \phi_c(t) = j | \varphi_0 = i] \mathbf{s}^{\mathbf{k}}, \quad 1 \leq i \leq n, 1 \leq j \leq m.$$

Consequently, $\hat{F}(\mathbf{1}, t) = (\mathbf{1} \otimes \boldsymbol{\alpha})$, as $\mathbb{P}[\phi_c(t) = j] = (\boldsymbol{\alpha} e^{A t})_j = \alpha_j$.

The following theorem is equivalent to Theorem 7.2.1. We indicate the major dissimilarity after its statement.

Theorem 8.2.1. *The forward Kolmogorov system of equations for the generating function $\hat{F}(\mathbf{s}, t)$ of an MBT with catastrophes is*

$$\begin{aligned} \frac{\partial}{\partial t} \hat{F}(\mathbf{s}, t) - \frac{\partial}{\partial \mathbf{s}^T} \hat{F}(\mathbf{s}, t) (I_m \otimes \mathbf{a}(\mathbf{s})) \\ &= \hat{F}(\mathbf{s}, t) A_0 + \hat{F}(\Delta \mathbf{s} + \boldsymbol{\varepsilon}, t) A_1, \\ \hat{F}(\mathbf{s}, 0) &= \mathbf{s} \cdot \boldsymbol{\alpha}, \end{aligned} \quad (8.1)$$

where $\mathbf{a}(\mathbf{s}) = \mathbf{d} + D_0 \mathbf{s} + B(\mathbf{s} \otimes \mathbf{s})$. \square

Notice the right-hand side of (8.1), which makes the main difference with (7.1) in the MRE case, and with (5.1) in the standard case. This time, the external influence affects the variable \mathbf{s} of the generating function, becoming $\Delta \mathbf{s} + \boldsymbol{\varepsilon}$, which is the generating function of the indicator that an individual survives a catastrophe.

We now extract the factorial moments of the population size from (8.1). The k th factorial moments of $\hat{\mathbf{Z}}(t)$ are defined as in (7.2) and (7.3), and the following properties are the analogues of Proposition 7.2.3 and Corollary 7.2.4.

Proposition 8.2.2. *The matrices $\hat{M}^{(k)}(t)$, for $k \geq 1$, are solutions of*

$$\begin{aligned} \frac{d}{dt} \hat{M}^{(k)}(t) &= \hat{M}^{(k)}(t) [(I_m \otimes \Omega \otimes I_{n^{k-1}}) A(k) + (A_0 \otimes I_{n^k}) + (A_1 \otimes \Delta^{(k)})] \\ &\quad + \hat{M}^{(k-1)}(t) [I_m \otimes B(I_{n^2} + I_{(n,n)}) \otimes I_{n^{k-2}}] C(k), \end{aligned} \quad (8.2)$$

with initial conditions $\hat{M}^{(1)}(0) = (\boldsymbol{\alpha} \otimes I_n)$, $\hat{M}^{(k)}(0) = 0$ for $k \geq 2$; $\Delta^{(k)}$ is the k th-fold Kronecker product of Δ with itself, and the $mn^k \times mn^k$ coefficient matrices $A(k)$ and $C(k)$ are the same as in Proposition 7.2.3. \square

Corollary 8.2.3. *The first two moments of the population size in an MBT with catastrophes are given by*

$$\begin{aligned} \hat{m}^{(1)}(t) &= (\boldsymbol{\alpha} \otimes I_n) e^{\hat{A} t} (\mathbf{1}_m \otimes I_n) \\ \hat{m}^{(2)}(t) &= (\boldsymbol{\alpha} \otimes I_n) X(t) (\mathbf{1}_m \otimes I_{n^2}), \end{aligned} \quad (8.3)$$

where $X(t)$ is the solution of the Lyapunov equation

$$\hat{A} X(t) - X(t) \hat{B} + [I \otimes B(I_{n^2} + I_{(n,n)})] e^{\hat{B} t} - e^{\hat{A} t} [I \otimes B(I_{n^2} + I_{(n,n)})] = 0,$$

with

$$\begin{aligned}\hat{\mathcal{A}} &= (I_m \otimes \Omega) + (A_0 \otimes I_n) + (A_1 \otimes \Delta), \\ \hat{\mathcal{B}} &= (I_m \otimes \Omega \otimes I_n) I_{(n, mn)} [I_{(m, n)} \otimes I_n] \\ &\quad + (A_0 \otimes I_{n^2}) + (A_1 \otimes \Delta^{(2)}).\end{aligned}\tag{8.4}$$

□

Extinction probability and time until extinction

Let \hat{q} denote the extinction probability of an MBT undergoing catastrophes, and let $\hat{F}(t) = \hat{F}(\mathbf{0}, t) \mathbf{1}$ be the distribution of the time until extinction, both given the phase of the initial individual. We have

$$\hat{q} = \lim_{t \rightarrow \infty} \hat{F}(t).$$

Again, the loss of independence between the individuals prevents us to write a simple fixed point equation for \hat{q} , and the usual almost sure extinction criteria do not hold anymore.

The condition $\mu(\hat{\mathcal{A}}) \leq 0$, where $\hat{\mathcal{A}}$ is defined in (8.4), is sufficient but not necessary to ensure the almost sure extinction of the process. From (8.3), we see that when $\mu(\hat{\mathcal{A}}) > 0$, the population grows to infinity with the time on the average, but almost sure extinction is still possible, as will be discussed in Remark 8.3.8 in the next section.

Total progeny size

We denote by $\hat{N}(t)$ the total progeny size until time t in an MBT undergoing catastrophes. The probability generating function of the joint process $(\hat{Z}(t), \hat{N}(t))$, given the initial phase of the MBT, is

$$\hat{G}(\mathbf{s}, z, t) = \sum_{\mathbf{k} \geq \mathbf{0}} \sum_{\ell \geq \mathbf{k} \cdot \mathbf{1}} \mathbb{P}[(\hat{Z}(t), \hat{N}(t)) = (\mathbf{k}, \ell), \phi_c(t) | \varphi_0] \mathbf{s}^{\mathbf{k}} z^{\ell}.$$

It satisfies the following partial differential system.

Proposition 8.2.4. *The forward Kolmogorov system of equations for the generating function $\hat{G}(\mathbf{s}, z, t)$ of an MBT undergoing catastrophes is*

$$\begin{aligned}\frac{\partial}{\partial t} \hat{G}(\mathbf{s}, z, t) - \frac{\partial}{\partial \mathbf{s}^T} \hat{G}(\mathbf{s}, z, t) \cdot (I_m \otimes \mathbf{a}(\mathbf{s}, z)) \\ = \hat{G}(\mathbf{s}, z, t) A_0 + \hat{G}(\Delta \mathbf{s} + \boldsymbol{\varepsilon}, z, t) A_1 \\ \hat{G}(\mathbf{s}, z, 0) = z \mathbf{s} \cdot \boldsymbol{\alpha},\end{aligned}\tag{8.5}$$

with $\mathbf{a}(\mathbf{s}, z) = \mathbf{d} + D_0 \mathbf{s} + z B(\mathbf{s} \otimes \mathbf{s})$.

□

The difference with Proposition 7.2.5 again lies in the right-hand side of the Kolmogorov equation.

We characterize below the k th factorial moment of the total progeny until time t ,

$$\hat{\mathbf{m}}_k(t) = \frac{\partial^k}{(\partial z)^k} \hat{G}(\mathbf{s}, z, t) |_{\mathbf{s}=\mathbf{1}, z=1} \cdot \mathbf{1}_m \quad k \geq 1,$$

obtained from successive derivatives of (8.5) with respect to z . This is to put in parallel with Proposition 7.2.6.

Proposition 8.2.5. *The vectors $\hat{\mathbf{m}}_k(t)$, for $k \geq 1$, are solutions of the following differential matrix equations*

$$\frac{d}{dt} \hat{\mathbf{m}}_k(t) = k \hat{M}_{k-1}^{(1)}(t) (\mathbf{1}_m \otimes B \mathbf{1}),$$

with initial conditions $\hat{\mathbf{m}}_1(0) = \mathbf{1}_n$ and $\hat{\mathbf{m}}_k(0) = \mathbf{0}$ for $k \geq 2$, and where $\hat{M}_0^{(1)}(t) = \hat{M}^{(1)}(t) = (\boldsymbol{\alpha} \otimes I_n) \exp(\hat{A}t)$, and $\hat{M}_k^{(1)}(t) = \partial^k / (\partial z)^k \partial / \partial \mathbf{s}^T \hat{G}(\mathbf{s}, z, t) |_{\mathbf{s}=\mathbf{1}, z=1}$ for $k \geq 1$. \square

Let us focus on the first moment $\hat{\mathbf{m}}_1(t)$ of the total progeny until time t :

$$\begin{aligned} \hat{\mathbf{m}}_1(t) &= \mathbf{1} + \int_0^t \hat{M}^{(1)}(u) du (\mathbf{1}_m \otimes B \mathbf{1}) \\ &= \mathbf{1} + (\boldsymbol{\alpha} \otimes I_n) \int_0^t e^{\hat{A}u} du (\mathbf{1}_m \otimes B \mathbf{1}), \end{aligned}$$

where \hat{A} is given by (8.4). If \hat{A} is nonsingular, then we obtain

$$\hat{\mathbf{m}}_1(t) = \mathbf{1} + (\boldsymbol{\alpha} \otimes I_n) (-\hat{A})^{-1} (I - e^{\hat{A}t}) (\mathbf{1}_m \otimes B \mathbf{1}).$$

When $t \rightarrow \infty$, we are led to two cases for the mean total progeny size

$$\hat{\mathbf{m}}_1(\infty) = \begin{cases} \infty & \text{if } \mu(\hat{A}) > 0 \\ \mathbf{1} + (\boldsymbol{\alpha} \otimes I_n) (-\hat{A})^{-1} (\mathbf{1}_m \otimes B \mathbf{1}) & \text{if } \mu(\hat{A}) < 0 \end{cases}.$$

In the case $\mu(\hat{A}) < 0$, by some algebraic manipulations using the fact that $B \mathbf{1} = -D_0 \mathbf{1} - \mathbf{d}$, we can rewrite $\hat{\mathbf{m}}_1(\infty)$ as

$$\hat{\mathbf{m}}_1(\infty) = (\boldsymbol{\alpha} \otimes I_n) (-\hat{A})^{-1} [(\mathbf{1}_m \otimes \mathbf{d}) + (A_1 \mathbf{1} \otimes \boldsymbol{\varepsilon})]. \quad (8.6)$$

Mean behaviour

As in the MRE case, we can associate a standard MBT to the MBT with catastrophes so that both processes have the same behaviour on the average.

The standard MBT has mn phases, which are the pairs (i, j) , for $1 \leq i \leq m$, $1 \leq j \leq n$. It is exactly as if each individual had *its own* catastrophe process and all

individuals thus behaved independently of each others. Here, an individual is in the state (i, j) if its associated catastrophe process is in state i , and the individual itself is in the “physical” phase j .

