



HAL
open science

Population dynamics and epidemic processes on a trade network

Pierre Montagnon

► **To cite this version:**

Pierre Montagnon. Population dynamics and epidemic processes on a trade network. Probability [math.PR]. Université Paris Saclay (COMUE), 2019. English. NNT : 2019SACLX025 . tel-02272853

HAL Id: tel-02272853

<https://theses.hal.science/tel-02272853>

Submitted on 28 Aug 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Dynamiques de populations et processus épidémiques sur des réseaux d'échanges

Thèse de doctorat de l'Université Paris-Saclay
préparée à l'École Polytechnique

Ecole doctorale n°574
École doctorale de mathématiques Hadamard (EDMH)
Spécialité de doctorat : Mathématiques appliquées

Thèse présentée et soutenue à Palaiseau, le 1^{er} Juillet 2019, par

PIERRE MONTAGNON

Composition du Jury :

Frank Ball Professeur, University of Nottingham	Rapporteur
Vincent Bansaye Professeur, École Polytechnique	Directeur de thèse
Tom Britton Professeur, Stockholm University	Examineur
Eva Löcherbach Professeur, Université de Cergy-Pontoise	Examinatrice
Sylvie Méléard Professeur, École Polytechnique	Présidente du jury
Étienne Pardoux Professeur émérite, Aix-Marseille Université	Rapporteur
Elisabeta Vergu Directrice de recherches, INRA	Directrice de thèse

*And now you press the second spot on the card
That stands for a situation in your life
And you imagine this situation
In the middle of this waterfall
Washed and cleaned by its amazing energy*

– Ivo Dimchev, *I-Cure*

Remerciements

Comment exprimer à mes deux directeurs la reconnaissance qu'ils méritent ? Évoquer leur patience, leur gentillesse et leur disponibilité est fort convenu et ne rend pas compte de leur endurance quasi-chrétienne face à un trublion parfois réfractaire (quoique bien intentionné), irrémédiablement nanterrien, malade plus souvent qu'à son tour et à l'efficacité aléatoire. Parvenir avec une telle bienveillance à dégager une dérive positive de mes fluctuations est un tour de force dont je leur serai durablement reconnaissant. J'ai peine à imaginer des directeurs plus à l'écoute et plus compétents que Elisabeta Vergu et Vincent Bansaye. Leur investissement, leur complémentarité et la confiance qu'ils inspirent sur le plan scientifique et humain ont été des moteurs essentiels de mon travail et de mon épanouissement durant ces trois dernières années.

I wish to express my deepest gratitude to MM. Ball and Pardoux for having accepted to report on my work. A short glance at any chapter of the present manuscript is enough to appreciate the importance of their theoretical results in the framework of my thesis. I am honored that such major contributors of the field of epidemiologic modeling agreed to evaluate my own research.

Obviously, this elite epidemiologist squad would not have been complete without the participation of M. Britton, whom I thank warmly for joining the jury.

Un grand merci à Eva Löcherbach et Sylvie Méléard d'avoir elles aussi bien voulu apporter leurs expertises respectives à l'examen de mon travail de thèse. Eva Löcherbach, qui l'apprendra sans doute en lisant ces remerciements, est à l'origine de mon émerveillement devant des systèmes de neurones en interaction et de mon intérêt pour les mathématiques appliquées à la biologie. Quant à Sylvie Méléard, je lui dois, ainsi qu'à la chaire MMB de façon plus générale, d'avoir baigné dans un environnement intellectuel particulièrement stimulant et varié durant un peu plus de trois ans.

Mes contacts avec les chercheurs et doctorants du CMAP et avec les membres de la chaire MMB ont été la source de découvertes scientifiques dont je suis profondément heureux. En particulier, je souhaite remercier Amandine Veber, Carl Graham, Joseba Dalmau, Michele Salvi et Adrien Prodhomme pour la qualité des différents groupes de travail auxquels ils ont contribué et de nos discussions passées.

Parmi mes deux laboratoires d'accueil, c'est néanmoins dans l'unité MaIAGE de l'INRA de Jouy-en-Josas que j'ai passé le plus de temps. Et quel temps ! Il n'est pas donné à tous les chercheurs de pouvoir travailler dans un repaire de cruciverbistes, musiciens ou joueurs de cartes par ailleurs à la pointe de leurs domaines de recherche respectifs, dans un havre pastoral doté à la fois d'un potager et d'un cluster de calcul, de troupeaux de vaches susceptibles et d'accès illimités à des centaines de revues scientifiques. Merci donc à Maxime, Leo, Halaleh, Aj-

mal et Romain pour leur amitié et leur capacité à ne pas perdre de vue les choses importantes de l'existence. Merci aussi à Jean-Pierre Gauchi, Patrick Hoscheit, Estelle Kuhn, Olivier David, Béatrice Laroche, Simon Labarthe, François Deslandes, Gaël Beaunée et tant d'autres, pour l'aperçu brillant et humain qu'ils m'ont offert du monde de la recherche.

C'est cependant la formidable expérience d'enseignement que j'ai vécue ces dernières années qui a achevé de me convaincre de m'engager dans la voie du professorat, et ce, malgré le dépit affiché par environ 50% de mes directeurs. Je suis profondément reconnaissant à Frédéric Pascal, Claudine Picaronny, Hugo Harari-Kermadec et Antoine Hémon de m'avoir permis d'effectuer mon monitorat à l'ENS de Cachan auprès de publics divers mais toujours du plus haut niveau. Préparer et assurer des cours, leçons et travaux dirigés dans les préparations à l'agrégation de mathématiques et de sciences sociales a été pour moi un défi ainsi qu'un honneur, et à ce jour la mission d'enseignement la plus stimulante et la plus jouissive qu'il m'ait été donné d'assurer.

Merci bien sûr, et surtout, à mes amis et à tous ceux qui partagent ma vie. À ceux que je retrouve en rentrant chez moi, à ceux que je rencontre avec un archet à la main ou une lampe au front, à ceux qui chantent et à ceux qui parlent, à ceux qui racontent des histoires, à ceux qui jouent, à ceux qui sont là, aux autres aussi. Merci à tous ceux du passé et à tous ceux du présent, merci à la vie qui avance. Merci à mes parents, pour leur amour et leur permanence.

Obrigado, a quem possa interessar, por fazer as perguntas certas, por expandir meu mundo, por me desafiar e confortar, por ser quem você é e não desistir do caminho mais difícil.

Je remercie enfin Nicolas Doduik, en marmonnant de façon quasi-ininterrompue

Contents

1	Introduction	11
1.1	Context and motivation	11
1.1.1	Context of cattle trade network analysis and available data	12
1.1.1.1	Analysis of cattle trade networks	12
1.1.1.2	The French National Cattle Database	12
1.1.2	Modeling context	14
1.1.2.1	Metapopulation models	14
1.1.2.2	Stochastic SIR epidemics on networks	15
1.1.2.3	Stochastic SIR epidemics with demography	16
1.2	Modeling approach	17
1.2.1	Piecewise deterministic metapopulation processes	17
1.2.2	Metapopulation Markovian jump processes	18
1.2.2.1	The branching population model	19
1.2.2.2	The logistic population model	20
1.2.3	The epidemic process	22
1.2.4	Questions raised by the models under study	24
1.3	Probabilistic concepts and main results of the thesis	25
1.3.1	Stability of Markov processes	26
1.3.1.1	Irreducibility, Harris recurrence and ergodicity	26
1.3.1.2	Sampled chains and petite sets	29
1.3.1.3	A Foster-Lyapunov criterion	31
1.3.1.4	Stability of the population models under study	31
1.3.2	Results on continuous-time multitype branching processes	32
1.3.2.1	Definition	32
1.3.2.2	Fundamental properties of a multitype branching process	33
1.3.2.3	Approximation of epidemic processes	38
1.3.3	Scaling limits	40
1.3.3.1	Scaling limits of density-dependent population processes	40
1.3.3.2	Scaling limits of population and epidemic processes	41
1.3.4	Metastability for scaled Markov jump processes	42
1.3.4.1	Exit time from a domain for a scaled Markov jump process	43
1.3.4.2	Large deviations of the processes under study	44
1.4	The tau-leaping simulation method	46

2	The population model	51
2.1	Piecewise deterministic Markovian metapopulation processes	51
2.1.1	Introductory remarks	51
2.1.2	Definition of the metapopulation PDMP	54
2.1.3	Multiplicative and unitary models	55
2.1.3.1	Additional assumptions	55
2.1.3.2	Multiplicative models	57
2.1.3.3	Unitary models	60
2.1.4	Stability criteria for the metapopulation PDMP	61
2.1.4.1	Criterion for boundedness	62
2.1.4.2	Criterion for petiteness	66
2.1.4.3	Criterion for ergodicity	69
2.1.5	Proof of stability Theorem 2.1.2	71
2.1.6	Proof of stability Theorem 2.1.5	76
2.1.7	Conclusion on metapopulation PDMP	78
2.2	The branching population model	78
2.2.1	Definition of the branching population model	79
2.2.2	Stability and scaling limit of the branching population process	80
2.3	The logistic population model	85
2.3.1	Definition of the logistic population model	85
2.3.2	Stability and scaling limit of the logistic population process	86
3	The epidemic model	89
3.1	The unitype (one-population) case	89
3.1.1	The unitype branching-driven SIR model	89
3.1.1.1	The case $p = 1$	90
3.1.1.2	The case $q > 0$	94
3.1.2	The unitype logistic-driven SIR model	96
3.1.2.1	The case $p = 1$	97
3.1.2.2	The case $q > 0$	98
3.2	The multitype case	100
3.2.1	The branching-driven SIR model	100
3.2.1.1	The case $p = 1$	102
3.2.1.2	The case $q \neq 0$	111
3.2.2	The logistic-driven SIR model	113
3.2.2.1	The case $p = 1$	115
3.2.2.2	The case $q \neq 0$	118
4	Network vulnerability assessment and numerical applications	121
4.1	Dataset description and parameter calibration	121
4.1.1	Dataset description	121
4.1.2	Calibration of the demographic parameters	122
4.2	Indicators of node criticality	127
4.2.1	Major outbreak probabilities	128
4.2.2	Mean number of contaminated nodes	130

4.2.3	Composite indicators	132
4.2.4	Simulation-based indicators	136
4.3	Elaboration, choice and evaluation of targeted control strategies	138
4.3.1	Assessing the severity of an epidemic event	139
4.3.1.1	The quest for a threshold parameter	139
4.3.1.2	Monte-Carlo estimation of the epidemic final outcome	140
4.3.2	Design of control strategies	140
4.3.2.1	Identification of critical nodes	141
4.3.2.2	Actions on critical nodes	142
4.3.3	Control strategies assessment	143
4.3.3.1	Screening at importation	143
4.3.3.2	Isolation	144
4.3.3.3	Vaccination	145
5	Conclusion and perspectives	147
6	Appendices	151
	Appendix A: On the invariant probability of X	151
	Appendix B: Invariant measure of the branching population process	153
7	Contexte et résultats de la thèse	157
7.1	Contexte scientifique et problématique pratique	157
7.1.1	Analyse des réseaux d'échanges de bovins et données empiriques	158
7.1.1.1	Analyse des réseaux d'échanges de bovins	158
7.1.1.2	La Base de Données Nationale d'Identification (BDNI)	160
7.1.2	Contexte de modélisation	160
7.1.2.1	Modèles de métapopulations	160
7.1.2.2	Processus stochastiques SIR sur des réseaux	161
7.1.2.3	Modèles SIR stochastiques avec démographie	163
7.2	Modélisation	164
7.2.1	Processus de métapopulations déterministes par morceaux	164
7.2.2	Processus de métapopulations markoviens à sauts	165
7.2.2.1	Le processus de population branchant	166
7.2.2.2	Le modèle de population logistique	167
7.2.3	Le processus épidémique	168
7.2.4	Questions soulevées par les modèles étudiés	171
7.3	Principaux résultats théoriques de la thèse	172
7.3.1	Stabilité des modèles de population étudiés	172
7.3.2	Approximation des processus épidémiques à l'étude par des processus de branchement	173
7.3.3	Limites d'échelle des processus étudiés	174
7.3.4	Résultats de grandes déviations pour les processus étudiés	176
	Bibliography	177

Notations

The following notations will be used throughout this work. Chapter-specific notations will be introduced in the corresponding sections.