The parameters of the standard MBT are

$$\begin{aligned} \mathbf{d}' &= (\mathbf{1}_m \otimes \mathbf{d}) + (A_1 \mathbf{1} \otimes \boldsymbol{\varepsilon}), \\ D'_0 &= (I_m \otimes D_0) + (A_1 \otimes \Delta) + (A_0 \otimes I_n), \end{aligned}$$

and the only nonzero entries in the birth rates matrix B' are the entries

$$B'_{(\ell,i),(\ell,j)(\ell,k)} = B_{i,jk},$$

so that we can write $B' = \mathcal{D}[\mathcal{B}^{(1)} \cdots \mathcal{B}^{(m)}]$, where $\mathcal{B}^{(i)}$ is an $n \times n^2 m$ matrix defined like in (7.12) with $B^{(i)}(j) = \bar{B}(j)$ for all $1 \leq i \leq m$ and $1 \leq j \leq n$.

It is easily seen that the matrix $\Omega' = D'_0 + B'(\mathbf{1} \oplus \mathbf{1})$ of the standard MBT coincides with the matrix $\hat{\mathcal{A}}$ defined in (8.4), so that the matrix of mean population size at time t in the standard MBT is given by $M'^{(1)}(t) = e^{\hat{\mathcal{A}}t}$, and the mean total progeny size vector in the subcritical case is given by $\mathbf{D}'^{(1)} = (-\hat{\mathcal{A}})^{-1} [(\mathbf{1}_m \otimes \mathbf{d}) + (A_1 \mathbf{1} \otimes \boldsymbol{\varepsilon})]$. If we only care about the physical phase of individuals, we respectively get (8.3) and (8.6).

Illustrations

Example 8.2.6. Let us illustrate the transient measures on an example of MBT with $n = 3$ phases.

Like in Example 7.2.7, we consider individuals whose lifetime is made up of three age classes. The rates are those of a supercritical country comparable to Congo:

$$\mathbf{d} = \begin{bmatrix} 0.018 \\ 0.013 \\ 0.05 \end{bmatrix}, \quad D_0 = \begin{bmatrix} * & 1/15 & \\ & * & 1/35 \\ & & * \end{bmatrix}, \quad B_{2,12} = 0.12,$$

the other entries of the matrix B being zero. The probability of dying from a catastrophe for each phase is given by the vector $\boldsymbol{\varepsilon} = [0.4, 0.2, 0.3]^T$.

We consider three catastrophe processes:

- a Poisson process with parameter β ;
- a phase-type renewal process (see Section 1.3) in which the inter-arrival times follow an Erlang distribution with $m = 3$ phases. This is a special case of MAP with

$$A_0 = \begin{bmatrix} -3\beta & 3\beta & \\ & -3\beta & 3\beta \\ & & -3\beta \end{bmatrix}, \quad A_1 = \begin{bmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 3\beta & 0 & 0 \end{bmatrix}.$$

We expect the time intervals between catastrophes to be relatively regular.

- a phase-type renewal process in which the inter-arrival times follow a hyperexponential distribution with $m = 3$ phases. This is a special case of MAP with

$$A_0 = \begin{bmatrix} -20\beta/39 & & \\ & -\beta & \\ & & -20\beta \end{bmatrix}, \quad A_1 = \begin{bmatrix} 20\beta/39 & & \\ & \beta & \\ & & 20\beta \end{bmatrix} \cdot [1/3, 1/3, 1/3].$$

We expect here much variability in the time intervals between catastrophes.

We have chosen the parameters of the catastrophe processes so that the expected time between catastrophes is the same in all three cases, and is equal to $1/\beta$. This will allow us to measure how the regularity between catastrophe times affects the population dynamics.

We show on Figure 8.2 the mean total family size for $\beta = 1/10$, if we start with one individual in phase 1 at time 0. We see that when the time between two catastrophes is highly variable, the population is more likely to grow than when the catastrophes occur at regular epochs.

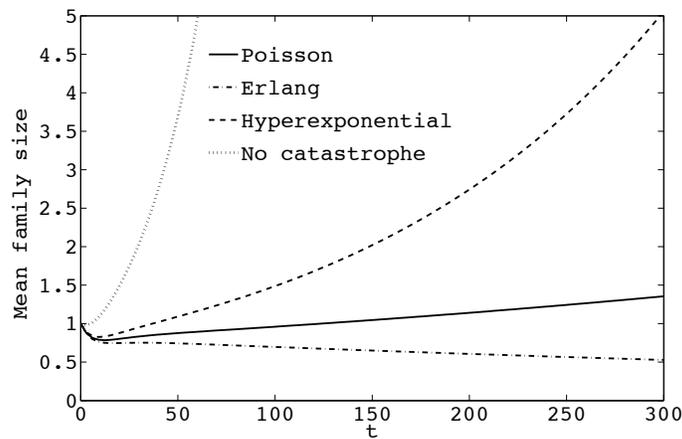


Figure 8.2: Comparison of the mean total family size as a function of time for three catastrophe processes with the same mean interval of time between catastrophes $1/\beta = 10$ years.

Then, we show on Figure 8.3 the mean total progeny size after a fixed $t = 200$ years, that is $\hat{m}_1(200)$, as a function of the average time between catastrophes $0 \leq 1/\beta \leq 500$, if we start with one individual in phase 1 at time 0. We compare the results obtained for the exponential and the hyperexponential inter-arrival distributions. For the latter, we distinguish between the three possible initial states of the MAP modeling the catastrophe process. We know that when we start the hyperexponential catastrophe process in its second phase, the mean time until the first catastrophe is $1/\beta$, like for the Poisson catastrophe process; both curves are quite close for all values of β . On the contrary, if the hyperexponential catastrophe process starts in its third phase, then the

mean time until the first catastrophe is $1/(20\beta)$, which gives much less opportunity to the population of growing; in that case, the mean total progeny size until 200 years is the smallest.

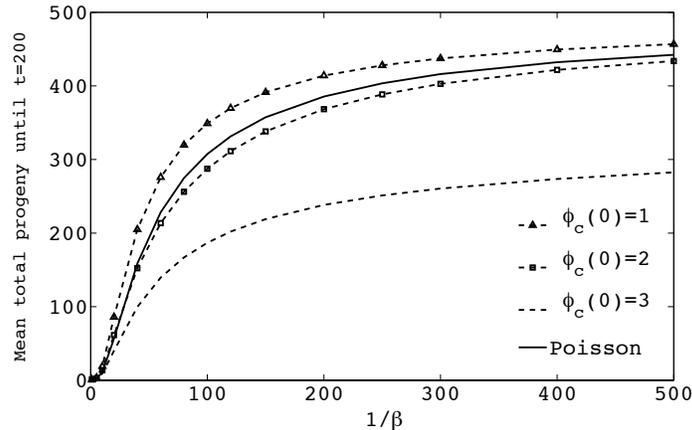


Figure 8.3: Evolution of the mean total progeny size until $t = 200$ years with the exponential and the hyperexponential inter-arrival distributions.

8.3 Extinction criteria

As for an MBT under MRE, we can classify an MBT with catastrophes into several categories and study the almost sure extinction criteria in each case. We shall separately consider the one-type and the multitype cases, as well as the Poisson(β) and the general MAP catastrophe cases.

When $n = 1$, the parameters of the exponential MBT are $d = \mu$, $B = \lambda$ and $D_0 = -\lambda - \mu$, and thus $\omega = \lambda - \mu$. We shall use the extinction criteria developed for *discrete-time* branching processes.

In a first discretization of the continuous-time MBT with catastrophes, we consider the embedded process at the times of catastrophe. This idea was already used by Bartoszyński *et al.* [7], Bühler and Puri [14], and Lee [49].

Let t_1, t_2, \dots be the successive epochs of catastrophes, and $\tau_i = t_i - t_{i-1}$ ($i \geq 1$) the intervals of time between catastrophes, with $t_0 = 0$. We define the embedded discrete-time branching process $\{\bar{Z}_k : k \in \mathbb{N}\}$ as $\bar{Z}_k = \hat{Z}(t_k^+)$. That is, the k th generation of the discrete-time branching process is made up of the survivors to the k th catastrophe in the initial continuous-time MBT.

Consequently, given τ_{k+1} , the progeny generating function of one individual from generation k in \bar{Z}_k is $F(\delta s + \varepsilon, \tau_{k+1})$, where $F(s, t)$ is the generating function of the population size at time t in a standard exponential MBT; the associated conditional

mean progeny is $m(k) = \exp(\omega \tau_{k+1})\delta$, which is random through the value of τ_{k+1} . The process \bar{Z}_k is thus a branching process in random environment, and the extinction criteria for an MBT with catastrophes follow from those for a branching process in random environment discussed in Section 7.3.

Let us first consider the case where catastrophes occur following a Poisson process with parameter β . The successive inter-arrival times between catastrophes $\{\tau_k\}$ are i.i.d. and exponentially distributed with parameter β .

Following the extinction criteria of a discrete-time branching process in i.i.d. random environment (Smith and Wilkinson [64]), we obtain that, provided $E|\log(1 - F(\varepsilon, \tau_1))| < \infty$, extinction of the process \bar{Z}_n is certain if and only if

$$0 \geq E[\log m(0)] = E[\log e^{\omega \tau_1} \delta] = \omega E[\tau_1] + \log \delta,$$

which finally gives the following criterion, previously obtained through another argument by Kaplan [36].

Corollary 8.3.1. *An exponential MBT with Poisson(β) catastrophes eventually becomes extinct with probability one if and only if*

$$\omega + \beta \log \delta \leq 0.$$

□

Now, suppose that the catastrophes occur following a MAP with characteristics A_0 and A_1 . Using the same discretization technique, we observe that the random environment is twofold and given by both the sequence of states of the MAP immediately after each catastrophe, that is $\phi_c(t_n^+)$, and the successive inter-arrival times between catastrophes $\{\tau_n\}$, which themselves depend on the states $\phi_c(t_n^+)$.

Let γ be the stationary distribution of the discrete process giving the phase of the MAP after each catastrophe, of which the transition probability matrix is given by $P = (-A_0)^{-1} A_1$; thus γ is such that $\gamma P = \gamma$, $\gamma \mathbf{1} = 1$.

Assume that at time 0, the catastrophic MAP starts with the initial distribution γ . In that case, the inter-arrival times between catastrophes $\{\tau_n\}$ are identically distributed following a phase-type distribution $\text{PH}(\gamma, A_0)$. The random environment is stationary and ergodic; we refer to Athreya and Karlin [5] for the almost sure extinction criterion, which is the same as in the Poisson catastrophe case, but this time the mean inter-arrival time is given by $E[\tau_1] = \gamma (-A_0)^{-1} \mathbf{1}$. This leads to the following criterion.

Corollary 8.3.2. *An exponential MBT with catastrophes following a MAP eventually becomes extinct with probability one if and only if*

$$\omega \gamma (-A_0)^{-1} \mathbf{1} + \log \delta \leq 0.$$

□

Another way to discretize the MBT with catastrophes is to apply the uniformization technique described in Section 7.3 to the MAP of catastrophes.

Let $c = \max_{1 \leq i \leq m} (-A_0)_{ii}$. Take a Poisson process of rate c and denote by $0 = t_0, t_1, t_2, \dots$ the epochs of events in that process, and by $\tau_i = t_i - t_{i-1}$ ($i \geq 1$) the intervals of times between events.

Define the discrete MAP with $K_0 = (1/c)A_0 + I$, $K_1 = (1/c)A_1$, and denote the phase at time k by $\bar{\phi}_k$; the discrete-time branching process is defined as $\bar{Z}_k = \hat{Z}(t_k)$. The stationary distribution of $\bar{\phi}_k$ is the same as that of the original continuous-time Markovian process $\phi_c(t)$, that is, α . The Markov chain $\bar{\phi}_k$ with initial distribution α is thus stationary and ergodic.

Let the indicator X_k be equal to 1 if the k th transition in $\bar{\phi}_k$ is associated with an event in the MAP, and to 0 otherwise. Conditionally given X_{k+1} and τ_{k+1} , the progeny generating function of one individual from generation k in the discrete-time branching process is $F(\delta s + \varepsilon, \tau_{k+1})$ if $X_{k+1} = 1$ or $F(s, \tau_{k+1})$ if $X_{k+1} = 0$, and is thus random through the time interval τ_{k+1} and the occurrence of event in the MAP at time $k + 1$. The random environment is thus again twofold and stationary ergodic, and the criterion becomes

Corollary 8.3.3. *An exponential MBT with catastrophes following a MAP eventually becomes extinct with probability one if and only if*

$$\omega + \alpha A_1 \mathbf{1} \log \delta \leq 0.$$

Proof. According to Athreya and Karlin [5], extinction is almost sure if and only if $E[\log m(0)] \leq 0$. Here,

$$\begin{aligned} E[\log m(0)] &= \sum_{i=1}^m \alpha_i E[\log m(0) \mid \phi_c(0) = i] \\ &= \sum_{i=1}^m \alpha_i E[\log m(0) \mid \phi_c(0) = i, X_1 = 0] P[X_1 = 0 \mid \phi_c(0) = i] \\ &\quad + \sum_{i=1}^m \alpha_i E[\log m(0) \mid \phi_c(0) = i, X_1 = 1] P[X_1 = 1 \mid \phi_c(0) = i] \\ &= \sum_{i=1}^m \alpha_i \{ \omega E[\tau_1] [(1/c)A_0 \mathbf{1} + \mathbf{1} + (1/c)A_1 \mathbf{1}]_i + \log \delta [(1/c)A_1 \mathbf{1}]_i \} \\ &= (1/c)(\omega + \alpha A_1 \mathbf{1} \log \delta), \end{aligned}$$

which proves the statement of the corollary. \square

Remark 8.3.4. The criteria in Corollaries 8.3.2 and 8.3.3 are actually based on the same expression. Indeed, we can write the vector α as

$$\alpha = \frac{\gamma (-A_0)^{-1}}{\gamma (-A_0)^{-1} \mathbf{1}},$$

since the j th component of the numerator is the mean time spent in phase j between two catastrophes, and the denominator is the mean time between two catastrophes.

So, we have $\alpha A_1 \mathbf{1} = 1/[\gamma (-A_0)^{-1} \mathbf{1}]$. This is quite intuitive since $\alpha A_1 \mathbf{1}$ may be interpreted as the average catastrophe rate.

Consider now the multitype case $n \geq 2$. Again, we look first at Poisson(β) catastrophes. As stated above, the successive inter-arrival times between catastrophes $\{\tau_k\}$ are i.i.d. The conditional progeny generating function of an individual from generation k in the discrete-time process \bar{Z}_k embedded at the times of catastrophes is given by $F(\Delta \mathbf{s} + \boldsymbol{\varepsilon}, \tau_{k+1})$ and the associated conditional mean progeny matrix is given by $A(k) = \exp(\Omega \tau_{k+1}) \Delta$.

We follow Athreya and Karlin [5]: provided that all entries of $A(0)$ and of the second factorial moment matrix are positive and finite with probability one, and that $E|\log(n - F(\boldsymbol{\varepsilon}, \tau_1)\mathbf{1})| < \infty$, we get

Corollary 8.3.5. *The extinction of an MBT undergoing Poisson catastrophes is almost sure if and only if*

$$\lim_{k \rightarrow \infty} \frac{1}{k} E \log \|e^{\Omega \tau_1} \Delta e^{\Omega \tau_2} \Delta \cdots e^{\Omega \tau_k} \Delta\| \leq 0, \quad (8.7)$$

for any matrix norm, where the τ_i 's are exponentially distributed with parameter β , for $i \geq 1$. \square

Now, consider the MAP catastrophe case. We can proceed as in the exponential MBT case by looking at the embedded branching process at the times of catastrophes, or at the events epochs of a Poisson process by using the uniformization technique. We then investigate the almost sure extinction criteria of a discrete-time multitype branching process \bar{Z}_k in a stationary and ergodic random environment, and we refer to Tanny [67] as in Section 7.3.

Using the first discretization, we conclude, under assumptions (i)–(iii) of Page 129, with the following criterion

Corollary 8.3.6. *The extinction of an MBT undergoing MAP catastrophes is almost sure if and only if*

$$\lim_{k \rightarrow \infty} \frac{1}{k} E \log \|e^{\Omega \tau_1} \Delta e^{\Omega \tau_2} \Delta \cdots e^{\Omega \tau_k} \Delta\| \leq 0, \quad (8.8)$$

where the τ_i 's are the intervals between observable events of the MAP; they are marginally $PH(\gamma, A_0)$ distributed, for $i \geq 1$. \square

Using the uniformization technique, the criterion becomes

$$\lim_{k \rightarrow \infty} \frac{1}{k} E \log \|A(0) A(1) \cdots A(k-1)\| \leq 0,$$

where $A(i) = e^{\Omega \tau_{i+1}} \Delta$ if $X_{i+1} = 1$, or $A(i) = e^{\Omega \tau_{i+1}}$ if $X_{i+1} = 0$, and τ_{i+1} is the $(i+1)$ th uniformization interval, exponentially distributed with parameter c , $i \geq 0$.

Remark 8.3.7. In the particular case of “uniform killing”, that is when $\delta_i = \delta$ for all i , the limits in (8.7) and in (8.8) may be computed explicitly. Indeed, in that case,

$$\|e^{\Omega \tau_1} \Delta e^{\Omega \tau_2} \Delta \dots e^{\Omega \tau_k} \Delta\| = \delta^k \|e^{\Omega(\tau_1 + \tau_2 + \dots + \tau_k)}\| \approx c \delta^k e^{\mu(\Omega)(\tau_1 + \tau_2 + \dots + \tau_k)},$$

asymptotically as $k \rightarrow \infty$, using the Jordan decomposition of the matrix Ω , where c is a positive constant (Gantmacher [21]), so that

$$\begin{aligned} & \lim_{k \rightarrow \infty} \frac{1}{k} \mathbf{E} \log \|e^{\Omega \tau_1} \Delta e^{\Omega \tau_2} \Delta \dots e^{\Omega \tau_k} \Delta\| \\ &= \log \delta + \lim_{k \rightarrow \infty} \frac{1}{k} \mu(\Omega) (\tau_1 + \tau_2 + \dots + \tau_k) \\ &= \log \delta + \mu(\Omega) \mathbf{E}[\tau] \\ &= \log \text{sp} \left[e^{\Omega \mathbf{E}[\tau]} \delta \right], \end{aligned}$$

by the Law of Large Numbers, with $\mathbf{E}[\tau] = 1/\beta$ in the Poisson case, and $\mathbf{E}[\tau] = \gamma(-A_0)^{-1} \mathbf{1}$ in the MAP catastrophe case.

Simplifying the limits in (8.7) and in (8.8) in the general case is more complicated, and is still a work in progress.

Remark 8.3.8. Recall that the condition $\mu(\hat{\mathcal{A}}) \leq 0$ is a sufficient but not necessary condition for the almost sure extinction of an MBT undergoing catastrophes. In the one-phase Poisson(β) catastrophe case, this condition becomes $\omega + \beta(\delta - 1) \leq 0$, and obviously

$$\omega + \beta \log \delta \leq \omega + \beta(\delta - 1),$$

since $\log x \leq x - 1$ for $0 < x \leq 1$. Thus, we can easily find an example where

$$\omega + \beta \log \delta \leq 0 < \omega + \beta(\delta - 1),$$

so that extinction is almost sure, and the mean size of the exponential MBT grows to infinity at the same time. Take for instance $\lambda = 4$, $\mu = 2$, so that $\omega = 2$, $\beta = 8$, and $\delta = 0.5$.

We now turn to numerical methods to compute the extinction probability vector $\hat{\mathbf{q}}$. This is the object of the next three sections.

8.4 Numerical partial differential equations

We briefly discuss the numerical techniques proposed in Section 7.4 in the context of an exponential MBT with Poisson(β) catastrophes.

The one-dimensional population size generating function $\hat{F}(s, t)$ satisfies the partial differential equation

$$\begin{aligned} \frac{\partial}{\partial t} \hat{F}(s, t) - a(s) \frac{\partial}{\partial s} \hat{F}(s, t) &= \beta [\hat{F}(\delta s + \varepsilon, t) - \hat{F}(s, t)], \\ \hat{F}(s, 0) &= s, \end{aligned} \quad (8.9)$$

Algorithm 8.4.1 Algorithm to compute the extinction probability \hat{q} of an exponential MBT with Poisson(β) catastrophes (recall that the function $[v]$ is defined by (7.24)).

```

 $\hat{F}_k^0 := s_k, \quad 0 \leq k \leq J$ 
 $\hat{q}^0 := \hat{F}_{J/2}^0$ 
for  $n = 0$  to  $n^* - 1$  do
   $\hat{F}_k^{n+\frac{1}{2}} := (8.13), \text{ or } (8.14)$ 
   $\hat{F}_k^{n+1} := \hat{F}_k^{n+\frac{1}{2}} + \beta \Delta t \left( \hat{F}_{[\delta s_k + \varepsilon]}^{n+\frac{1}{2}} - \hat{F}_k^{n+\frac{1}{2}} \right), \quad 1 \leq k \leq J - 1$ 
   $\hat{F}_0^{n+1} := \hat{F}_1^{n+1}$ 
   $\hat{F}_J^{n+1} := 1$ 
   $\hat{q}^{n+1} := \hat{F}_{J/2}^{n+1}$ 
end for
 $\hat{q} := \hat{q}^{n^*}$ 

```

where $a(s) = \mu - (\lambda + \mu)s + \lambda s^2$.