Symbol	Meaning
n	Number of nodes
$\llbracket 1, n \rrbracket$	$\{1, \dots, n\}$
\mathcal{I}	Edges set $\{(i, j) \in \llbracket 1, n \rrbracket^2 : i \neq j\}$
E^c	Complement of a subset E in the ambient space
1_E	Indicator function of a subset or an event E in the ambient space
$\langle \cdot, \cdot \rangle$	Usual scalar product of \mathbb{R}^n
$\ \cdot\ _1$	l_1 norm on \mathbb{R}^n
$\ \cdot\ _2$	l_2 (Euclidean) norm on \mathbb{R}^n
$\ \cdot\ _\infty$	l_∞ (uniform) norm on \mathbb{R}^n
$\mathcal{B}_i(x, \delta)$	Open ball with center x and radius δ for norm $\ \cdot\ _i$
$\mathcal{B}(E)$	Borel σ -algebra on a Borel subset E of \mathbb{R}^n
tA	Transpose of matrix A
$\text{diag}(\lambda_1, \dots, \lambda_n)$	Diagonal $n \times n$ matrix with diagonal coefficients $\lambda_1, \dots, \lambda_n$
(e_1, \dots, e_n)	Canonical basis of \mathbb{R}^n
x_i	i -th coordinate of vector $x \in \mathbb{R}^n$ or \mathbb{R}^n -valued function x
X_i	i -th coordinate of \mathbb{R}^n -valued process X
$a \wedge b$	$\min(a, b)$
$a \vee b$	$\max(a, b)$
a_+	$0 \vee a$
$\lfloor x \rfloor$	$(\lfloor x_1 \rfloor, \dots, \lfloor x_n \rfloor)$ (with $x = (x_1, \dots, x_n) \in \mathbb{R}^n$)

1

Introduction

The present work is devoted to the mathematical analysis of continuous-time stochastic metapopulation models coupled with stochastic epidemic processes on a graph. We first investigate on the modeling of population dynamics within a network of exchanging cattle holdings (Chapter 2), considering transfers occurring at random times and examining both deterministic and stochastic regimes for local population evolution. Focusing on Markovian jump population processes, we define corresponding epidemic models suitable to describe the spread of an epidemic over the trade network (Chapter 3). Theoretical results derived from these models make it possible to assess the vulnerability to the epidemic of a real cattle exchange network and to design and evaluate control strategies (Chapter 4).

This introduction is structured as follows. Section 1.1 states the scientific context and practical motivations of this work. In Section 1.2, we sketch the metapopulation and epidemic models under study. Section 1.3 presents the mathematical concepts used in the next chapters as well as an overview of the main theoretical results of this thesis. Lastly, Section 1.4 presents a fast simulation method for Markov jump processes, that will be used in numerical applications in Chapter 4.

1.1

Context and motivation

Animal movements due to trade are a major vector of epidemic spread between cattle holdings at large spatial scales [KDGK06]. The practical motivation for the present work stems from a research project named Cadence, funded by the French National Research Agency (ANR). It is focused on the statistical study, mathematical modeling, vulnerability assessment and epidemic control for cattle infectious diseases spreading through animal movements on French cattle trade networks.

Networks are quite natural representations of exchanging cattle holdings, that play the role of nodes while trade relationships can be represented as directed links. These networks are weighted according to the number of animals exchanged, and time-varying since activated links and their weight are not permanent over time, expressing the variability of trade relationships.

Epidemic dynamics on cattle trade networks are likely to exhibit *endemicity* — that is, persistence of the infection at a moderate level over large time scales. Indeed, particular livestock demographics entail a fast population renewal, and therefore a steady flow of new individuals potential pathogen hosts entering the system. When modeling epidemics on a cattle trade network, it is therefore necessary to take into consideration imports, births and deaths of animals occurring on the same time scale as epidemic dynamics. Thus, we shall be aiming for a unified modeling framework coupling metapopulation dynamics and epidemic propagation among network-structured populations.

Before presenting the models under study, we proceed to an overview of the applicative problematics and the modeling context to which they relate.

1.1.1 Context of cattle trade network analysis and available data

This subsection presents elements on empirical cattle trade networks analysis and a presentation of the dataset upon which the numerical analysis presented in Chapter 4 will be conducted.

1.1.1.1 Analysis of cattle trade networks

The important amount of data collected by European authorities over the last two decades consecutively to the BSE crisis makes it possible to track the position over time of every single piece of cattle within national territories [Ver11, DEV14]. This allows for very detailed descriptions of the properties of the cattle trade network observed on arbitrarily fine time intervals [VK09, Ver11, DEV14], but also for building and calibrating models for pathogen spread [PGPSV12, BVE15, HGM⁺16] that can eventually lead to designing control strategies [BVJE17].

Studying the connectivity of an empirical trade network is a first step towards the evaluation of its vulnerability to an infectious disease (see [RDD11] for an analysis of the size of connected components of a real network and [HS12] for a review on the more sophisticated *reachability ratio* accounting for time-varying characteristics of the network). Such a study also helps design containment strategies [DEV14] that limit the disruptions of market mechanisms [MGM⁺16]. The structure of the network itself can be predicted using suitable microeconomic models [HGM⁺16] or using more general activity-based models [PGPSV12].

Another approach, that we will follow in the rest of this work, consists in interpreting the characteristics of the observable network as realizations of a Markovian metapopulation process. In this case, it is possible to derive theoretical results on epidemic dynamics coupled with this process to evaluate quantities related to the network vulnerability induced by various nodes. Instances of such quantities are the probability of a major epidemic outbreak, the total size of an epidemic, or the expected number of holdings reached by the infection, when the epidemic is started by one initial infective in a given node.

1.1.1.2 The French National Cattle Database

Modeling choices and control strategies evaluation in the next chapters will be guided by empirical observations from the French National Cattle Database (FNCD), maintained by the

French Ministry of Agriculture. This database traces back the path of every piece of cattle within the French territory between 2005 and 2015 [RDD11, DEV14] and was already used for calibrating models and for designing and assessing control strategies in the past few years [BVE15, QVDE17, BVJE17].

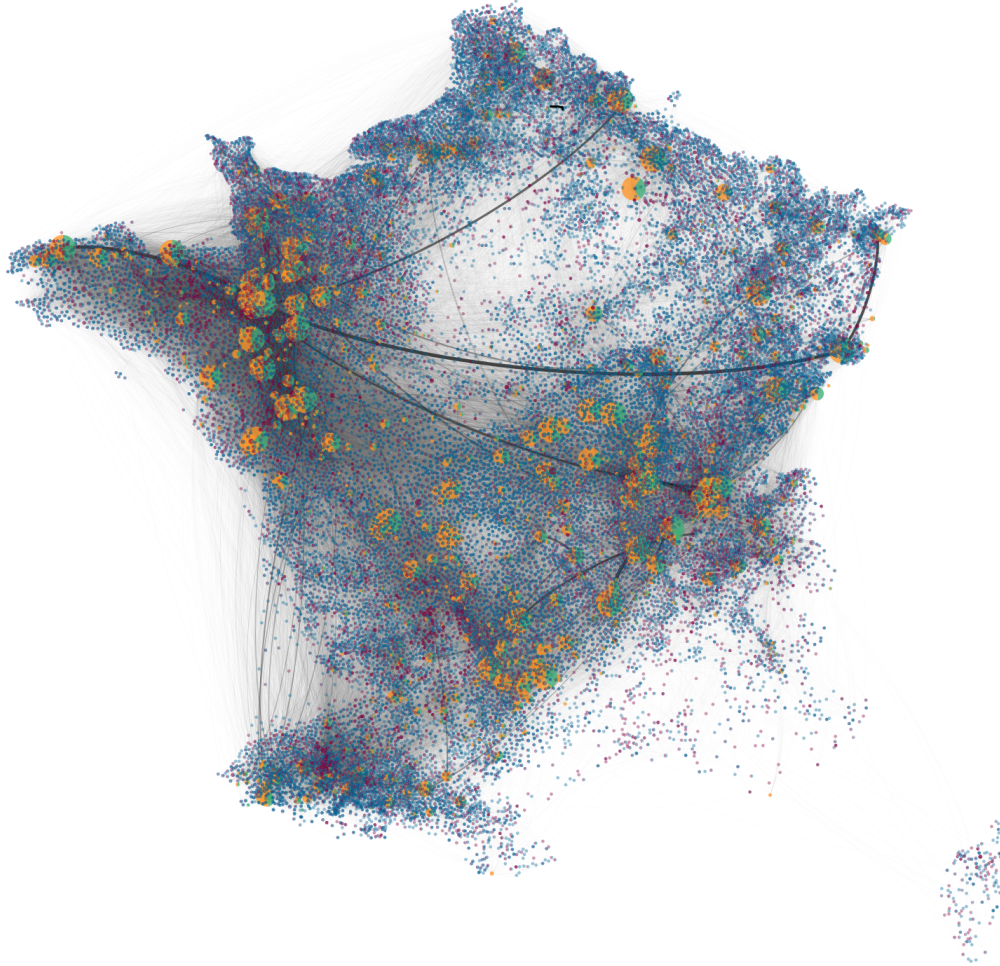


Figure 1.1: Representation of the cattle trade network of France in 2008. Exchanging cattle holdings are aggregated at the commune level. The size of a node represents its mean population over the year. Colours on the nodes represent the share of buying (orange for operators and red for farms) and selling (green for operators and blue for farms). The edges represent the existence of a movement between two holdings in the dataset, with their width indicative of the observed trading volume along this edge. The picture is courtesy of Gaël Beaunée.

The raw data available consist in five layers of information [DEV14]. The first layer is the detention record of various holdings over time, displaying among other information the national identification number of animals held, their date and cause of entry into the holding (either by birth or by purchase), and their date and cause of exit from the holding (either by death or sale). The second layer contains the life history of every animal, with its national identification number, its date and holding of birth, its sex, its race and the date of its first calving. The other three layers contain information about markets and assembling centers (that we will refer to as

operators) and about slaughterhouses. As in [DEV14], in the processing of the data we treated slaughterhouses as sinks unlikely to play a role in the spread of infectious diseases, so deaths and transfers to slaughterhouses were considered as movements of the same nature. These raw data make it possible to build a full record of cattle trade exchanges on the French territory between 2005 and 2015, tracing for each movement its date, its origin and destination (in terms of holding type and identification), and the identification number of animals involved. From this record, it is possible to build and represent the empirical cattle trade network over any period of time (see Figure 1.1).

1.1.2 Modeling context

The modeling approach of the present work and its mathematical contributions lie in the field of metapopulation models and epidemiological models on graphs. The following subsections give a brief (and far from exhaustive) overview of the existing literature on these topics.

1.1.2.1 Metapopulation models

Metapopulation models describe the behavior of a population naturally or artificially split into spatially distant patches connected through individual movements. Although the reality of distant but connected populations had been studied by biologists since the 1950s [AB54, Huf58, MW67], the term itself was coined and defined in 1969 by Levins, who studied a deterministic model describing the evolution of the total number of patches occupied by a species over time [Lev69, Lev70]. Important refinements on the initial models were introduced, such as a distinction between some patches as *sources* of population that can survive thanks to their own growth and others as *sinks* that go extinct in the absence of dispersal [Pul88], the incorporation of the *rescue effect* through which small populations are compensated by immigration in order to avoid their extinction [Han83, HMG96, Eti00], or the fact of taking landscape patterns into account by exploiting the explicit spatial distribution of patches [Pul88, Kar90, KW95, Rit97]. Metapopulations models nowadays appear in numerous biological contexts, especially in the study of biodiversity, thanks to their ability to mix spatial informations and individual typologies [JS03, BWG⁺09, WCC⁺16]. More complete reviews on the various extensions of the original Levins model and their applications can be found in [HG91, HS97, Han99, Eti02].

Stochastic metapopulation models will be of paramount interest for the present work. Hanski's Incidence Function Model [Han94, VtN00] first introduced some degree of stochasticity in the dispersion of individuals across patches. Yet it describes the state of a metapopulation as a vector of binary occupancy indicators and does not consider local, intra-patch demographics (see also [GS94, EN02]). Other models, based on Markov processes, take into account local population dynamics (births and deaths) and/or transfers between patches happening at random times, with transition rates either estimated directly on the available data [VLM91] or given by a parametric population model (see [PDGM00] for a metapopulation model with logistic population growth, to be compared with the deterministic [Ayd17]). The population models we will introduce in the next section belong to this latter class. So do multitype branching processes, that enjoy many theoretical properties due to the very strong branching assumption [Ath68, Mod71, AN72] and can be used to describe metapopulations [GL00, BL13, HJK16, Ada16] without being limited to this use, as we shall see in the next section.

1.1.2.2 Stochastic SIR epidemics on networks

SIR (Susceptible – Infected – Removed) compartmental models introduced as ODE systems by Kermack and McKendrick [KM27] and their stochastic counterparts [Bar49, Ken56] are widely used in epidemiology to describe diseases with lifelong immunity upon recovery (for instance measles, rubella, mumps and pertussis in the case of human health). In these models, alive individuals can be assigned three sanitary statuses: they are either Susceptible (S) and never yet hit by the disease, Infected (I) and potentially at the origin of infectious contacts that turn susceptible individuals into infected ones, or Removed (R) after recovering from an infection and permanently immune to it. During their lifetime, individuals may move between compartments from Susceptible to Infected (in the case of an infection event) or from Infected compartment to Removed (in the case of a recovery). In the original SIR models, the population is assumed to be *homogeneously mixing*, which means that each infective is homogeneously in contact with all other individuals of the population, and therefore equally likely to infect any susceptible individual. A large panel of variations on the SIR model was developed, taking into account for instance additional types of health statuses, eventual loss of immunity, age structure or heterogeneous mixing (see the monography [KR07] for an extensive presentation of such models, specifically developed for various applicative contexts).

Given the application we have in mind, we will be particularly interested in models accounting for the spreading of SIR epidemics on contact networks. There has been important literature about such models since three decades. While many models represent individuals themselves as nodes (see for instance [BN08, DF15]), some use nodes to represent subpopulations corresponding to different *types* [Bal86, BC93, Cla94, BC95, Cla96, Nea12]. These types can be thought of as biologically distinct subpopulations within the same space, but can also be seen as groups of individuals located in geographically distinct patches. With this interpretation, multitype SIR models are couplings of epidemiological and metapopulation models. Yet, even within such frameworks, intra-nodal population dynamics related to births or deaths are seldom taken into account, thus resulting in fixed-size models in which infectives may [BC93, Cla94, Cla96, Nea12] or may not [Bal86, BC95, AB00a] move across nodes. According to cases, infectives may [Bal86, BC95, AB00a] or may not [BC93, Cla94, Cla96, Nea12] make infectious contacts with individuals from other nodes. For such models, the focus is generally put on describing the first stages of the epidemic as well as its final outcome. [Cla96, Nea12] approximate the epidemic process by a multitype branching process in the first stages of the epidemic as the typical population size N tends to infinity, and distinguish between two types of epidemic behavior according to whether the branching process survives (a *major epidemic outbreak*) or not (a *minor epidemic outbreak*). For some fixed-sized models, exact results for the *final size of the epidemic* — that is, the total number of individuals infected during the course of the epidemic — can be derived using the so-called *Sellke construction*, that consists in associating each individual with a critical level of exposure to the epidemic under which it is Susceptible and over which it becomes Infected (see [Sel83] and Chapter 6 of [AB00a]). In [BC93, Cla94, BC95], asymptotic estimations under the $N \rightarrow +\infty$ limit are derived for the final size of the epidemic, generalizing the proofs of [Sca85, Sca90] to the multitype case. We will be aiming at similar results when studying epidemiological models in Chapter 3.

Among the models we just described, the *dynamic epidemic model* studied in [Nea12] is the closest demography-free counterpart to the settings we will study. It represents the spread of an SIR epidemic among a population divided into subpopulations between which individuals move according to a Markov transition matrix, regardless of their health status. In this model, infectives can only make infectious contacts with members of their current subpopulation. Neal computes the moment generating function of the offspring of one infective individual for a branching process approximating the epidemic in its first stages (see [Cla96]). Knowing an analytic expression for this function allows to compute numerically the probability of a major epidemic outbreak. It also yields an estimate for a classic epidemiological parameter, the *basic reproduction number* R_0 , that roughly describes the average number of infections caused by an infective in an initially fully susceptible population during its lifetime. We will adapt this approach to our models with population renewal in Chapter 3.

In the past few decades, there has been debate on the relevance of the R_0 parameter in the context of networks or small-sized, homogeneously mixing subpopulations (also known as *household-organized networks*) [BN08, BST09, BST10, PBT11, BBH⁺15, BPT16, BS18]. Active research has been led on an alternative *threshold parameter* that would help classify the behavior of an epidemic on such networks, and a variety of new quantities have been defined and compared [BPT16]. They will inspire our investigation on indicators for network vulnerability in Chapter 4.

1.1.2.3 Stochastic SIR epidemics with demography

Our goal is to provide models that account for population evolution by immigration, births, deaths and migration between patches on one side, allowing to generate plausible dynamics in agreement with observations, and for local SIR epidemic dynamics on the other side. It has been shown [VHG95, VH97, Nå99, AB00b] that such *open* SIR models differ from their demography-free counterparts in that they allow for endemicity, so the epidemic persists over a given threshold when a major epidemic outbreak occurs ([Bar56]; on the importance of endemicity as a current topic of study for epidemiology, see [Bri10]). The probability of a major epidemic outbreak (Chapter 4 of [AB00a], [Cla96, Nea12]), as well as the extinction time and the total size of an epidemic in the case of a major outbreak, are therefore essential quantities of interest in the study of the epidemic process, especially from a control perspective. However, the Sellke construction and other techniques used in [Sca85, Sca90, BC93, BC95, AB00a] to derive explicit results on the final size of the epidemic in the fixed-size case fail to transpose in the multitype open setting, in which the exposure of individuals to infection starts at various times, varies as populations move on the graph, and eventually ends at random times. As a result, a large part of the literature on open SIR models rather focuses on obtaining estimates for the extinction time of the epidemic [AB00b, O’N96] and describing the qualitative behavior of the process after a major outbreak episode [VHG95, VH97].

Some authors consider open demographic dynamics coupled with epidemic processes but mostly deal with single-type models — that is, with one single, uniformly mixing population. Most of such models either rely on a population process with population-proportional [O’N96, CG07] or constant [Nå99, AB00b] entry rates. In all these specifications, the set of disease-free states is absorbing and the extinction of the epidemic in finite time is almost sure. [AB00b] and

[Nå99] study the *quasi-stationary distribution* (QSD) of the epidemic process, that is, the long-time limit of its distribution conditionally on not being extinct, as well as the extinction time of an epidemic having this QSD as initial distribution. [O’N96] approximates the extinction time of the epidemic by that of a birth and death process as a population scaling parameter N tends to infinity, yet without estimating its distribution for fixed values of N . Part of our focus in Chapter 3 will be on the time scale over which the epidemic goes extinct in our open SIR setting. We will show that under the endemicity regime, the extinction time is greater than an exponential function of N with probability tending to 1.

In Chapters 3 and 4, we will study a multitype SIR model coupled with metapopulation dynamics where transition rates are either affine (the so-called *branching-driven SIR model*) or logistic (the *logistic-driven SIR model*). A similar open multitype setting with affine rates is studied in the case of a SI model in [BS16] using a mostly numerical approach. Various deterministic counterparts of our stochastic SIR branching model can be found in [MA07, LS09, MEK13, TL15, TIK18]. SIR models with a logistic population evolution are less common. We refer to [WZJ10, LTW⁺17, MMZB17, GS18] for deterministic specifications, and to [ZH15] for a model with Brownian stochasticity. To the best of our knowledge, models similar to our stochastic logistic-driven SIR setting have not yet been considered in the literature.

1.2

Modeling approach

Our first task is to define a general metapopulation model on a network. Depending on the size of the populations considered and the time steps at which they are observed, different modeling approaches can be used to represent their evolution. We consider a piecewise deterministic Markovian metapopulation process (a *metapopulation PDMP*, Subsection 1.2.1) describing a deterministic local evolution of controlled populations between stochastic inter-patches transfers. Then, relaxing assumptions on the deterministic control of local demographics, we examine a fully-stochastic regime that results in a more tractable \mathbb{Z}_+^n -valued pure jump process specifications (Subsection 1.2.2) that we couple with a stochastic SIR model (Subsection 1.2.3).

1.2.1 Piecewise deterministic metapopulation processes

When the populations under study are typically large, with an evolution controlled in a deterministic way (as is the case in cattle holdings) and transfers between nodes occurring at random times (for instance because of exogenous economical dynamics), it is natural to model the population of the system patches as a \mathbb{R}_+^n -valued Markovian metapopulation process $X = (X_1, \dots, X_n)$ driven both by a continuous flow and by a set of jump processes. The resulting mathematical object is known as a *piecewise deterministic Markov process* (PDMP).

In this metapopulation model, we therefore consider that the population of each patch i is associated with an autonomous growth function ϕ_i (meaning that $dX_i(t) = \phi_i(X(t))dt$ when no jump occurs), and that an instantaneous transfer from patch i to patch j at population x occurs at state-dependent rate $\theta_{i,j}(x)$, its amplitude being drawn according to a $[0, x_i]$ -supported law $\mu_{i,j}(x, \cdot)$.

This model will be defined in a general framework in Section 2.1. For now, we consider the two following motivating examples, that emerged from the modeling of cattle trade network dynamics. Set $n \geq 1$ and $\mathcal{G} = (\llbracket 1, n \rrbracket, \mathcal{A})$ a strongly connected directed graph on $\llbracket 1, n \rrbracket$ (where \mathcal{A} is a subset of $\mathcal{S} := \{(i, j) \in \llbracket 1, n \rrbracket^2 : i \neq j\}$), define $(c_1, \dots, c_n) \in \mathbb{R}^n \setminus \{0\}$ and consider the constant-growth settings defined by:

Multiplicative uniform setting

$$\phi_i(x) = \begin{cases} c_i & \text{if } c_i \geq 0 \\ c_i 1_{x_i > 0} & \text{if } c_i < 0 \end{cases} \quad \text{and} \quad \begin{cases} \theta_{i,j}(x) = \theta_{i,j} \\ \mu_{i,j}(x, \cdot) = \mathcal{U}([0, x_i]) \end{cases} \quad (1.1)$$

with $\theta_{i,j} > 0$ if $(i, j) \in \mathcal{A}$ and $\theta_{i,j} = 0$ otherwise, or:

Unitary power setting

$$\phi_i(x) = \begin{cases} c_i & \text{if } c_i \geq 0 \\ c_i 1_{x_i > 0} & \text{if } c_i < 0 \end{cases} \quad \text{and} \quad \begin{cases} \theta_{i,j}(x) = (1 \vee x_i)^\alpha \\ \mu_{i,j}(x, \cdot) = \delta_{1 \wedge x_i} \end{cases} \quad (1.2)$$

for some $\alpha \in (0, 1]$.

Specification (1.1) corresponds to the case of patches transferring at constant temporal rate a random fraction of their population to each other. It fits to empirical data on cattle trade observed over large time steps, but is not mechanistically realistic since the actual size of cattle transfers is bounded by transportation capacities. Specification (1.2) corresponds to unitary population transfers occurring at population-dependent rates, which is a natural framework for modeling cattle trade movements observed on a daily basis. Note that the latter setting only differs from an open Jackson network [Jac57, MD94, Dai95] by its continuous state space and the deterministic growth flow defined by the ϕ_i .

1.2.2 Metapopulation Markovian jump processes

When populations are not large or do not exhibit low local stochasticity, their evolution between transfers cannot be described using an ordinary differential equation and is better modeled by a Markovian jump process with unitary jumps. This approach does not allow for macroscopic jumps, nor does it account for the fact that population dynamics, in the application we have in mind, are still controlled to some extent by holding management. Yet, very large jumps are not likely to happen when populations are observed on a small enough time scale. Moreover, the Markovian jump process approach allows to consider integer-valued populations, which is more realistic and makes stability analysis easier. As we will see in Subsection 1.2.3, it will also make the coupling of the population dynamics with a Poisson process-driven epidemic model quite natural.

We will only allow unitary transfers in the density-dependent jump processes we will consider — that is, immigration, birth, death or exchange events concerning exactly one individual.

Therefore, as typical populations get larger, we expect to retrieve a continuous, deterministic limit for the scaled population process; this justifies the introduction of a scaling parameter N in the models below.

In the next two subsections, we will assume that all \mathbb{Z}_+^n -valued jump processes are defined using a unique set of Poisson point measures, and that the same holds for $(\mathbb{Z}_+^n)^3$ -valued jump processes. Explicit constructions will be provided in Chapters 2 and 3.

1.2.2.1 The branching population model

We may model the population dynamics using a \mathbb{Z}_+^n -valued multitype continuous-time branching process with immigration, simply referred to as the *branching population model* in the rest of this work. For any $N \geq 1$, we define $(X^N(t))_{t \geq 0}$ as a \mathbb{Z}_+^n -valued jump process defined on (Ω, \mathcal{A}) with initial value $X^N(0) = \lfloor Nx(0) \rfloor$ for some $x(0) \in \mathbb{R}_+^n$ and the following transition rates under \mathbb{P} , with $\theta_{i,j}, b_i, B_i, d_i \in \mathbb{R}_+$:

Transition	Rate at state x	
$x \rightarrow x + e_i$	$NB_i + b_i x_i$	(1.3)
$x \rightarrow x - e_i$	$d_i x_i$	
$x \rightarrow x - e_i + e_j$	$\theta_{i,j} x_i$	

Table 1.1: Branching population process jump rates chart.