To solve this non-homogeneous hyperbolic partial differential equation, we follow the same approaches as in the MRE case: we use the fractional-step method to split the equation into a homogeneous partial differential equation

$$\frac{\partial}{\partial t} \hat{F}(s, t) - a(s) \frac{\partial}{\partial s} \hat{F}(s, t) = 0, \quad (8.10)$$

that we solve with a finite difference scheme or with the semi-Lagrangian method, and an ordinary differential equation

$$\frac{\partial}{\partial t} \hat{F}(s, t) = \beta [\hat{F}(\delta s + \varepsilon, t) - \hat{F}(s, t)] \quad (8.11)$$

that we solve using the forward Euler method.

Recall the definition of the two-dimensional grid (s_k, t^n) from Section 7.4. Let \hat{F}_k^n be a numerical approximation of $\hat{F}(s_k, t^n)$ for $0 \leq k \leq J$, where J is even, and $n \geq 0$. The index $k = J/2$ of s corresponds to the particular value $s = 0$, and we successively compute $\hat{q}^n = \hat{F}_{J/2}^n$ for $n \geq 0$, which are approximations of $\hat{F}(0, t^n)$; the limit \hat{q}^∞ is thus an approximation of the extinction probability. In practice, we stop at n^* such that $|\hat{q}^{n^*} - \hat{q}^{n^*-1}| < \epsilon$ for a fixed error ϵ .

In the context of finite difference methods, recall that the space and time steps must satisfy the CFL condition for the scheme to be stable. Here, it asks that for all values of s_k in the domain of computation,

$$|a(s_k)| \Delta t \leq \Delta s.$$

In practice, we thus take

$$\Delta t = \Delta s / \max_k |a(s_k)|. \quad (8.12)$$

The upwind scheme obtained using (7.18) and (7.19) is summarized by Algo-

rithm 8.4.1 with

$$\begin{aligned} \hat{F}_k^{n+\frac{1}{2}} &:= \hat{F}_k^n + \frac{1}{2} \frac{\Delta t}{\Delta s} \left[(\hat{F}_{k+1}^n - \hat{F}_k^n) \cdot |\text{sign}[-a(s_k)] - 1| \cdot a(s_k) \right. \\ &\quad \left. + (\hat{F}_k^n - \hat{F}_{k-1}^n) \cdot |\text{sign}[-a(s_k)] + 1| \cdot a(s_k) \right]. \end{aligned} \quad (8.13)$$

The semi-Lagrangian scheme is given by Algorithm 8.4.1 with

$$\hat{F}_k^{n+\frac{1}{2}} := \hat{F}_{[X(0; s_k, \Delta t)]}^n, \quad (8.14)$$

where

$$X(0; s, t) = \begin{cases} 1 + \frac{(\mu - \lambda)(s - 1)}{\lambda(s - 1) + (\mu - \lambda s) \exp[(\mu - \lambda)t]}, & \text{if } \lambda \neq \mu, \\ 1 + \frac{(s - 1)}{1 - \lambda t(s - 1)}, & \text{if } \lambda = \mu. \end{cases}$$

Recall that no CFL condition is required for that scheme, but so far, no rule exists for the optimal choice of the time step Δt .

Numerical examples

Let us apply the methods discussed above on two examples of exponential MBT with catastrophes; in the first example, the system is subcritical, in the second one it is supercritical.

Example 8.4.1. Take the subcritical MBT undergoing Poisson(β) catastrophes whose mean population size explodes as discussed in Remark 8.3.8, where $\lambda = 4$, $\mu = 2$, $\beta = 8$, and $\delta = 0.5$. We plot on the curve A of Figure 8.4 the approximations \hat{q}^n obtained with the upwind scheme for $J = 15 \cdot 10^2$ and Δt given by (8.12). The results obtained with the semi-Lagrangian method for $J = 7 \cdot 10^5$ and $\Delta t = 0.1$ are the same and are not represented.

Example 8.4.2. Take now a supercritical MBT undergoing Poisson(β) catastrophes with $\lambda = 20$, $\mu = 12$, $\beta = 5$ and $\delta = 0.5$. We show on the curve B of Figure 8.4 the approximations \hat{q}^n obtained with the upwind scheme for $J = 15 \cdot 10^2$ and Δt given by (8.12). Again, those obtained with the semi-Lagrangian method for $J = 7 \cdot 10^5$ and $\Delta t = 0.001$ are roughly the same and are thus not represented. The approximations of the extinction probability are respectively $\hat{q} = 0.7692$ and $\hat{q} = 0.7721$.

8.5 Integral equations approach

Bartoszynski *et al.* [7] show by analytical arguments that the probability generating function $\hat{F}(\mathbf{s}, t)$ of the population size at time t in a multitype branching process undergoing Poisson(β) catastrophes satisfies the integral equation

$$\hat{F}(\mathbf{s}, t) = \mathbf{F}(\mathbf{s}, t) + \beta \int_0^t \hat{F}(\Delta \mathbf{F}(\mathbf{s}, t - u) + \boldsymbol{\varepsilon}, u) - \hat{F}(\mathbf{F}(\mathbf{s}, t - u), u) du,$$

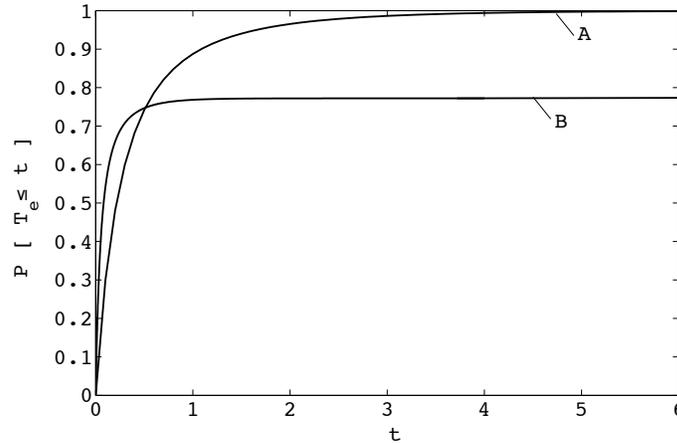


Figure 8.4: Distribution of the time until extinction of two exponential MBTs.

where $\mathbf{F}(\mathbf{s}, t)$ is the generating function of the population size at time t in the corresponding branching process without catastrophes. This integral equation is shown to be an implicit solution of the partial differential equation (8.1) for $m = 1$, and it yields the iterative scheme

$$\hat{\mathbf{F}}_n(\mathbf{s}, t) = \mathbf{F}(\mathbf{s}, t) + \beta \int_0^t \hat{\mathbf{F}}_{n-1}(\Delta \mathbf{F}(\mathbf{s}, t-u) + \boldsymbol{\varepsilon}, u) - \hat{\mathbf{F}}_{n-1}(\mathbf{F}(\mathbf{s}, t-u), u) du,$$

with $\hat{\mathbf{F}}_0(\mathbf{s}, t) = \mathbf{F}(\mathbf{s}, t)$.

Recall the definitions of the norm of the approximation error $\hat{e}_n(t)$ and of the R-factor $\hat{R}(t)$ respectively given by (7.27) and (7.29) in Section 7.5. Using the Stirling formula $n! \sim \sqrt{2\pi n} (n/e)^n$, we get $\hat{R}(t) = 0$ for all $t \geq 0$, which ensures a R-superlinear convergence of the sequence $\hat{\mathbf{F}}_n(\mathbf{s}, t)$ for all t (Ortega and Rheinboldt [58]).

However, this iterative method does not seem to have any probabilistic interpretation. For that reason, we go further and we analyze for catastrophes the analogue of the two sequences defined in Section 7.5 for MRE.

Thus, we propose two recursive integral equations with physical interpretation, in order to obtain numerical approximations for the extinction probability of an MBT with catastrophes. The first integral equation also provides us with the distribution of the time until extinction, while the second one allows us to compute the distribution of the total number of catastrophes occurring before extinction, given that the process eventually becomes extinct.

Let $M(t)$ denote the number of observable transitions occurring in the MAP of catastrophes during the time interval $[0, t[$. The probability generating function of the population size at time t in the MBT on the paths with at most n catastrophes until

that time, is given by

$$(\hat{F}_n)_{ij}(\mathbf{s}, t) = \sum_{\mathbf{k} \geq \mathbf{0}} \mathbb{P}[\hat{\mathbf{Z}}(t) = \mathbf{k}, \phi_c(t) = j, M(t) \leq n \mid \varphi_0 = i] \mathbf{s}^{\mathbf{k}}.$$

Recall that $\boldsymbol{\alpha}$ is the initial probability vector of the catastrophe process. We have

$$\hat{F}_0(\mathbf{s}, t) = \mathbf{F}(\mathbf{s}, t) \cdot \boldsymbol{\alpha} e^{A_0 t},$$

since with probability $\boldsymbol{\alpha} e^{A_0 t}$, no catastrophe occurs before time t , and in that case, the population size at time t is that of a standard MBT.

For $n \geq 1$, the generating function $\hat{F}_n(\mathbf{s}, t)$ satisfies the integral recursive equation

$$\hat{F}_n(\mathbf{s}, t) = \hat{F}_0(\mathbf{s}, t) + \int_0^t \hat{F}_{n-1}(\Delta \mathbf{F}(\mathbf{s}, t-u) + \boldsymbol{\varepsilon}, u^-) A_1 e^{A_0(t-u)} du. \quad (8.15)$$

This is obtained by decomposing on the time of the *last* catastrophe before time t . Indeed, either no catastrophe occurred yet at time t which is recorded by $\hat{F}_0(\mathbf{s}, t)$, or the last catastrophe occurs at time u in $(0, t)$, which happens with probability $A_1 e^{A_0(t-u)} du$. In that case, the population at time t is made up of the descendants of the survivors to the last catastrophe among the living individuals at time u^- , under the restriction of at most $n-1$ catastrophes until time u^- , these descendants evolving independently during a time interval of length $t-u$.

The limit when $n \rightarrow \infty$ of (8.15),

$$\hat{F}(\mathbf{s}, t) = \mathbf{F}(\mathbf{s}, t) \cdot \boldsymbol{\alpha} e^{A_0 t} + \int_0^t \hat{F}(\Delta \mathbf{F}(\mathbf{s}, t-u) + \boldsymbol{\varepsilon}, u^-) A_1 e^{A_0(t-u)} du,$$

is also an implicit solution of the partial differential equation (8.1) with initial condition $\hat{F}(\mathbf{s}, 0) = \mathbf{s} \cdot \boldsymbol{\alpha}$.