The $b_i x_i$ might be considered as Malthusian birth rates and the NB_i as constant immigration rates. All rates are represented in the synthetic Figure 1.2.

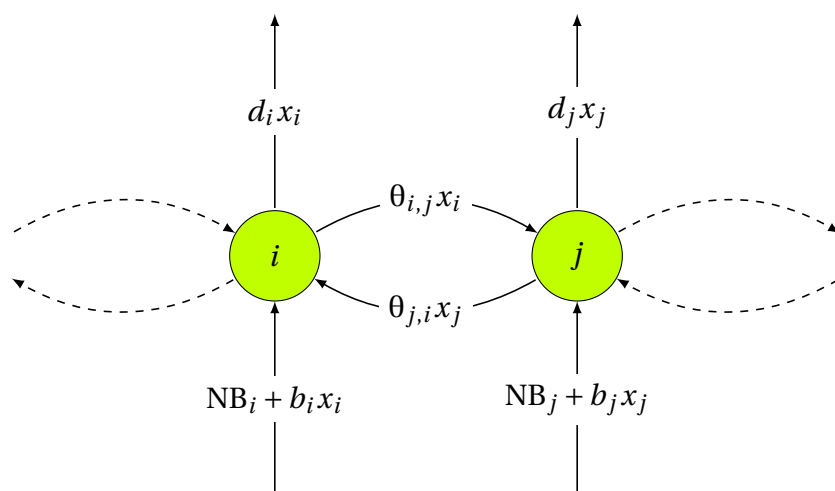


Figure 1.2: Schematic representation of the branching population process. Coefficients in the arrows are instant transition rates.

In order to focus on non-trivial cases relevant for the application we have in mind, we assume that $B = (B_1, \dots, B_n) \neq 0$ so 0 is not an absorbing state for the population processes, and that the directed graph with vertices set $\llbracket 1, n \rrbracket$ and edges set $\{(i, j) : \theta_{i,j} > 0\}$ is strongly connected so that for any i and j , any individual born in node i can get to node j with positive probability during its lifetime.

Finally, defining

$$A = \begin{pmatrix} b_1 - d_1 - \sum_{j \neq 1} \theta_{1,j} & \theta_{2,1} & \cdots & \theta_{n,1} \\ \theta_{1,2} & b_2 - d_2 - \sum_{j \neq 2} \theta_{2,j} & \ddots & \vdots \\ \vdots & \ddots & \ddots & \theta_{n,n-1} \\ \theta_{1,n} & \cdots & \theta_{n-1,n} & b_n - d_n - \sum_{j \neq n} \theta_{n,j} \end{pmatrix}, \quad (1.4)$$

we assume that all eigenvalues of A have negative real parts.

In this framework, immigration of individuals to node i occurs at rate NB_i , and individuals in node i give birth at rate b_i , die at rate d_i and move to node j at rate $\theta_{i,j}$, independently from other individuals in the network. The lineage of a single individual is a \mathbb{Z}_+^n -valued branching process with transition rates given by (1.3) with the B_i replaced by 0. Once they enter the system, individuals give birth to independent lineages that do not interact, so the number of such lineages, and therefore the typical size of the population process, is proportional to the immigration flux per unit of time, that is, to N .

The theory of continuous-time multitype branching processes presented in Subsection 1.3.2 allows for an easy characterization of the asymptotic behavior of the X^N . Since A has only eigenvalues with negative real parts, X^N appears like the superposition of subcritical branching processes initiated at rate NB , which entails stability properties. Moreover, we will see in Section 1.3.3 that the scaled limit of X^N/N (as N tend to infinity) is a deterministic process x of the simplest kind, solution of the differential equation $\dot{x} = Ax + B$.

1.2.2.2 The logistic population model

Despite its tractability, the branching population process we just presented lacks realism for the purpose we have in mind. Indeed, it does not take into account saturation phenomena that naturally limit the population of holdings with respect to their individual carrying capacity. We therefore introduce a second, more complex metapopulation jump process on \mathbb{Z}_+^n , that we will refer to as the *logistic population model*. For every node i , we define a capacity $NK_i > 0$ that intervenes both in the logistic rates of importation to node i , in its local population logistic growth rate and in the "pseudo-logistic" rates of transfers directed towards i .

For any $N \geq 1$, we define $(X^N(t))_{t \geq 0}$ as a \mathbb{Z}_+^n -valued jump process defined on (Ω, \mathcal{A}) with initial value $X^N(0) = \lfloor Nz(0) \rfloor$ for some $z(0) \in \mathbb{R}_+^n$, and with the following transition rates under \mathbb{P} :

Transition	Rate at state x	
$x \rightarrow x + e_i$	$\left(B_i + \frac{b_i}{N} x_i\right) (NK_i - x_i)_+$	(1.5)
$x \rightarrow x - e_i$	$d_i x_i$	
$x \rightarrow x - e_i + e_j$	$\frac{\theta_{i,j}}{N} x_i (NK_j - x_j)_+$	

Table 1.2: Logistic population process jump rates chart.

All rates corresponding to the logistic population process are represented in the synthetic Figure 1.3. Note that the scaling parameter N does no longer appear in the importation rate since the typical size of the system is now determined by the carrying capacity of nodes rather than by the population inflow. We let it intervene in the birth rates and transfer rates in order to obtain scaling limit results in Subsection 1.3.3.2.

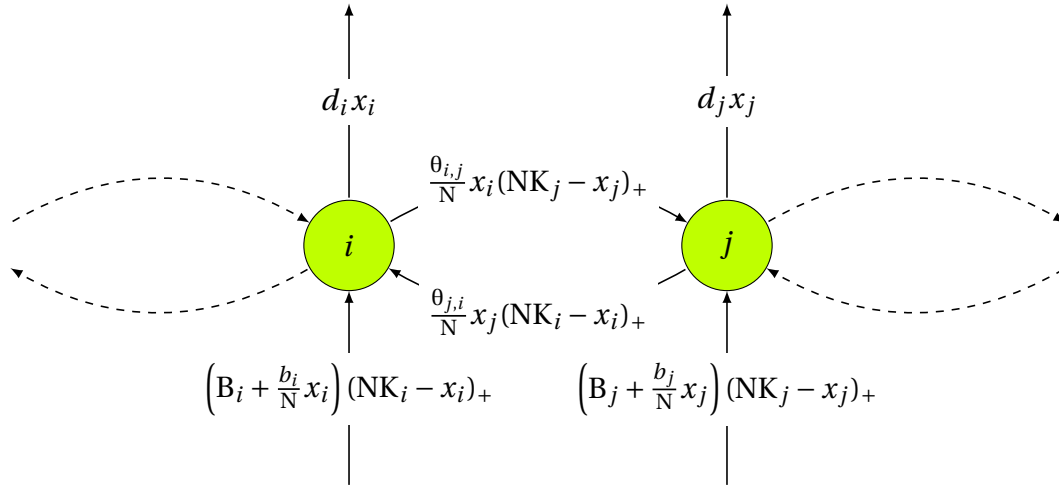


Figure 1.3: Schematic representation of the logistic population process. Coefficients in the arrows are instant transition rates.

Once again, we assume that $B = (B_1, \dots, B_n) \neq 0$ so 0 is not an absorbing state for the population process, and that the directed graph with vertices set $\llbracket 1, n \rrbracket$ and edges set $\{(i, j) : \theta_{i,j} > 0\}$ is strongly connected, so that for any i and j , any individual born in node i can get to node j with positive probability during its lifetime. We also assume that $d \neq 0$ so $NK = N(K_1, \dots, K_n)$ is not an absorbing state. Under these assumptions, X^N in an irreducible Markov jump process on $\prod_{i=1}^n \llbracket 0, \lceil NK_i \rceil \rrbracket$. It is therefore ergodic.

1.2.3 The epidemic process

We now proceed to the definition of the epidemic model, that we couple with the jump population processes introduced above.

For any N , i and t , the population $X_i^N(t)$ of the i -th node at time t is divided into three subpopulations: $S_i^N(t)$ susceptibles, $I_i^N(t)$ infectives and $R_i^N(t)$ removed individuals. Movements between nodes, births and deaths — that is, population dynamics — are assumed to be independent from health status and therefore described by the population process (branching or logistic, see chart below and Figure 1.4). All individuals born from other individuals in the system are assigned the susceptible status, that is to say that we exclude vertical disease transmission. However, infectives may enter the system through immigration; every animal imported in node i has the Susceptible status with probability p_i , the Infectious status with probability q_i , and the Removed status with probability $r_i = 1 - p_i - q_i$.

When alive and in node i , each infected individual makes contacts with individuals chosen independently and uniformly from node i , at rate β_i . Such contacts may only occur within a given node, so an infective from node i cannot make an contact with an individual from node j if $i \neq j$. Contacted individuals that are still susceptible get infected; otherwise their status does not change. Independently, infectious individuals alive in node i recover at rate γ_i and then enter the Removed compartment.

Let us write the canonical basis of \mathbb{R}^{3n} as $(e_1^s, \dots, e_n^s, e_1^i, \dots, e_n^i, e_1^r, \dots, e_n^r)$. We consider for every $N \geq 1$ a $(\mathbb{Z}_+^n)^3$ -valued Markovian pure jump process $(S^N(t), I^N(t), R^N(t))_{t \geq 0}$ defined on (Ω, \mathcal{A}) and described by the following transition rates at state (s, i, r) where $x_j = s_j + i_j + r_j$ for all $j \in \llbracket 1, n \rrbracket$:

Transition	Rate (branching case)	Rate (logistic case)
$(s, i, r) \rightarrow (s, i, r) + e_j^s$	$p_j N B_j + b_j x_j$	$\left(p_j B_j + \frac{b_j}{N} x_j\right) (N K_j - x_j)_+$
$(s, i, r) \rightarrow (s, i, r) + e_j^i$	$q_j N B_j$	$q_j B_j (N K_j - x_j)_+$
$(s, i, r) \rightarrow (s, i, r) + e_j^r$	$r_j N B_j$	$r_j B_j (N K_j - x_j)_+$
$(s, i, r) \rightarrow (s, i, r) - e_j^s$	$d_j s_j$	$d_j s_j$
$(s, i, r) \rightarrow (s, i, r) - e_j^i$	$d_j i_j$	$d_j i_j$
$(s, i, r) \rightarrow (s, i, r) - e_j^r$	$d_j r_j$	$d_j r_j$
$(s, i, r) \rightarrow (s, i, r) + e_k^s - e_j^s$	$\theta_{j,k} s_j$	$\frac{\theta_{j,k}}{N} s_j (N K_k - x_k)_+$
$(s, i, r) \rightarrow (s, i, r) + e_k^i - e_j^i$	$\theta_{j,k} i_j$	$\frac{\theta_{j,k}}{N} i_j (N K_k - x_k)_+$
$(s, i, r) \rightarrow (s, i, r) + e_k^r - e_j^r$	$\theta_{j,k} r_j$	$\frac{\theta_{j,k}}{N} r_j (N K_k - x_k)_+$
$(s, i, r) \rightarrow (s, i, r) + e_j^i - e_j^s$	$\beta_j \frac{i_j s_j}{x_j}$	$\beta_j \frac{i_j s_j}{x_j}$
$(s, i, r) \rightarrow (s, i, r) + e_j^r - e_j^i$	$\gamma_j i_j$	$\gamma_j i_j$

Table 1.3: Branching and logistic-driven SIR processes rates chart.

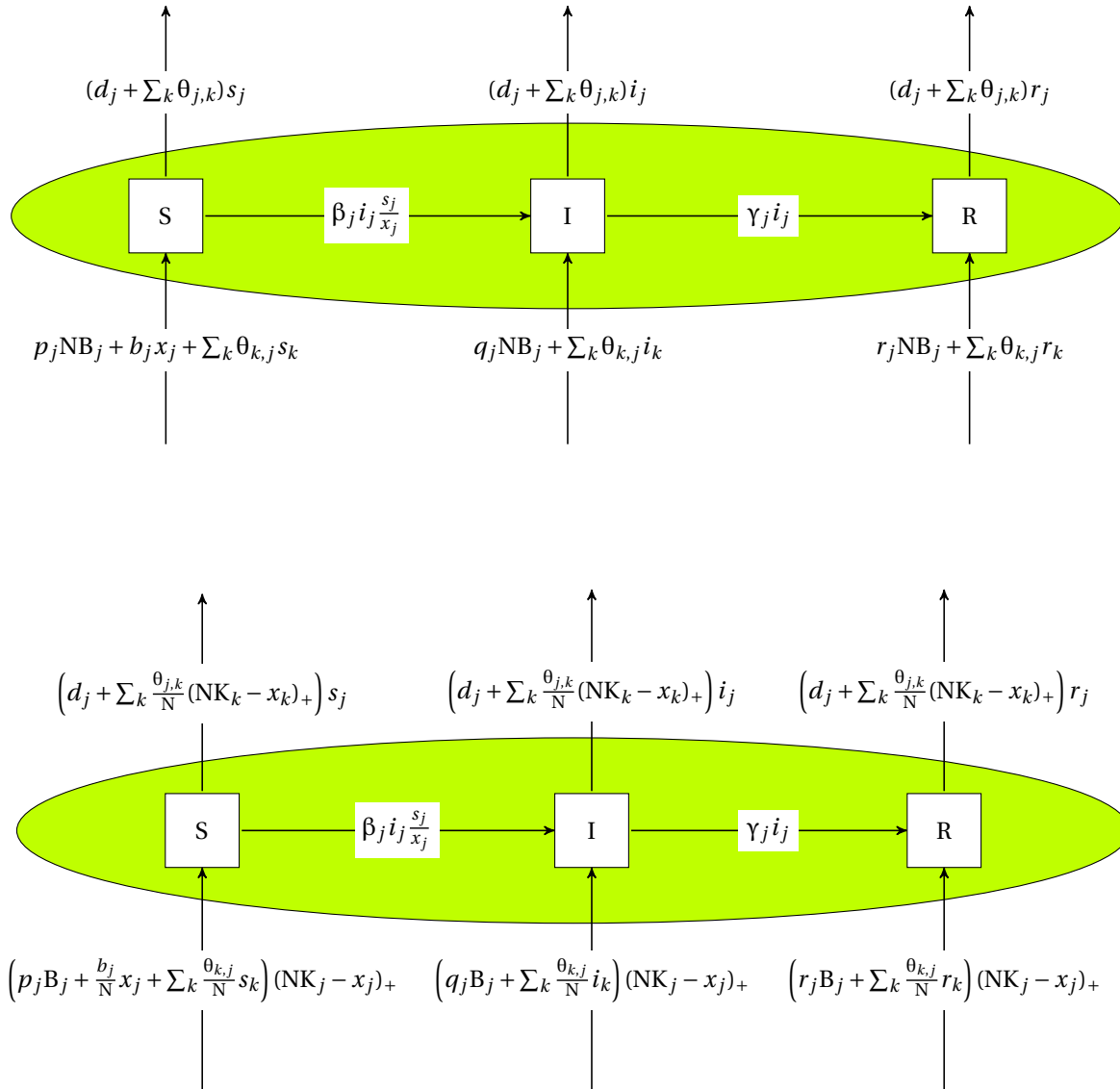


Figure 1.4: On top, schematic representation of an SIR compartmental model coupled with a branching population process (a *branching-driven SIR*). Below, schematic representation of an SIR compartmental model coupled with a logistic population process (a *logistic-driven SIR*). All three compartments are inside the same node j (pictured as a green ellipse). Coefficients on the arrows are instant transition rates. Horizontal arrows stand for transfers from one compartment to another within node j , while vertical arrows represent flows in and out of node j .

One of our focuses will be on the behavior of an epidemic started by a small number of individuals in the case $p_j = 1$ (so $q_j = r_j = 0$), that is, when immigration of infectives is ruled out, so we do not necessarily assume $I^N(0)$ to be proportional to N . In the latter case, we will instead consider that \mathbb{P} -almost surely

$$I^N(0) = I(0), \quad S^N(0) = X^N(0) - I^N(0) = X^N(0) - I(0) \quad \text{and} \quad R^N(0) = 0$$

with a fixed $I(0) \in \mathbb{Z}_+^n \setminus \{0\}^n$ (typically e_i for some i).

1.2.4 Questions raised by the models under study

In Chapter 2, we will investigate the recurrence and ergodicity properties of the population processes introduced in Subsections 1.2.1 and 1.2.2. In the case of jump population processes, we will consider two additional questions:

- By what deterministic processes can they be approximated when the typical population tends to infinity?
- Over which time scale can we consider that the population is stable?

In Chapter 3, we will study the epidemic processes introduced in Subsection 1.2.3, coupled to demographic processes studied in Chapter 2. In the case where no immigration of infectives is allowed ($p = \mathbb{1}$) and the epidemic is initiated by a fixed number of infectives accidentally introduced in the system, we will answer the following:

- By what simpler mathematical object can the epidemic process be approximated within its first stages?
- What is the probability of a major epidemic outbreak to occur?
- Over which time scale does the epidemic go extinct, and what is the total size of the epidemic?

In the case where individuals entering the system through immigration can have an infectious status with positive probability ($q \neq 0$), our focus will be on the following issues:

- What is the behavior of the epidemic process when the typical population is large?
- On which time scales can the endemicity phenomenon be observed, and to what level does the prevalence of the disease stabilize?

Chapter 4 will finally provide numerical illustrations and applications of the results on the logistic-driven SIR process derived in Chapter 3 to a real cattle trade network, organized around two guiding questions:

- How can we derive computable indicators from the analytical results of Chapter 3 to assess the network's vulnerability to an epidemic?
- What node-based control strategies can we design to reduce this vulnerability, how to assess them and which of these strategies are the most efficient?

In the next section, we introduce mathematical concepts and methods necessary to address these questions.

1.3

Probabilistic concepts and main results of the thesis

This section is devoted to presenting some mathematical theories we used and sometimes extended to study our models of interest. This presentation is strictly reduced to the notions and results that serve the purpose of the present work and does not aim at exhaustivity. At the end of each subsection, we present the main theoretical results of this work derived from the corresponding theory. In order to make novel results easier to identify, theorems and propositions from the existing literature are presented on shaded frames, while original results proved in the present work are framed.

From now on, we will consider a probabilistic space $(\Omega, \mathcal{A}, \mathbb{P})$, that we assume to be big enough so we can define all \mathbb{R}^n -valued processes and independent Poisson random measures introduced in the rest of this work.

Let E be a Borel subset of \mathbb{R}^n . We first introduce the notion of *Markov family*, that will mostly allow for a greater simplicity of notation.

DEFINITION 1.3.1 (Markov family). — A Markov family on a filtered space $(\Omega, \mathcal{A}, (\mathcal{F}_t)_{t \geq 0})$ associated with a semigroup $(P^t)_{t \geq 0}$ on $E \times \mathcal{A}$ is a family $(X, (\mathbb{P}_x)_{x \in E})$, where X is a $(\mathcal{F}_t)_{t \geq 0}$ -adapted process on (Ω, \mathcal{A}) and $(\mathbb{P}_x)_{x \in E}$ is a family of probabilities on (Ω, \mathcal{A}) such that for any $x \in E$, X is a Markov process with semigroup $(P^t)_{t \geq 0}$ and almost sure initial value x under \mathbb{P}_x .

In the framework of this definition, for any $x \in E$ we will denote by \mathbb{E}_x the expectation associated with \mathbb{P}_x .

DEFINITION 1.3.2 (Strongly Markovian Markov family). — We say that a Markov family $(X, (\mathbb{P}_x)_{x \in E})$ on $(\Omega, \mathcal{A}, (\mathcal{F}_t)_{t \geq 0})$ is strongly Markovian (or satisfies the strong Markov property) if for all $(\mathcal{F}_t)_{t \geq 0}$ -stopping time T , all $t \geq 0$, all $x \in E$ and all $A \in \mathcal{B}(E)$ (the Borel σ -algebra on E), \mathbb{P}_x -almost surely

$$\mathbb{P}_x(X(T+t) \in A \mid \mathcal{F}_T) 1_{T < +\infty} = \mathbb{P}_{X(T)}(X(t) \in A) 1_{T < +\infty}.$$

In the next subsections, all stochastic processes X will be considered defined on $(\Omega, \mathcal{A}, \mathbb{P})$ and belonging to a strongly Markovian Markov family $(X, (\mathbb{P}_x)_{x \in E})$ on $(\Omega, \mathcal{A}, (\mathcal{F}_t)_{t \geq 0})$ associated to a semigroup denoted $(P^t)_{t \geq 0}$, with $(\mathcal{F}_t)_{t \geq 0}$ the augmented filtration obtained from the $(\sigma(X(s), s \leq t))_{t \geq 0}$ filtration generated by X .

If $A \in \mathcal{B}(E)$, we denote by $\tau_A = \inf\{t \geq 0 : X(t) \in A\}$ the hitting time of A by X . It is then known from [Bas10] that τ_A is a $(\mathcal{F}_t)_{t \geq 0}$ -stopping time.

If μ is a Borel measure on E , $f : E \rightarrow \mathbb{R}$ is a bounded Borel function and $t \geq 0$, we define the Borel measure μP^t and function $P^t f : E \rightarrow \mathbb{R}$ by:

$$\mu P^t : A \mapsto \int_E P^t(x, A) d\mu(x)$$

and

$$P^t f : x \mapsto \mathbb{E}_x [f(X(t))] = \int_E f(y) P^t(x, dy).$$

We now introduce a technical condition required by theoretical results of [MT93b] and [DMT95] that we will present in next section.

DEFINITION 1.3.3 (Borel right process, [Dav93] p.77). — *X is said to be Borel right if:*

- (i) *For all $t \geq 0$ and all bounded Borel-measurable function $f : \mathbb{R}^n \rightarrow \mathbb{R}$, $P^t f$ is bounded and Borel-measurable.*
- (ii) *X is almost surely right-continuous.*
- (iii) *If $f : \mathbb{R}^n \rightarrow \mathbb{R}$ is a nonnegative Borel-measurable function that is α -excessive for the semi-group for some $\alpha > 0$, that is, if $e^{-\alpha t} P^t f \leq f$ for all $t \geq 0$ and $e^{-\alpha t} P^t f \uparrow f$ as $t \downarrow 0$, then $f(X)$ is almost surely right-continuous.*

In the rest of this work, we will always assume that the processes we consider are Borel right.

Subsection 1.3.1 below deals with the recurrence and ergodicity of \mathbb{R}^n -valued processes. This stability theory, mostly due to Meyn and Tweedie, helps describe the long-term behavior of (the distribution of) the various population processes we will consider. In Subsection 1.3.2, we define and give some fundamental results on continuous-time branching processes, that will be applied both to the study of branching population processes and to the approximation of infection processes defined in Section 1.2.3 during the first stages of an epidemic. Subsection 1.3.3 will provide with deterministic approximations of scaled Markov jump processes on finite time intervals, that we will apply to our population and epidemic jump processes. Finally, the long-term deviation of processes from these limits will be dealt with in Subsection 1.3.4.

1.3.1 Stability of Markov processes

Let us first review some concepts and results on the long-term stability of \mathbb{R}^n -valued Markov processes.

1.3.1.1 Irreducibility, Harris recurrence and ergodicity

For any Borelian part A of E, we set

$$\eta_A := \int_0^{+\infty} 1_{X(t) \in A} dt.$$

The following definition extends the notion of irreducibility of a Markov chain with a countable set space to the case of a E-valued Markov chain:

DEFINITION 1.3.4 (ϕ -irreducibility of a Markov chain). — *If ϕ is a nontrivial σ -finite Borel measure on E, we say that a E-valued Markov chain $Z = (Z_k)_{k \geq 0}$ is ϕ -irreducible if for all $A \in \mathcal{B}(E)$ the following holds:*

$$\phi(A) > 0 \quad \Rightarrow \quad \forall x \in E, \exists k \in \mathbb{N}^* : \mathbb{P}_x(Z_k \in A) > 0.$$

We simply say that Z is *irreducible* if the definition above holds for some ϕ .

The definition of irreducibility for a continuous-time process is more constraining and involves sojourn times of the process in A :

DEFINITION 1.3.5 (ϕ -irreducibility for a continuous-time Markov process). — *If ϕ is a nontrivial σ -finite Borel measure on E , we say that X is ϕ -irreducible if for all $A \in \mathcal{B}(E)$ the following holds:*

$$\phi(A) > 0 \quad \Rightarrow \quad \forall x \in E, \quad \mathbb{E}_x [\eta_A] > 0.$$

Here again, we say that X is *irreducible* if the definition above holds for some ϕ .