The distribution of the time until extinction $\hat{F}(t) = \mathbb{P}[T_e \leq t \mid \varphi_0]$ and the extinction probability \hat{q} are computed exactly in the same way as in the MRE case in Section 7.5; the only difference lies in the practical choice of the maximal time T_c at which we evaluate the functions: here we choose it such that the probability of extinction after time T_c of the standard MBT without catastrophes is smaller than ϵ_1 , that is

$$T_c = \inf \{t \geq 0 : \|\mathbf{q} - \mathbf{F}(\mathbf{0}, t)\| < \epsilon_1\}.$$

Proceeding as in Section 7.5, we investigate the convergence rate of the sequence $\hat{F}_n(\mathbf{s}, t)$ to $\hat{F}(\mathbf{s}, t)$. We have $\hat{e}_o(t) \leq 2$ for all $t \geq 0$, and for $n \geq 1$,

$$\hat{e}_n(t) \leq \int_0^t \hat{e}_{n-1}(u) \|A_1\| \|e^{A_0(t-u)}\| du.$$

Let $0 < \beta_0 = -\mu(A_0)$. We have

$$\|e^{A_0(t-u)}\| = e^{-\beta_0(t-u)} \|e^{(\beta_0 I + A_0)(t-u)}\|,$$

and since $\lim_{t \rightarrow \infty} e^{A_0 t} = \mathbf{0}$, the matrix $e^{(\beta_0 I + A_0)(t-u)}$ is bounded, so there exists a constant $c < \infty$ which should not be very large, such that

$$c = \sup_{t \geq 0} \|e^{(\beta_0 I + A_0)t}\|, \quad (8.16)$$

and we get

$$\hat{e}_n(t) \leq c \|A_1\| \int_0^t \hat{e}_{n-1}(u) e^{-\beta_0(t-u)} du.$$

We can show by induction on n that

$$\hat{e}_n(t) \leq 2 \left(\frac{c \|A_1\|}{\beta_0} \right)^n e^{-\beta_0 t} \left[e^{\beta_0 t} - \sum_{i=0}^{n-1} \frac{(\beta_0 t)^i}{i!} \right], \quad n \geq 1.$$

The factor in square brackets is the remainder of the Taylor expansion of $e^{\beta_0 t}$, and thus by the Taylor-Lagrange formula, we have

$$\hat{e}_n(t) \leq 2 \frac{(c \|A_1\| t)^n}{n!} e^{-\beta_0(t-\zeta)},$$

for $n \geq 1$, where $0 < \zeta < t$. We can show that the convergence of the sequence $\hat{F}_n(\mathbf{s}, t)$ is thus also R-superlinear. In the Poisson(β) catastrophe case, $\beta_0 = \|A_1\| = \beta$, and $c = 1$.

Let t_n be the time of the n th catastrophe, for $n \geq 1$. The probability generating function of the population size just after the n th catastrophe is given by $\hat{\varphi}_n(\mathbf{s}) = \hat{F}(\mathbf{s}, t_n^+)$, that is,

$$(\hat{\varphi}_n)_{ij}(\mathbf{s}) = \sum_{\mathbf{k} \geq \mathbf{0}} \mathbb{P}[\hat{\mathbf{Z}}(t_n^+) = \mathbf{k}, \phi_c(t_n^+) = j \mid \varphi_0 = i] \mathbf{s}^{\mathbf{k}}.$$

The generating function $\hat{\varphi}_n(\mathbf{s})$ satisfies the integral recursive equation

$$\hat{\varphi}_n(\mathbf{s}) = \int_0^\infty \hat{\varphi}_{n-1}(\mathbf{F}(\Delta \mathbf{s} + \boldsymbol{\varepsilon}, u)) e^{A_0 u} A_1 du, \quad (8.17)$$

for $n \geq 1$, with $\hat{\varphi}_0(\mathbf{s}) = \mathbf{s} \cdot \boldsymbol{\alpha}$. This integral equation is obtained by conditioning on the time u between the $(n-1)$ th and the n th catastrophe. Indeed, the population after the n th catastrophe is made up of the survivors among the descendants of individuals still living after the $(n-1)$ th catastrophe, which evolve independently during a time interval of length u .

The convergence of the sequence $\hat{\varphi}_n(\mathbf{s})$ to its limit $\hat{\varphi}_\infty(\mathbf{s}) = \hat{\mathbf{q}} \cdot \boldsymbol{\alpha}$ when $\mathbf{s} < \mathbf{1}$ (or $\hat{\varphi}_\infty(\mathbf{1}) = \mathbf{1} \cdot \boldsymbol{\alpha}$) is ensured by its probabilistic interpretation. A convergence rate study leads to

$$\hat{e}_n \leq \frac{c \|A_1\|}{\beta_0} \hat{e}_{n-1}$$

for $n \geq 1$, where $\hat{e}_n = \sup_{\mathbf{s}} \|\hat{\varphi}_n(\mathbf{s}) - \hat{\varphi}_\infty(\mathbf{s})\|$, $\beta_0 = -\mu(A_0)$, and where c is defined in (8.16). This inequality may not be exploited here since we cannot tell much about the constant $c \|A_1\|$, which depends on the system. In the general catastrophe case, the convergence rate is thus not clearly defined.

In the Poisson(β) catastrophe case, we get $\hat{e}_n \leq \hat{e}_{n-1}$, which shows that the sequence is (sub-)linear.

Again, the extinction probability and the cumulated total number of catastrophes before extinction, given extinction occurs, are computed like in the MRE case in Section 7.5, except that here, in practice, the upper bound T_c^* in the integral in (8.17) is taken such that

$$T_c^* = \inf \{u \geq 0 : \|e^{A_0 u} A_1\| < \epsilon_1\},$$

for some fixed error ϵ_1 .

Example 8.5.1. Let us consider a supercritical exponential MBT with parameters $\lambda = 100$, $\mu = 75$, undergoing catastrophes following a MAP characterized by

$$A_0 = \begin{bmatrix} -52 & 10 \\ 40 & -95 \end{bmatrix} \quad A_1 = \begin{bmatrix} 30 & 12 \\ 50 & 5 \end{bmatrix},$$

and such that $\varepsilon = 0.3$.

We compare on Figure 8.5 the distributions of the time until extinction of this MBT with catastrophes, obtained with the first integral method, and of the standard MBT with the same mean behaviour (see on page 151), obtained by numerically solving (5.20). The extinction probabilities are respectively $\hat{q} = 0.9125$, $q = 0.8835$.

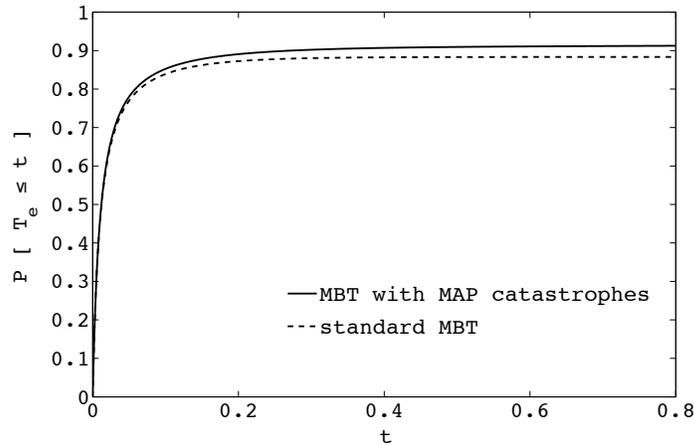


Figure 8.5: Distribution of the time until extinction of two MBTs.

8.6 Structured Markov chain approach

An MBT undergoing catastrophes governed by a MAP may be represented by a structured Markov chain $\{(\hat{X}(t), \hat{\varphi}(t)) : t \in \mathbb{R}^+\}$, where the level $\hat{X}(t)$ is the total number of individuals living at time t , and the phase is an $(n + 1)$ -uple $\hat{\varphi}(t) = (\phi_c(t), \hat{Z}(t))$, the first entry being the state of the catastrophic MAP at time t , and $\hat{Z}(t)$ giving the number of individuals in phases 1 to n at time t .

The phase space $\hat{L}(k)$ at level k is defined like in (7.31) and is of cardinality $|\hat{L}(k)| = m \binom{k+n-1}{n-1}$.

Since catastrophes may kill several individuals at the same time, here transitions from level k to any lower level $k - m$, $1 \leq m \leq k$, are permitted, so that the generator has the following structure

$$Q = \begin{bmatrix} A & 0 & 0 & 0 & 0 & \cdots \\ Q_{10} & Q_{11} & Q_{12} & 0 & 0 & \cdots \\ Q_{20} & Q_{21} & Q_{22} & Q_{23} & 0 & \cdots \\ Q_{30} & Q_{31} & Q_{32} & Q_{33} & Q_{34} & \cdots \\ & & \vdots & & & \ddots \end{bmatrix}.$$

We call this kind of process a level-dependent G/M/1-type Markov chain. For the sake of clarity, here we shall use the notation Q_{ij} instead of the usual notation $A_{j-i}^{(i)}$.

If the catastrophe process starts with the initial distribution α , the extinction probability of the MBT undergoing catastrophes, given the phase of the initial individual, is given by

$$\hat{q} = (\alpha \otimes I_n) G_1 \mathbf{1}_m,$$

where G_1 is the $mn \times m$ matrix of first passage probabilities from level 1 to level 0 defined in Section 6.2.

We now explain how to compute G_1 in a level-dependent G/M/1-type process. Recall from Section 6.2 that $G_1 \mathbf{1} = \lim_{M \rightarrow \infty} G_1(M) \mathbf{1}$, where

$$G_1(M) \mathbf{1} = \mathbb{P} \left[\gamma(0) < \gamma(M+1) \mid \hat{X}(0) = 1, \hat{\varphi}(0) \right],$$

and corresponds to the probability that the MBT with catastrophes eventually becomes extinct with a number of individuals at most equal to M at any time.

We first adapt the algorithm L described in Section 6.2 to the present context. Later, we propose two improvements of this method.