DEFINITION-PROPOSITION 1.3.6 (Harris recurrence, Theorem 1.1 of [MT92a]). — *We say that X is Harris recurrent if there exists a nontrivial, sigma-finite Borel measure ϕ on E such that for all $A \in \mathcal{B}(E)$ with $\phi(A) > 0$ the following holds:*

$$\forall x \in E, \quad \mathbb{P}_x(\eta_A = +\infty) = 1$$

or equivalently:

$$\forall x \in E, \quad \mathbb{P}_x(\tau_A < +\infty) = 1.$$

We note that if X is Harris recurrent, then X is irreducible.

The following result is the counterpart to the theorem of existence and unicity of an invariant measure for a recurrent Markov chain on a countable state space.

THEOREM 1.3.7 (Existence and unicity of an invariant measure for a Harris recurrent Markov process, [ADR69]). — *If X is Harris-recurrent, then there exists a Borel measure μ on E , unique up to a multiplicative constant, such that:*

$$\forall t \geq 0, \quad \mu P^t = \mu.$$

Such a measure is said to be invariant for semigroup $(P^t)_{t \geq 0}$, and we say that X is positive Harris recurrent if there exists a finite invariant measure for $(P^t)_{t \geq 0}$.

We observe the Cesàro mean convergence of the time spent by a positive Harris recurrent process on a given Borel subset of E towards the measure of this subset for the invariant probability. More generally, we have the following Birkhoff theorem:

THEOREM 1.3.8 (Ergodic Birkhoff theorem, [ADR67] p.169). — *If X is positive Harris recurrent with invariant probability π , then for all $x \in E$ and all $f \in L^1(E, \mathcal{B}(E), \pi)$ the following holds:*

$$\mathbb{P}_x - \text{a.s.}, \quad \lim_{t \rightarrow +\infty} \frac{1}{t} \int_0^t f(X(s)) ds = \int f d\pi.$$

It is yet worth noting that this latter convergence result does not, in general, imply that of the law of $X(t)$ towards π as t tends to infinity. In order to study this last phenomenon, we introduce the notion of ergodicity:

DEFINITION 1.3.9 (Ergodicity of a Markov process, [MT93a] p.508). — *If X is positive Harris recurrent with invariant probability π , we say that X is ergodic if for any $x \in E$ we have:*

$$\lim_{t \rightarrow +\infty} \|P^t(x, \cdot) - \pi\|_{TV} = 0$$

where $\|\cdot\|_{TV}$ is the total variation convergence norm, that is:

$$\|P^t(x, \cdot) - \pi\|_{TV} = \sup_{\substack{g : E \rightarrow \mathbb{R}_+ \\ g \text{ measurable} \\ |g| \leq 1}} |P^t g - \pi g|. \quad (1.6)$$

We can obtain a much stronger ergodicity concept by changing the upper bound in the supremum of Definition 1.6. Let us first introduce the notion of f -norm:

DEFINITION 1.3.10 (f -norm). — *For any measurable function $f : E \rightarrow [1, +\infty[$, the f -norm $\|\cdot\|_f$ on the set of Borel measures on E is defined by:*

$$\|\mu\|_f := \sup_{\substack{g : E \rightarrow \mathbb{R}_+ \\ g \text{ measurable} \\ g \leq f}} \left| \int g d\mu \right|.$$

For instance, the total variation norm $\|\cdot\|_{TV}$ is the 1-norm.

We then define:

DEFINITION 1.3.11 (f -ergodicity). — *If $f : E \rightarrow [1, +\infty[$ is a measurable function, we say that X is f -ergodic if X positive Harris recurrent with invariant probability π such that*

$$\lim_{t \rightarrow +\infty} \|P^t(x, \cdot) - \pi\|_f = 0$$

for all $x \in E$.

Another development of the notion of ergodicity consists in precisising the convergence speed in (1.6) by demanding an exponentially fast convergence:

DEFINITION 1.3.12 (f -uniform exponential ergodicity). — *If $f : E \rightarrow [1, +\infty[$ is a measurable function, we say that X is f -uniformly exponentially ergodic if there exist $\rho \in [0, 1)$ and $M \geq 0$ such that:*

$$\forall t \geq 0, \forall x \in \mathbb{R}_+^n, \quad \|P^t(x, \cdot) - \pi\|_f \leq M f(x) \rho^t.$$

In the case of a continuous-time Markov process with a countable set space, jump times are (possibly degenerate) exponential variables, ensuring aperiodicity and ergodicity results in the recurrent positive case. At the opposite, positive Harris recurrence does not necessarily entail ergodicity for a continuous-time Markov process with an uncountable state space. We must

therefore state new recurrence and ergodicity criteria for X ; this is the aim of the following paragraphs, built on results from [MT93a], [MT93b] and [DMT95].

Recurrence and ergodicity criteria in [MT93a] are build around the notions of *sampled chains* and *petite sets*, which are introduced in the first paragraph below. We then give a powerful result from [DMT95], known as the *Foster-Liapounov criterion for uniform exponential ergodicity*, that allows to obtain the strongest form of ergodicity from the study of the infinitesimal generator of an irreducible aperiodic Markov process.

1.3.1.2 Sampled chains and petite sets

The strategy followed by Meyn and Tweedie in [MT93a] consists in deriving the properties of X from these of sampled chains $(X(A_k))_{k \geq 0}$, that is, of Markov chains obtained by observing X at random times A_k , where $(A_k)_{k \geq 0}$ is an increasing sequence of \mathbb{R}_+ -valued random variables independent from X and with stationary independent increments.

It is the meaning of the following definition:

DEFINITION 1.3.13 (Sampled chains, skeleton chains and resolvent). — *Let a be a Borel probability measure on \mathbb{R}_+ . We define the transition function K_a on $E \times \mathcal{B}(E)$ by:*

$$K_a(x, A) := \int P^t(x, A) da(t).$$

We then call K_a -chain any E -valued Markov chain with transition function K_a .

In the case $a = \delta_\Delta$ with $\Delta > 0$, the K_a -chain is called Δ -skeleton of X .

In the case where $a = \mathcal{E}(1)$ is the exponential distribution with mean 1, the K_a -chain is denoted R and called resolvent of X .

The Δ -skeleton of X is the chain obtained by observing X at regular time intervals of length Δ , and its resolvent is the chain obtained by waiting an exponential time of mean 1 between each observation. It seems intuitive that we can derive less information from the study of the Δ -skeleton of X , that by definition fails to account for the behavior of X on intervals of the form $(k\Delta, (k+1)\Delta)$, than from the study of the resolvent of X that samples it at "truly random" times. This intuition is partly true, and X has tight bonds with its resolvent that it does not share with its skeleton chains (see [MT93a] for more detail). Yet, we will see that under some assumptions on the local behavior of X , observing its skeleton chains makes is sufficient to prove its Harris recurrence and its ergodicity.

Let us now introduce the crucial concept of *petite set* :

DEFINITION 1.3.14 (Petite set). — *If a is a Borel probability measure on \mathbb{R}_+^* and if ν_a is a non-trivial Borel measure on E , we say that a set $C \in \mathcal{B}(E)$ is ν_a -petite if $K_a(x, \cdot) \geq \nu_a$ for all $x \in C$. One simply says that C is petite for the K_a -chain if there exists a nontrivial Borel measure ν_a on E such that C is ν_a -petite, and that C is petite if there exists a Borel probability measure a on \mathbb{R}_+^* such that C is petite for the K_a -chain.*

Petiteness is a *mixing* condition: it means that if at some point in time X takes a value in C , any observation of X realized after an independent waiting time of law a has a positive proba-

bility to be projected on the support of ν_a and distributed according to ν_a . It is therefore easy to conceive that X is Harris recurrent as soon as it almost surely reaches a given petite set. This is the meaning of the following theorem:

THEOREM 1.3.15 (Petite sets and Harris recurrence, [MT93a] p.503). — *If there exists a petite set $C \in \mathcal{B}(E)$ such that $\mathbb{P}_x(\tau_C < +\infty) = 1$ for all $x \in E$, then X is Harris recurrent.*

It is possible to derive a stronger result by controlling the mean time spent by X outside of compact subsets of E :

DEFINITION 1.3.16 (Boundedness in probability on average). — *X is said to be bounded in probability on average if for all $x \in E$ and all $\varepsilon > 0$ there exists a compact subset C of E such that*

$$\liminf_{t \rightarrow +\infty} \frac{1}{t} \int_0^t \mathbb{P}_x(X(s) \in C) ds \geq 1 - \varepsilon.$$

THEOREM 1.3.17 (Condition for positive Harris recurrence, Theorem 3.2 (ii) and Theorem 4.1 (i) of [MT93a]). — *If $\mathbb{P}_x(\|X\|_1 \rightarrow +\infty) < 1$ for some $x \in E$, if all compacts of E are petite and if X is bounded in probability on average, then X is positive Harris recurrent.*

The ergodicity of X can then be derived from the study of its skeleton chains:

THEOREM 1.3.18 (Ergodicity condition for a positive Harris recurrent Markov process, [MT93a] p.509). — *If X is positive Harris recurrent and if one its skeleton chains is irreducible, then X is ergodic.*

We finally state a f -ergodicity result:

THEOREM 1.3.19 (f -ergodicity condition for a positive Harris recurrent Markov process, Theorems 7.1 and 7.2 of [MT93a]). — *Let us assume that X is Harris recurrent, and let μ be one of its nontrivial invariant measures. If there exist a Borel function $h : E \rightarrow [1, +\infty)$, a closed petite set C and $\delta > 0$ such that*

$$\sup_{x \in C} \mathbb{E}_x \left[\int_0^{\tau_C(\delta)} h(X(t)) dt \right] < +\infty$$

where $\tau_C(\delta) := \inf\{t \geq \delta : X(t) \in C\}$, then X is positive Harris recurrent and h is μ -integrable.

If in addition X has an irreducible skeleton chain, if

$$\mathbb{E}_x \left[\int_0^{\tau_C} h(X(t)) dt \right] < +\infty$$

for all $x \in E$ and if there exists a Borel function $f : E \rightarrow [1, +\infty)$ such that $P^s f \leq h$ for all $s \in [0, \delta]$, then X is f -ergodic.

The results above give very useful criteria for the study of long time behavior of Markov process. Yet, they do not give information on the convergence speed of the distribution of $X(t)$ towards the invariant probability in the ergodic case. Next subsection introduces a condition yielding such results.

1.3.1.3 A Foster-Lyapunov criterion

Foster-Lyapunov conditions draw a link between properties of the infinitesimal generator of X and the propensity of the process to reach petite sets in a quick time. Various criteria of non-explosivity, positive Harris recurrence and uniform exponential ergodicity derived from these conditions are given in [MT93b]. The one we state here, taken from [DMT95], yields a strong uniform exponential ergodicity result.

Aperiodicity is the condition insuring the ergodicity of irreducible positive recurrent Markov chains. We first need to extend to continuous-time Markov processes.

DEFINITION 1.3.20 (Aperiodicity of a continuous-time Markovian process). — *If X is ϕ -irreducible, X is said to be aperiodic if there exist $T \geq 0$ and a petite set $C \in \mathcal{B}(E)$ such that $\phi(C) > 0$ and $P^t(x, C) > 0$ for all $t \geq T$ and all $x \in C$.*

We then have the following exponential ergodicity criterion:

THEOREM 1.3.21 (Criterion for uniform exponential ergodicity of X , Theorem 5.2 (c) of [DMT95]). — *If X is ϕ -irreducible and aperiodic and if there are $b, c > 0$, a petite set $C \in \mathcal{B}(E)$ and a measurable function $V : E \rightarrow [1, +\infty)$ belonging to the domain of the infinitesimal generator \mathfrak{A} of X such that:*

$$\mathfrak{A}V \leq -cV + b1_C,$$

then X is positive Harris recurrent, V is integrable under the invariant probability of X and X is V -uniformly exponentially ergodic.

It is worth noting that unlike the results stated in [MT93b], the latter theorem only requires the existence of *one* petite set C (not necessarily for a skeleton chain of X but for any sampled chain).

1.3.1.4 Stability of the population models under study

The main results derived from the stability theory presented above in the context of the present work are the following. The first statement stems from Theorems 2.1.2 and 2.1.5:

THEOREM 1.3.22 (Ergodicity of multiplicative uniform and unitary power settings). — *A multiplicative uniform or unitary power metapopulation PDMP (defined by equation 1.1 or 1.2) is positive Harris recurrent if and only if*

$$\sum_{i=1}^n c_i < 0$$

in which case it is also F -ergodic, where

$$F : \begin{cases} \mathbb{R}_+^n & \longrightarrow & \mathbb{R}_+ \\ x & \longmapsto & e^{\eta \|x\|_1} \end{cases}$$

for some $\eta > 0$.