Recall from Section 6.2 that $G_1(M) \mathbf{1} = \mathbf{1} - F_M \mathbf{1}$, with $F_M = L_1 L_2 \cdots L_M$, where the matrix L_i holds the probability to reach level $i+1$ before level 0, starting from level i , that is,

$$L_i = \mathbb{P}[\gamma(i+1) < \gamma(0), \hat{\varphi}(\gamma(i+1)) \mid \hat{X}(0) = i, \hat{\varphi}(0)].$$

These matrices may still be computed recursively, but now, since the process can reach from level i any lower level in one transition, we have $L_1 = (-Q_{11})^{-1} Q_{12}$, and for $i \geq 2$,

$$\begin{aligned} L_i &= (-Q_{ii})^{-1} [Q_{i(i+1)} + Q_{i(i-1)} L_{i-1} L_i + Q_{i(i-2)} L_{i-2} L_{i-1} L_i + \cdots \\ &\quad + Q_{i1} L_1 L_2 \cdots L_{i-1} L_i], \end{aligned}$$

which can be rewritten as

$$L_i = \left[I - (-Q_{ii})^{-1} \sum_{j=1}^{i-1} Q_{i(i-j)} \prod_{i-j \leq k \leq i-1} L_k \right]^{-1} (-Q_{ii})^{-1} Q_{i(i+1)}. \quad (8.18)$$

Recall that we can then write $G_1(1) \mathbf{1} = (-Q_{11})^{-1} Q_{10} \mathbf{1}$, and

$$G_1(M) \mathbf{1} = G_1(M-1) \mathbf{1} + F_{M-1} (\mathbf{1} - L_M \mathbf{1})$$

for $M \geq 2$. We see that, at the M th iteration, the probability $G_1(M) \mathbf{1}$ that the process started in level 1 eventually reaches level 0 before level $M+1$, is decomposed in two terms: the probability $G_1(M-1) \mathbf{1}$ that the process eventually reaches level 0 before level M , and the probability $F_{M-1} (\mathbf{1} - L_M \mathbf{1})$ that the process eventually reaches level M before level 0, and then eventually reaches level 0 under the taboo of level $M+1$.

We can improve this algorithm by allowing the process to go over level M in a controlled manner, and thus considering more paths at each iteration.

For that purpose, we need to define the matrix \bar{C}_k , for $1 \leq k \leq M$, as the generator of the restriction \bar{S}_k of the G/M/1-type process observed only during those intervals of time spent at level k , before it moves for the first time to level $k+1$ or to level 0. We also define the matrices Γ_{nm} , $1 \leq n < m \leq M+1$, as follows: $(\Gamma_{nm})_{ij}$ is the probability that, starting from level n in phase i , the process reaches level m before level 0, and the first phase visited at level m is the phase j . They are recursively given by

$$\begin{aligned} \bar{C}_1 &= Q_{11} \\ \Gamma_{12} &= (-\bar{C}_1)^{-1} Q_{12}, \end{aligned}$$

and for $2 \leq k \leq M$,

$$\begin{aligned} \bar{C}_k &= Q_{kk} + \sum_{i=1}^{k-1} Q_{ki} \Gamma_{ik} \\ \Gamma_{k(k+1)} &= (-\bar{C}_k)^{-1} Q_{k(k+1)} \\ \Gamma_{i(k+1)} &= \Gamma_{ik} \Gamma_{k(k+1)} \quad \text{for } 1 \leq i \leq k-1. \end{aligned}$$

(see Latouche, Jacobs and Gaver [46]).

We define a first improved sequence $\{\mathbf{x}_M^{(1)}\}_{M \geq 1}$ as follows

$$\mathbf{x}_M^{(1)} = G_1(M) \mathbf{1} + \mathbf{T}_M^{(1)},$$

where the additional term $\mathbf{T}_M^{(1)}$ gives the probability that the process eventually reaches level $M+1$, and that the $M+1$ individuals then act independently of each others, and generate a tree which becomes extinct with the probability given by the last approximation $\mathbf{x}_{M-1}^{(1)}$, so that the process eventually gets extinct by reaching level 0.

To do this, we define a vector $\mathbf{X}_{M+1}^{(1)}$ whose entries are the probability that each of the $M+1$ individuals at level $M+1$ independently generates a tree which eventually becomes instnct under the constraints of the last approximation. That is, the entry of $\mathbf{X}_{M+1}^{(1)}$ corresponding to the state (i, S_1, \dots, S_n) with $S_1 + \dots + S_n = M+1$ is given by $(\mathbf{x}_{M-1}^{(1)})_1^{S_1} \dots (\mathbf{x}_{M-1}^{(1)})_n^{S_n}$, independently of i .

The additional term $\mathbf{T}_M^{(1)}$ is then given by

$$\mathbf{T}_M^{(1)} = F_{M-1} (-\bar{C}_M)^{-1} Q_{M(M+1)} \mathbf{X}_{M+1}^{(1)}.$$

We define a second improved sequence $\{\mathbf{x}_M^{(2)}\}_{M \geq 1}$ as follows

$$\mathbf{x}_M^{(2)} = G_1(M) \mathbf{1} + \mathbf{T}_M^{(2)},$$

where the additional term $\mathbf{T}_M^{(2)}$ now gives the probability that the process reaches level M , and then teeters in the following way between levels M and $M + 1$, before finally reaching level 0: when the process moves from level M to level $M + 1$, the new child generates a subtree which eventually becomes extinct with the probability given by the last approximation $\mathbf{x}_{M-1}^{(2)}$, while the other M individuals are frozen until the extinction of that subtree, so that the process eventually returns to level M .

We then define a square matrix $X_M^{(2)}$ of which the entries are the rate at which a new child is produced at level M which generates a tree eventually becoming extinct under the constraints of the last approximation. For instance, in a two-phases MBT, the nonzero elements of $X_M^{(2)}$ are

Transitions	Rates
$(i, S_1, S_2) \rightarrow (i, S_1 + 1, S_2 - 1)$	$S_2 \left(B_{2,11}(\mathbf{x}_{M-1}^{(2)})_1 + B_{2,21}(\mathbf{x}_{M-1}^{(2)})_2 \right)$
$(i, S_1, S_2) \rightarrow (i, S_1 - 1, S_2 + 1)$	$S_1 \left(B_{1,22}(\mathbf{x}_{M-1}^{(2)})_2 + B_{1,12}(\mathbf{x}_{M-1}^{(2)})_1 \right)$
$(i, S_1, S_2) \rightarrow (i, S_1, S_2)$	$S_1 \left(B_{1,11}(\mathbf{x}_{M-1}^{(2)})_1 + B_{1,21}(\mathbf{x}_{M-1}^{(2)})_2 \right)$ $+ S_2 \left(B_{2,12}(\mathbf{x}_{M-1}^{(2)})_1 + B_{2,22}(\mathbf{x}_{M-1}^{(2)})_2 \right),$

with $S_1 + S_2 = M$.

The additional term $\mathbf{T}_M^{(2)}$ is then given by

$$\mathbf{T}_M^{(2)} = F_{M-1} \sum_{n \geq 1} \left[(-\bar{C}_M)^{-1} X_M^{(2)} \right]^n (\mathbf{1} - L_M \mathbf{1}).$$

These two improved sequences are heuristically shown to converge to the extinction probability \hat{q} , and we observe that $\mathbf{T}_M^{(2)} \geq \mathbf{T}_M^{(1)}$, as illustrated in the first example below, so that the second sequence $\mathbf{x}_M^{(2)}$ is actually faster than the first one.

Example 8.6.1. Take the supercritical exponential MBT with Poisson(β) catastrophes with parameters $\lambda = 20$, $\mu = 12$, $\beta = 5$, and $\delta = 0.5$ from Example 8.4.2. We represent on Figure 8.6 the approximations $G_1(M)$, $x_M^{(1)}$ and $x_M^{(2)}$, as a function of the level M . For $M = 112$, we obtain $\hat{q} = 0.7728$ with a precision of 10^{-5} , which is in accord with the results obtained using the numerical methods for partial differential equations.

We see that the two improved sequences converge to \hat{q} . However, it is more complicated to show that they are monotone increasing, since the additional terms themselves are not monotone increasing, as we see on Figure 8.7.

It is not easy to show that $\mathbf{T}_M^{(2)} \geq \mathbf{T}_M^{(1)}$ either: we would have to show that the set of paths measured by $\mathbf{T}_M^{(1)}$, where an independence assumption is used, is included in the set of paths measured by $\mathbf{T}_M^{(2)}$; this is still a work in progress.

We plot on Figure 8.8 the logarithm (in basis 10) of the approximation errors $E_M = \hat{q} - G_1(M)$, $E_M^{(1)} = \hat{q} - x_M^{(1)}$ and $E_M^{(2)} = \hat{q} - x_M^{(2)}$ as functions of the level M . This shows that convergences are linear.

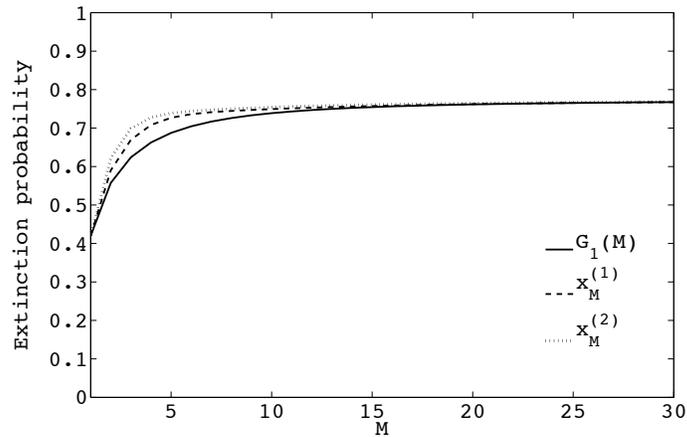


Figure 8.6: Approximations of the extinction probability \hat{q} as a function of M , using the algorithm L and the two improved sequences.

We now fix $\beta\varepsilon = 2.5$. This means that the rate at which deaths occur by catastrophic events remains constant. We let the probability ε of dying due to a catastrophe vary in the interval $]0, 0.5]$, and we plot on Figure 8.9 the extinction probability obtained as a function of ε . We see that when ε tends to 0, the extinction probability of the MBT undergoing catastrophes decreases to the extinction probability $q = 0.725$ of the standard MBT (without catastrophes) which has the same mean behaviour, that is with death rate $\mu' = \mu + \beta\varepsilon = 14.5$ (see on page 151).

Indeed, Batoszynski *et al.* [7] already observed that frequent small catastrophes affecting a branching process are in some sense equivalent to modifying the death rate in the standard branching process.

Together with Example 8.5.1, it seems that the extinction probability of the standard MBT with the same behaviour as the MBT undergoing catastrophes is a lower bound of the extinction probability of the latter. Also observe that $\mu(\hat{A}) \leq 0$ implies $\hat{q} = q = 1$, but that $\mu(\hat{A}) > 0$ implies $q < 1$ but not necessarily $\hat{q} < 1$.

Example 8.6.2. Let us return to the MBT from Example 8.2.6 which models the evolution of a female population undergoing catastrophes. From now on, our interest lies in the extinction probability of this family, therefore the third phase in which the fertility rate is zero is not useful anymore and we gather the two last phases together, which leads to the following parameters

$$\mathbf{d} = \begin{bmatrix} 0.018 \\ 0.026 \end{bmatrix}, D_0 = \begin{bmatrix} * & 1/15 \\ & * \end{bmatrix}, B_{2,12} = 0.077,$$

the other entries of B being zero. We consider Poisson catastrophes with parameter β .