The following result is Proposition 2.2.1:

PROPOSITION 1.3.23 (Ergodicity of the branching population process). — *Let $N \geq 1$. The branching population process X^N defined in Subsection 1.2.2.1 is positive recurrent and $(\|\cdot\|_1 + 1)$ -uniformly exponentially ergodic. Moreover, for every $x(0) \in \mathbb{R}_+^N$,*

$$\lim_{t \rightarrow +\infty} \mathbb{E}(X^N(t)) = \int x d\pi(x) = -NA^{-1}B$$

where A is defined by (1.4) and $B = (B_1, \dots, B_n)$.

As evoked after defining the logistic population process, its (exponential) ergodicity is trivial since it is an irreducible continuous-time Markov process on a finite state space. We nevertheless state it for the sake of symmetry. It can be found in section 2.3 as Proposition 7.3.3:

PROPOSITION 1.3.24 (Ergodicity of the logistic population process). — *Let $N \geq 1$. The logistic population process X^N defined in Subsection 1.2.2.2 is positive recurrent and exponentially ergodic.*

1.3.2 Results on continuous-time multitype branching processes

This subsection deals with the long-time behavior of continuous-time multitype branching processes, defined in a way that slightly differs from the usual setting of [Ath68, Mod71, AN72]. It also provides with the explicit calculation of the moment generating function of the offspring matrix of a multitype branching processes.

1.3.2.1 Definition

In the rest of this work, we denote $\mathcal{I} = \{(i, j) \in \llbracket 1, n \rrbracket^2 : i \neq j\}$.

Let $\Theta = (\theta_{i,j})_{i,j \in \llbracket 1, n \rrbracket}$ be a matrix with nonnegative coefficients, and for any $i \in \llbracket 1, n \rrbracket$, let b_i and d_i be nonnegative real numbers. Throughout this work, we will assume that for any $(i, j) \in \llbracket 1, n \rrbracket^2$ there exists a positive integer k such that $\Theta_{i,j}^k > 0$ (which is a *connectivity assumption* meaning that any individual born in node i can follow a path to node j with positive probability during its lifetime), and that the $\theta_{i,i}$ coefficients are zero. We say that a continuous-time \mathbb{Z}_+^n -valued Markovian jump process is a multitype branching process with birth rates b_i , death rates d_i and movements matrix Θ whenever its jump intensities are given by the following chart:

Transition	Rate at state $x \in \mathbb{Z}_+^n$	
$x \rightarrow x + e_i$	$b_i x_i$	(1.7)
$x \rightarrow x - e_i$	$d_i x_i$	
$x \rightarrow x - e_i + e_j$	$\theta_{i,j} x_i$	

Table 1.4: Multitype branching process rates chart.

Such a process $X = (X(t))_{t \geq 0}$ models the evolution over time of a population scattered among n nodes, with $X_i(t)$ denoting the population in node i at time t , such that individuals behave independently from each other and, while in node i , give birth at rate b_i to an individual starting an independent line of descent, die at rate d_i and move to node j at rate $\theta_{i,j}$.

It is quite classical that such a jump process almost surely does not explode in finite time (and is therefore well defined as a process on \mathbb{R}_+), since

$$\sum_{x \in \mathbb{Z}_+^n} \sum_{i=1}^n \frac{1}{b_i x_i + d_i x_i + \sum_{j=1}^n \theta_{i,j} x_i} = +\infty.$$

Note that the difference with the continuous-time setting studied in [AN72] and [Ath68] only lies in the fact that individuals do not create new lineages in various nodes at the time of their death but move across nodes and give birth in their current node *during their lifetime*. Now individuals are assumed to behave independently from each other, so the effective position of an individual over time does not affect the behavior of others. As a result, the Markov chains obtained by sampling the processes defined here and in [Ath68] at the times of deaths of individuals have the same distribution. This makes it possible to derive the results of Subsection 1.3.2.2 below directly from [Ath68].

Until the end of this section, we assume that X is a continuous-time multitype branching process with birth rates b_i , death rates b_i and movements matrix Θ , and that at least one b_i or one d_i is positive (which rules out the case of a constant population of immortal and sterile individuals).

1.3.2.2 Fundamental properties of a multitype branching process

It follows from the Perron-Frobenius theorem (see [AN72] p.185 and [Kar59]) that the matrix

$$A = \begin{pmatrix} b_1 - d_1 - \sum_{j \neq 1} \theta_{1,j} & \theta_{2,1} & \cdots & \theta_{n,1} \\ \theta_{1,2} & b_2 - d_2 - \sum_{j \neq 2} \theta_{2,j} & \ddots & \vdots \\ \vdots & \ddots & \ddots & \theta_{n,n-1} \\ \theta_{1,n} & \cdots & \theta_{n-1,n} & b_n - d_n - \sum_{j \neq n} \theta_{n,j} \end{pmatrix}$$

has a simple (real) eigenvalue with maximal real part, that we denote ρ . We say that the multitype branching process X is subcritical if $\rho < 0$, critical if $\rho = 0$ and supercritical if $\rho > 0$.

Let $\zeta \in [0, 1]^n$ be the vector of extinction probabilities of the multitype branching process for populations initiated by one single individual in various nodes, defined by:

$$\forall i \in [1, n], \quad \zeta_i = \mathbb{P}_{e_i}(\exists t \geq 0 : X(t) = 0)$$

where we recall that $\mathbb{P}_{e_i}(X(0) = e_i) = 1$.

Since all lineages started at time $t = 0$ evolve independently from each other, it is clear that for any $x \in \mathbb{Z}_+^n$ we have:

$$\mathbb{P}_x(\exists t \geq 0 : X(t) = 0) = \prod_{i=1}^n \zeta_i^{x_i}.$$

For any $i, j \in \llbracket 1, n \rrbracket$, we denote by $W_{i,j} = \lim_{t \rightarrow +\infty} M_{i,j}(t)$, where $(E_i(t), M_{i,j}(t))_{t \geq 0}$ is a $\mathbb{Z}_+^n \times \mathbb{Z}_+$ Markov jump process with initial value $(e_i, 0)$ and with the following rate intensities:

Transition	Rate at state $(x, m) \in \mathbb{Z}_+^n \times \mathbb{Z}_+$
$(e_j, m) \rightarrow (e_j, m + 1)$	b_j
$(e_k, m) \rightarrow (0, m)$	d_k
$(e_k, m) \rightarrow (e_l, m)$	$\theta_{k,l}$

$W_{i,j}$ can be seen as the total first-generation offspring in node j of an individual of a population modeled by the multitype branching process born in node i .

We define $G : [0, 1]^n \rightarrow [0, 1]^n$ as the moment generating function (MGF) of the $W_{i,j}$, given by

$$G : [0, 1]^n \longrightarrow [0, 1]^n$$

$$s \longmapsto \left(\mathbb{E} \left[\prod_{j=1}^n s_j^{W_{1,j}} \right], \dots, \mathbb{E} \left[\prod_{j=1}^n s_j^{W_{n,j}} \right] \right).$$

We shall see that this function is of paramount interest in approximating the major outbreak probability vector in the supercritical case, in addition of making a great number of explicit calculations possible (for instance that of the expected number of nodes in which an individual born in node i will have offspring, which will be useful in Chapter 4). [Nea12] puts forward a procedure to compute G numerically when the d_i are identical across nodes. However, in our setting the life duration of individuals is not independent from their trajectory, hampering the integration of the conditional expectancy obtained by Theorem 1 of [DM68] (see equations (11) and (12) of [Nea12]). The alternative method we use to compute G strongly relies on the Markov property. It yields the following:

PROPOSITION 1.3.25 (MGF of the $W_{i,j}$). — For any $s = (s_1, \dots, s_n)$,

$$G(s) = (\text{diag}(\lambda_1(s), \dots, \lambda_n(s)) - \Theta)^{-1} \mathbf{d} \tag{1.8}$$

where $\lambda_i(s) = (1 - s_i) b_i + \Sigma_i$ with $\Sigma_i = d_i + \sum_{j \neq i} \theta_{i,j}$ for any $i \in \llbracket 1, n \rrbracket$.

Proof of Proposition 1.3.25.— Let $i \in \llbracket 1, n \rrbracket$. For all $j \in \llbracket 1, n \rrbracket$, we consider the random time

$$Q_{i,j} = \int_0^{+\infty} \mathbf{1}_{E_i(s)=e_j} \, ds$$

spent in node j by an individual of the population described by the multitype branching process

born in node i at time 0. We recall that $W_{i,j}$ is the total offspring of this individual in node j . Then conditionally on the $Q_{i,j}$, the $W_{i,j}$ are independent and have law Poisson with mean $b_j Q_{i,j}$. Therefore, for any $s \in [0, 1]^n$:

$$\begin{aligned}
G_i(s) &:= \mathbb{E} \left(\prod_{j=1}^n s_j^{W_{i,j}} \right) \\
&= \mathbb{E} \left[\mathbb{E} \left(\prod_{j=1}^n s_j^{W_{i,j}} \mid Q_{i,1}, \dots, Q_{i,n} \right) \right] \\
&= \mathbb{E} \left[\prod_{j=1}^n \mathbb{E} \left(s_j^{W_{i,j}} \mid Q_{i,j} \right) \right] \\
&= \mathbb{E} \left[\prod_{j=1}^n \exp \left(-(1-s_j) \beta_j Q_{i,j} \right) \right], \tag{1.9}
\end{aligned}$$

Let us denote by T_1, \dots, T_τ the jump times of E_i , τ being the time of absorption of the underlying Markov chain by 0. Using the law of total probability and the strong Markov property at T_1 , we get that for any $(a_1, \dots, a_n) \in \mathbb{R}_+^n$:

$$\begin{aligned}
\mathbb{E} \left(e^{-\sum_{j=1}^n a_j Q_{i,j}} \right) &= \mathbb{E} \left(e^{-a_1 T_1} \right) \left(\sum_{k=1}^n \mathbb{P}(E_i(T_1) = k) \mathbb{E} \left(e^{-\sum_{j=1}^n a_j Q_{k,j}} \right) + \mathbb{P}(\tau = 1) \right) \\
&= \frac{\Sigma_i}{a_i + \Sigma_i} \left(\sum_{k=1}^n \frac{\theta_{i,k}}{\Sigma_i} \mathbb{E} \left(e^{-\sum_{j=1}^n a_j Q_{k,j}} \right) + \frac{d_i}{\Sigma_i} \right) \\
&= \sum_{k=1}^n \frac{\theta_{i,k}}{a_i + \Sigma_i} \mathbb{E} \left(e^{-\sum_{j=1}^n a_j Q_{k,j}} \right) + \frac{d_i}{a_i + \Sigma_i} \tag{1.10}
\end{aligned}$$

since T_1 is exponentially distributed with mean Σ_i^{-1} . Combining (1.9) and (1.10) shows that $G(s)$ is such that

$$(\text{diag}(\lambda_1(s), \dots, \lambda_n(s)) - \Theta) G(s) = d,$$

but $\text{diag}(\lambda_1(s), \dots, \lambda_n(s)) - \Theta$ is a diagonally dominant matrix that can be proved to be invertible using the connectivity assumption for Θ , which ends the proof of Proposition 1.3.25. \square

It is possible to show (see [AN72] p.202) that defining $m_{i,j}(t) = \mathbb{E}_{e_i}(X_j(t))$ for all i, j and t as the expected population in node j for a multitype branching process initiated by one individual in node i at time $t = 0$, then the matrices $M(t) = (m_{i,j}(t))_{i,j}$ satisfy the differential equation $\dot{M}(t) = AM(t)$, and therefore, as $M(0) = I_n$, that $M(t) = \exp(tA)$ for all $t \geq 0$. This suggests that the sign of ρ will prove crucial in determining the asymptotic behavior of the branching process, that should, by Fatou's lemma, get extinct with probability 1 as soon as the process is subcritical.

In fact, a much stronger result holds (Theorem 2, p.186 of [AN72]):

THEOREM 1.3.26 (Extinction probability of a multitype branching process). —

1. If the multitype branching process X is subcritical or critical, it goes extinct with probability 1 regardless of its initial condition : $\zeta = \mathbb{1}$.
2. If the multitype branching process X is supercritical, $\zeta_i < 1$ for any $i \in \llbracket 1, n \rrbracket$, and ζ is the only fixed point of the generating function G in $[0, 1]^n$. Moreover, for any $s \in [0, 1]^n \setminus \mathbb{1}$:

$$\lim_{n \rightarrow +\infty} G^n(s) = \zeta$$

where G^n stands for n -th iteration of G .