In the first numerical experimentation, we fix at $\varepsilon = [0.6, 0.4]^T$ the probabilities of dying at a catastrophe epoch in each phase, and we represent on Figure 8.10 the

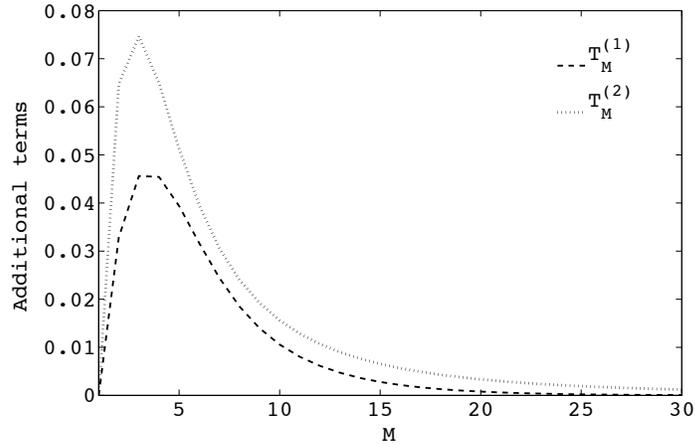


Figure 8.7: Additional terms $T_M^{(1)}$ and $T_M^{(2)}$ corresponding to the two improved sequences $\mathbf{x}_M^{(1)}$ and $\mathbf{x}_M^{(2)}$, as a function of the level M .

successive approximations of the extinction probability for three values of β : the plain line corresponds to $\beta = 1/10$, the dashed line corresponds to $\beta = 1/50$, and the dotted line corresponds to $\beta = 1/120$. In each pair of curves, the upper curve shows the extinction probability given the process starts with one child (phase 1), and the lower curve is given that it starts with one adult (phase 2).

As expected, the higher the catastrophe rate, the higher the extinction probability. We also observe that the probability for a family to get extinct with a maximal size M is higher if we start with one child and the catastrophes occur at rate $\beta = 1/120$ than if we start with one adult and the catastrophes occur at rate $\beta = 1/50$, for $M \leq 7$.

In our second experimentation, we fix the catastrophe rate at $\beta = 1/50$, and we let the two components of ε vary between 0 and 1. The resulting extinction probability given the process starts with one child is plotted on Figure 8.11. We see that the extinction probability is more affected by the variation from 0 to 1 of the component ε_2 than by that of ε_1 . It turns out that it is more important that the catastrophes keep adults alive than children, the adults being able to procreate directly, and the children having a high mortality rate.

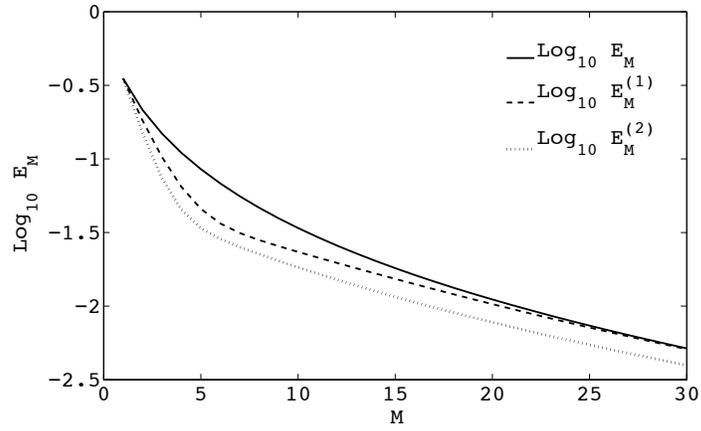


Figure 8.8: Logarithm of the approximation errors as a function of M , using the algorithm L and the two improved sequences.

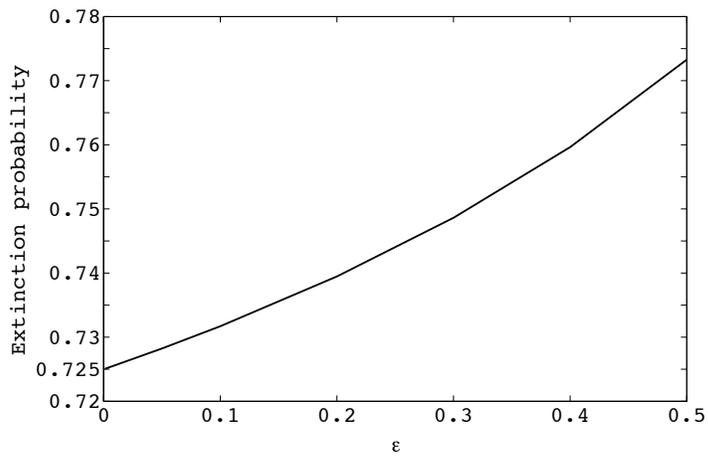


Figure 8.9: Extinction probability as a function of ε with $\beta\varepsilon = 2.5$.

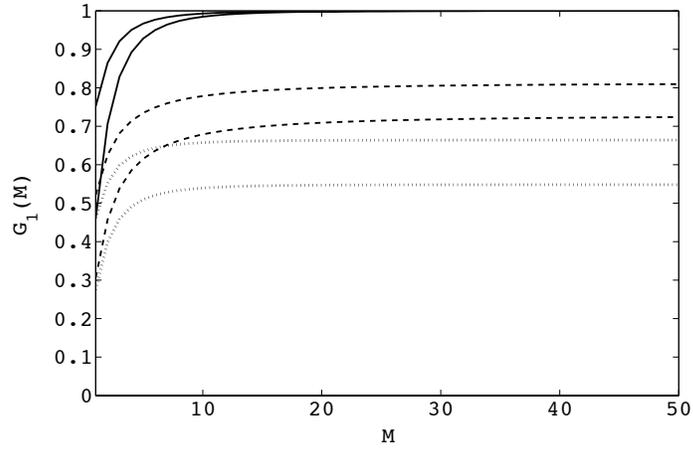


Figure 8.10: Probability that the process eventually becomes extinct with a maximum population size M , as a function of M , for three values of the parameter β : $\beta = 1/10$ (plain line), $\beta = 1/50$ (dashed line), and $\beta = 1/120$ (dotted line).

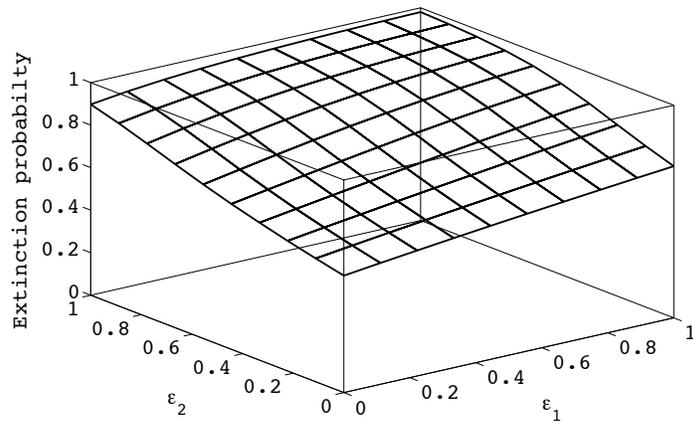


Figure 8.11: Extinction probability as a function of the entries of the vector ϵ .

Conclusion and perspectives

Branching processes form a very rich field of applied probabilities, for which a large amount of literature exists. Questions on branching processes are numerous, and the sphere of applications is wide-ranging.

It is now apparent that algorithmic approaches based on matrix analytic methods, as well as on numerical analysis, are suitable to investigate various questions about branching processes. Here, we mainly focused on the extinction probability of a special class of multitype branching processes; we also showed how to compute some of their transient measures.

When individuals behave independently, the study of the extinction probability actually boils down to finding the minimal nonnegative solution of a fixed point matrix equation. We applied well-known methods, such as linear functional and Newton iterations, but we did not settle for that: we went further by giving a probabilistic interpretation to each algorithm. The physical interpretation and the convergence analysis of the algorithms allowed us to better understand the properties of the branching processes themselves.

When independence is lost due to external influences, the methods used previously are no longer appropriate, and we have experienced much more difficulties to numerically evaluate the extinction probability.

We first turned to purely numerical methods to solve partial differential systems. Plunging into that field was an interesting experience, as well as interacting with numerical analysts in order to solve a problem in probability. As already mentioned, we are currently still working on those techniques; we would like to generalize them to the multiphase case, and to find a rule for the optimal choice of the time step to ensure the convergence of the semi-Lagrangian method.

Then, we returned to probabilistic methods; we analyzed in depth the behaviour of the branching process when imposing constraints on the external process. We also used the structured Markov chain approach, which is actually shown to be a very efficient method to compute the extinction probability, as well as transient measures, when the number of phases in the lifetime of individuals is small.

Again, going far in the numerical and probabilistic analysis of branching processes under external influences allowed us to well understand how these processes really work.

As pointed out in the text, other interesting questions arise from our developments, especially in the last two chapters. For instance, in Sections 7.2 and 8.2, we defined a standard MBT which behaves on the average like an MBT under external influence; other transient measures of the two processes and their extinction probability should be compared; we also refer to Sections 7.3 and 8.3 where we exposed the extinction criteria of an MBT under external influence as a limit that we would like to simplify, and to Section 8.6 where we presented two improved sequences to evaluate the extinction probability, of which the convergence and the comparison still need to be theoretically studied.

We applied the model of the Markovian binary tree to telecommunications [30, 31] and to demography, which are two fields for which real data were easy to obtain. After discussing with several biologists, we realized that real data about animal or cell populations are much more difficult to find. Nevertheless, we still hope to be able to use the MBT, as well as the theory related to reducible branching processes, to model real biological phenomena.

Bibliography

- [1] J. Abate and W. Whitt. Numerical inversion of probability generating functions. *Operations Research Letters*, 12(4):245–251, 1992.
- [2] S. R. Adke. The maximum population size in the first N generations of a branching process. *Biometrics*, 20(3):649–651, 1964.
- [3] A. Agresti. Bounds on the extinction time distribution of a branching process. *Advances in Applied Probability*, 6(2):322–335, 1974.
- [4] S. Asmussen and G. Koole. Marked point processes as limits of markovian arrival streams. *Journal of Applied Probability*, 30(2):365–372, 1993.
- [5] K. B. Athreya and S. Karlin. On branching processes with random environments: I extinction probabilities. *The Annals of Mathematical Statistics*, 42(5):1499–1520, 1971.
- [6] K. B. Athreya and P. E. Ney. *Branching Processes*. Springer-Verlag, New York, 1972.
- [7] R. Bartoszynski, W. J. Bühler, W. Chan, and D. K. Pearl. Population processes under the influence of disasters occurring independently of population size. *Journal of Mathematical Biology*, 27:167–178, 1989.
- [8] N. G. Bean, N. Kontoleon, and P. G. Taylor. Algorithms for determining the probability of eventual extinction of a Markovian binary tree. Technical report, University of Adelaide & University of Melbourne, 2004.
- [9] N. G. Bean, N. Kontoleon, and P. G. Taylor. Markovian trees: Properties and algorithms. *Annals of Operations Research*, 160(1):31–50, 2008.

-
- [10] D. A. Bini, G. Latouche, and B. Meini. *Numerical Methods for Structured Markov Chains*. Oxford University Press, 2005.
- [11] J. Bishir. Maximum population size in a branching process. *Biometrics*, 18(3):394–403, 1962.
- [12] F. T. Bruss. A note on extinction criteria for bisexual Galton-Watson processes. *Journal of Applied Probability*, 21(4):915–919, 1984.
- [13] M. Bush and M. L. Pernoll. Multiple pregnancy. *Current Obstetric & Gynecologic, Diagnosis & Treatment*, pages 315–326, 2006.
- [14] W. J. Bühler and P. S. Puri. The linear birth and death process under the influence of independently occurring disasters. *Probability Theory and Related Fields*, 83:59–66, 1989.
- [15] R. Cogburn and W. C. Torrez. Birth and death processes with random environments in continuous time. *Journal of Applied Probability*, 18(1):19–30, 1981.
- [16] L. de Lagrange. Nouvelle méthode pour résoudre des équations littérales par le moyen des séries. *Mém. Acad. Roy. Sci. Belles-Lettres de Berlin*, 24, 1770.
- [17] J. R. Dormand and P. J. Prince. A family of embedded runge-kutta formulae. *Journal of Computational and Applied Mathematics*, 6(1):19–26, 1980.
- [18] M. Dwass. The total progeny in a branching process and a related random walk. *Journal of Applied Probability*, 6(3):682–686, 1969.
- [19] M. Falcone and R. Ferretti. Convergence analysis for a class of high-order semi-Lagrangian advection schemes. *SIAM Journal on Numerical Analysis*, 35(3):909–940, 1998.
- [20] M. Falcone and R. Ferretti. Semi-Lagrangian schemes for Hamilton-Jacobi equations, discrete representation formulae and Godunov methods. *Journal of Computational Physics*, 175:559–575, 2002.
- [21] F. R. Gantmacher. *The Theory of Matrices*. Chelsea Publishing company, New York, 1974.
- [22] D. P. Gaver, P. A. Jacobs, and G. Latouche. Finite birth-and-death models in randomly changing environments. *Advances in Applied Probability*, 16:715–731, 1984.
- [23] M. Gonzalez, R. Martinez, and M. Mota. Multitype population size-dependent branching processes with dependent offspring. *Statistics and Probability Letters*, 70:145–154, 2004.
- [24] I. J. Good. The Lagrange distributions and branching processes. *Journal of Applied Mathematics*, 28(2):270–275, 1975.

-
- [25] P. Haccou, P. Jagers, and V. A. Vatutin. *Branching Processes: Variation, Growth, and Extinction of Populations*. Cambridge University Press, 2005.
- [26] T. E. Harris. *The Theory of Branching Processes*. Dover, New York, 1963.
- [27] S. Hautphenne, G. Latouche, and M.-A. Remiche. Newton's iteration for the extinction probability of a Markovian Binary Tree. *Linear Algebra and its Applications*, 428:2791–2804, 2008.
- [28] S. Hautphenne, G. Latouche, and M.-A. Remiche. Algorithmic approach to the extinction probability of branching processes. *Methodology and Computing in Applied Probability*, 2009. To appear.
- [29] S. Hautphenne, G. Latouche, and M.-A. Remiche. Transient features for Markovian binary trees. 2009. *SMCtools '09: Proceeding from the 2009 workshop on tools for solving structured Markov chains*. To appear.
- [30] S. Hautphenne, K. Leibnitz, and M.-A. Remiche. Extinction probability in Peer-to-Peer file diffusion. *ACM SIGMETRICS Performance Evaluation Review*, 34(2):3–4, 2006.
- [31] S. Hautphenne, K. Leibnitz, and M.-A. Remiche. Modeling of P2P file sharing with a level-dependent QBD process. *Advances in Queueing Theory and Network Applications*, 2009.
- [32] S. Hautphenne and B. van Houdt. On a link between Markovian trees and tree-structured Markov chains. *European Journal of Operational Research*, 201(3):791–798, 2010.
- [33] D. Heinzmann. Extinction times in multitype markov branching processes. *Journal of Applied Probability*, 46(1):296–307, 2009.
- [34] D. M. Hull. A survey of the literature associated with the bisexual Galton-Watson branching process. *Extracta Mathematicae*, 18(3):321–343, 2003.
- [35] P. Jagers. *Branching processes with biological applications*. John Wiley & Sons, 1975.
- [36] N. Kaplan, A. Sudbury, and T. S. Nilsen. A branching process with disasters. *Journal of Applied Probability*, 12(1):47–59, 1975.
- [37] S. Karlin and H. M. Taylor. *A First Course in Stochastic Processes*. 2nd ed., Academic Press, New York, 1975.
- [38] H. Kesten and B. P. Stigum. A limit theorem for multidimensional Galton-Watson processes. *The Annals of Mathematical Statistics*, 37:1211–1223, 1966.
- [39] H. Kesten and B. P. Stigum. Limit theorems for decomposable multi-dimensional Galton-Watson processes. *Journal of Mathematical Analysis and Applications*, 17:309–338, 1967.

-
- [40] M. Kimmel and D. E. Axelrod. *Branching Processes in Biology*. Springer-Verlag, New York, 2002.
- [41] J. F. C. Kingman. Subadditive ergodic theory. *Annals of Probability*, 1:893–909, 1973.
- [42] F. C. Klebaner. On population-size-dependent branching processes. *Advances in Applied Probability*, 16:30–55, 1984.
- [43] N. Kontoleon. *The Markovian Binary Tree: A Model of the Macroevolutionary Process*. PhD thesis, The University of Adelaide, 2005.
- [44] B. K. Kumar, A. Vijayakumar, and B. Thilaka. Multitype branching processes with disasters II: Total sojourn time and number of deaths. *Mathematical and Computer Modelling*, 28(11):103–114, 1998.
- [45] K. Lange, M. Boehnke, and R. Carson. Moment computations for subcritical branching processes. *Journal of Applied Probability*, 18(1):52–64, 1981.
- [46] G. Latouche, P. A. Jacobs, and D. P. Gaver. Finite Markov chain models skip-free in one direction. *Naval Research Logistics Quarterly*, 31:571–588, 1984.
- [47] G. Latouche and V. Ramaswami. *Introduction to Matrix Analytic Methods in Stochastic Modeling*. ASA-SIAM Series on Statistics and Applied Probability, SIAM, Philadelphia, PA, 1999.
- [48] G. Latouche, M.-A. Remiche, and P. G. Taylor. Transient Markov arrival processes. *The Annals of Applied Probability*, 13(2):628–640, 2003.
- [49] C. Lee. The density of the extinction probability of a time homogeneous linear birth and death process under the influence of randomly occurring disasters. *Mathematical Biosciences*, 164:93–66, 2000.
- [50] R. J. Leveque. *Finite Volume Methods for Hyperbolic Problems*. Cambridge Texts in Applied Mathematics, 2002.
- [51] T. Lindvall. On the maximum of a branching process. *Scandinavian Journal of Statistics*, 3(4):209–214, 1976.
- [52] E. C. MacRae. Matrix derivatives with an application to an adaptive linear decision problem. *The Annals of Statistics*, 2(2):337–346, 1974.
- [53] R. M. M. Mattheij, S. W. Rienstra, and J. H. M. ten Thijs Boonkkamp. *Partial differential equations: modeling, analysis, computation*. SIAM, 2005.
- [54] C. J. Mode. *Multitype Branching Processes, Theory and Applications*. Elsevier, 1971.
- [55] S. V. Nagaev and V. Vakhtel. Probability inequalities for a critical Galton-Watson process. *Theory of Probability and Its Applications*, 50(2):225–247, 2006.

- [56] M. F. Neuts. *Matrix-Geometric Solutions in Stochastic Models: An Algorithmic Approach*. The Johns Hopkins University Press, Baltimore, MD, 1981.
- [57] M. F. Neuts. *Structured Stochastic Matrices of M/G/1 Type and Their Applications*. Marcel Dekker, New York, 1989.
- [58] J. M. Ortega and W. C. Rheinboldt. *Iterative Solution of Nonlinear Equations in Several Variables*. Academic Press, New York, San Francisco, London, 1970.
- [59] A. G. Pakes. Some limit theorems for the total progeny of a branching process. *Advances in Applied Probability*, 3(1):176–192, 1971.
- [60] A. G. Pakes. On markov branching processes with immigration. *Sankhya: The Indian Journal of Statistics, Series A*, 37(1):129–138, 1975.
- [61] A. G. Pakes. Remarks on the maxima of a martingale sequence with application to the simple critical branching process. *Journal of Applied Probability*, 24(3):768–772, 1987.
- [62] V. Ramaswami and P. G. Taylor. Some properties of the rate operators in level dependent quasi-birth-and-death processes with a countable number of phases. *Communications in Statistics: Stochastic Models*, 12(1):143–164, 1996.
- [63] R. Sedgewick. *Algorithms*. Addison-Wesley, 1988.
- [64] W. L. Smith and W. E. Wilkinson. On branching processes in random environments. *The Annals of Mathematical Statistics*, 40(3):814–827, 1969.
- [65] Belgian National Institute of Statistics. Web page, <http://www.statbel.fgov.be/pub/>, 26th Jan, 2009.
- [66] J. Strain. Semi-Lagrangian methods for level set equations. *Journal of Computational Physics*, 151:498–533, 1999.
- [67] D. Tanny. On multitype branching processes in a random environment. *Advances in Applied Probability*, 13(3):464–497, 1981.
- [68] B. Thilaka, B. K. Kumar, and A. Vijayakumar. Multitype branching processes with disasters I: The number of particles in the system. *Mathematical and Computer Modelling*, 28(11):87–102, 1998.
- [69] J. W. Thomas. *Numerical partial differential equations: Finite difference methods*. Springer, 1995.
- [70] V. A. Topchii and V. A. Vatutin. Maximum of the critical Galton-Watson processes and left-continuous random walks. *Theory of Probability and Its Applications*, 42(1):17–27, 1998.
- [71] World population prospects: The 2006 revision. Web page, United Nations Population Division, <http://esa.un.org/unpp/>, 20th Sept, 2007.

-
- [72] R. S. Varga. *Matrix Iterative Analysis*. Prentice-Hall, Engelwood Cliffs, NJ, 1962.
- [73] R. C. Wang. The extinction time of Markov branching processes. *Journal of Applied Probability*, 13(2):345–347, 1976.
- [74] WHO statistical information system (WHOSIS). Web page, World Health Organization, <http://www.who.int/whosis/en/>, 4th Dec, 2008.
- [75] X. Yang and G. de Veciana. Performance of peer-to-peer networks: Service capacity and role of resource sharing policies. *Performance Evaluation*, 63(22):175–194, 2006.