In the one-dimensional case $n = 1$, Proposition 1.3.25 yields $G(s) = \frac{d_1}{(1-s)b_1 + \gamma_1}$ and therefore

$$\zeta_1 = \frac{d_1}{b_1}$$

when the process is supercritical, that is, when $b_1 > d_1$. This result will be used as a reference in Chapter 4 when discussing the behavior of a multitype branching process in quasi-isolated nodes (that is, nodes with very low $\sum_{j=1}^n \theta_{i,j}$).

The following Proposition states an equivalent characterization of subcritical, critical and supercritical multitype branching process, reminiscent of the usual mean-based criterion for one-dimensional Galton-Watson processes (see Theorem 1, p.7 of [AN72]).

PROPOSITION 1.3.27 (Mean offspring matrix). — *The matrix $C = (\mathbb{E}(W_{i,j}))_{i,j \in \llbracket 1, n \rrbracket}$ is given by*

$$C = (\text{diag}(\Sigma_1, \dots, \Sigma_n) - \Theta)^{-1} \text{diag}(b_1, \dots, b_n). \quad (1.11)$$

Let R_0 denote the largest real eigenvalue of C . Then the multitype branching process is subcritical if $R_0 < 1$, critical if $R_0 = 1$ and supercritical if $R_0 > 1$.

Proof of Proposition 1.3.27.— We take up the notations of the proof of Proposition 1.3.25 above. For any $i, j \in \llbracket 1, n \rrbracket$, we denote by $W_{i,j}^k$ the offspring of the individual in node j during times T_k and T_{k+1} . Then:

$$\begin{aligned} \mathbb{E}(W_{i,j}) &= \mathbb{E} \left(\sum_{k=0}^{+\infty} W_{i,j}^k \mathbf{1}_{E_i(T_k)=j} \right) = \sum_{k=0}^{+\infty} \mathbb{E} \left[\mathbb{E} \left(W_{i,j}^k \mid E_i(T_k) = j \right) \mathbf{1}_{E_i(T_k)=j} \right] \\ &= \sum_{k=0}^{+\infty} b_j \mathbb{E} \left(T_k \mathbf{1}_{E_i(T_k)=j} \right) = b_j \sum_{k=0}^{+\infty} \mathbb{E} \left[\mathbf{1}_{E_i(T_k)=j} \mathbb{E} \left(T_k \mid E_i(T_k) = j \right) \right]. \end{aligned}$$

Now the T_k follow an exponential distribution with mean Σ_j^{-1} conditionally on $(E_i(T_k) = j)$, so

$$\mathbb{E}(W_{i,j}) = \frac{b_j}{\Sigma_j} \mathbb{E} \left(\sum_{k=0}^{+\infty} 1_{E_i(T_k)=j} \right),$$

and $\mathbb{E} \left(\sum_{k=0}^{+\infty} 1_{E_i(T_k)=j} \right) = \mathbb{E} \left(\sum_{k=0}^{T-1} 1_{E_i(T_k)=j} \right)$ is the expected number of visits of j by the underlying Markov chain starting from i before absorption. This number is known (see for instance [GH60], Chapter 3) to be $(I_n - T)_{i,j}^{-1}$ where T is the matrix defined by

$$T_{i,j} = \begin{cases} 0 & \text{if } i = j \\ \frac{\theta_{i,j}}{\Sigma_i} & \text{if } i \neq j \end{cases}$$

so

$$\mathbb{E}(W_{i,j}) = \frac{b_j}{\Sigma_j} (I_n - T)_{i,j}^{-1} = b_j (\text{diag}(\Sigma_1, \dots, \Sigma_n) - \Theta)_{i,j}^{-1}$$

and (1.11) follows.

Alternatively, a conditioning argument similar to the one used in the proof of Proposition 1.3.25 can be used to derive (3.10), by writing that

$$\mathbb{E}(Q_{i,j}) = \sum_{k=1}^n \frac{\theta_{i,k}}{\Sigma_i} \mathbb{E}(Q_{k,j}) + \frac{1}{\Sigma_i}$$

and using the fact that $\mathbb{E}(W_{i,j}) = b_j \mathbb{E}(Q_{i,j})$ for all i, j . A third method would be to retrieve the formula for C by differentiating G using the expression given by Proposition 1.3.25.

The statements concerning R_0 are derived from a simple comparison with the splitting-at-death model developed in [AN72] p.202. \square

In Chapter 3, we will be interested in the behavior of a supercritical multitype branching process conditionally on its non-extinction. By the Perron-Frobenius theorem (see [AN72] p.185 and [Kar59]), there exists a left eigenvector v of A associated to the eigenvalue ρ with positive coefficients. Theorems 1 and 2 of [Ath68] yield the following analogous of Kesten-Stigum's theorem [KS67]:

THEOREM 1.3.28 (Asymptotic behavior of a multitype branching process). — *There exists a real-valued random variable W such that*

$$\lim_{t \rightarrow +\infty} X(t) e^{-\rho t} = W v$$

almost surely.

If the multitype branching process is supercritical, then

$$\mathbb{P}(W > 0 \mid \forall t \geq 0, X(t) \neq 0) = 1$$

so:

$$\forall i \in \llbracket 1, n \rrbracket, \quad X_i(t) \underset{t \rightarrow +\infty}{\sim} W v_i e^{\rho t}$$

almost surely on the event of non-extinction.

1.3.2.3 Multitype branching approximation of epidemic processes

We will apply some of the results we just saw to the approximation of epidemic processes introduced in Subsection 1.2.3 when the epidemic is started by a fixed number of individuals. Recall that for all $i \in \llbracket 1, n \rrbracket$, p_i denotes the probability for an individual arriving in node i through immigration to have the Susceptible health status, q_i its probability to be Infected and $r_i = 1 - p_i - q_i$ its probability to be Removed. In this paragraph, we assume that $p = \mathbb{1}$, $I^N(0) = I(0) \in \mathbb{Z}_+^n$, $S^N(0) = X^N(0) - I(0)$ and therefore $R^N(0) = 0$.

In the branching and logistic-driven SIR frameworks, the set of disease-free states $\mathbb{Z}_+^n \times \{0\}^n \times \mathbb{Z}_+^n$ is reachable from any point of the state space, and the assumption we just made makes this set absorbing, so the positive recurrence of the population processes X^N implies that disease extinction in finite time is almost sure. We call *extinction time* of the epidemic the hitting time of $\mathbb{Z}_+^n \times \{0\}^n \times \mathbb{Z}_+^n$ by the epidemic process, and *total size of the epidemic* the total number of individuals infected during the course of the epidemic.

Theorems 1.3.29 and 1.3.31 below are generalizations of Theorem 2.1 of [Cla96] and Theorem 3.3 of [O'N96] to a multitype open setting with density-dependent population inflow. They rely on the idea that if N is large, the early stages of the epidemic look like a multitype branching process because the probability for the first infectives of drawing non-susceptible individuals to make contact with vanishes (see [Bar55] p.141 or [Ken56, Bal83]). The "birth" of an individual in this branching process corresponds to the infection of a susceptible individual by an infective, while the "death" of an individual means either the actual death or the recovery of the corresponding infective in the epidemic process. The following result can be found as Theorem 3.2.1 in Section 3.2.1:

THEOREM 1.3.29 (Finite-time convergence to a multitype branching process (branching case)). — *It is possible to define a branching-driven epidemic process $(S^N(t), I^N(t), R^N(t))_{t \geq 0}$ on \mathbb{Z}_+^{3n} and a \mathbb{Z}_+^n -valued multitype branching process $(I'(t))_{t \geq 0}$ on $(\Omega, \mathcal{A}, \mathbb{P})$ with $I'(0) = I(0)$, describing a population of individuals moving from node i to node j at rate $\theta_{i,j}$ and, while in node i , giving birth at rate β_i and dying at rate $d_i + \gamma_i$, such that for any time $T \geq 0$, \mathbb{P} -almost surely:*

$$\exists N_0 \in \mathbb{Z}_+^* : \forall N \geq N_0, \forall u \in [0, T], \quad I^N(u) = I'(u).$$

In particular, if τ^N (resp. Z^N) denotes the extinction time (resp. total size) of the epidemic (S^N, I^N, R^N) and τ' (resp. Z') that of the branching process I' , then

$$\tau^N \xrightarrow{N \rightarrow +\infty} \tau' \quad \text{and} \quad Z^N \xrightarrow{N \rightarrow +\infty} Z'$$

\mathbb{P} -almost surely.

Following traditional terminology (see Chapter 4 of [AB00a]), we will say that the epidemic undergoes a *minor outbreak* when the branching process I' goes extinct and a *major outbreak* if it does not. As Theorem 1.3.29 indicates, the epidemic's extinction time and total size are of the same order of those of the branching process in the minor outbreak case and tend to infinity with N in the major outbreak case.

Such branching approximations are common in epidemiology, but also in population genetics [CFM05, BCF⁺16, BS19]. In the latter framework, invasion of rare mutants in the global population corresponds to the epidemiological notion of major epidemic outbreak, while their fixation is analogous to the stabilization of the epidemic to an endemic state.

The next proposition, which can be bound as Proposition 3.2.2 in Section 3.2.1, characterizes the behavior of the limiting branching process and gives an iterative method to compute its probability of survival, that is the probability of a major epidemic outbreak:

PROPOSITION 1.3.30 (Major outbreak probability of an SIR branching-driven epidemic). — *For any $i, j \in \llbracket 1, n \rrbracket$, let $W_{i,j}$ denote the number of offspring in node j of an individual born in node i for the branching process I' . Also set $\Sigma_i = \gamma_i + d_i + \sum_{j \neq i} \theta_{i,j}$ for any $i \in \llbracket 1, n \rrbracket$. Let Θ be the $n \times n$ matrix defined by $\Theta_{i,j} = \theta_{i,j}$ if $i \neq j$ and $\Theta_{i,i} = 0$. Then:*

1. *The matrix $C = (\mathbb{E}(W_{i,j}))_{1 \leq i, j \leq n}$ is given by*

$$C = (\text{diag}(\Sigma_1, \dots, \Sigma_n) - \Theta)^{-1} \text{diag}(\beta_1, \dots, \beta_n).$$

2. *Let R_0 denote the eigenvalue of C with the largest real part, that we will call the basic reproduction number of the epidemic process. It is real, and the MBP I' is subcritical if $R_0 < 1$, critical if $R_0 = 1$ and supercritical if $R_0 > 1$.*
3. *If the MBP I' is subcritical or critical, then the major outbreak probability is 0. If it is supercritical, then this probability is strictly positive and equals $1 - \prod_{k=1}^n \zeta_k^{1k(0)}$, where ζ is the only fixed point in $[0, 1]^n$ of the moment generating function*

$$G: \quad [0, 1]^n \quad \longrightarrow \quad [0, 1]^n \\ s = (s_1, \dots, s_n) \quad \longmapsto \quad \left(\mathbb{E} \left[\prod_{j=1}^n s_j^{W_{1,j}} \right], \dots, \mathbb{E} \left[\prod_{j=1}^n s_j^{W_{n,j}} \right] \right).$$

4. *Function G has explicit expression*

$$G(s) = (\text{diag}(\lambda_1(s), \dots, \lambda_n(s)) - \Theta)^{-1} (\gamma + d)$$

where $\lambda_i(s) = (1 - s_i)\beta_i + \Sigma_i$.

5. *The iterated sequence $(G^k(s))_{k \geq 0}$ converges to ζ for any $s \in [0, 1]^n$.*

The same results holds for the logistic-driven SIR model, provided that its population starts at its equilibrium value so rates of migrations between nodes are stable over time. The following result is the combination of Theorem 3.2.10 and Proposition 3.2.11 from Subsection 3.2.2

THEOREM 1.3.31 (Branching approximation in the logistic case). — *Theorem 1.3.29 and Proposition 1.3.30 hold for the limiting branching process of a logistic-driven SIR process, adding the condition that $z(0)$ is an equilibrium point z^* of dynamical system (\mathcal{S}'_{pop}) defined in Subsection 1.3.3.2 below, and individual movement rates $\theta_{i,j}$ by $\tilde{\theta}_{i,j} = \theta_{i,j}(\mathbf{K}_j - z_j^*)_+$ in the definition of Θ , Σ_i and λ_i .*

1.3.3 Scaling limits

Scaling limits are a powerful tool in the study of density-dependent pure jump Markovian population processes with large typical populations, that can be approximated by the deterministic solutions of a dynamical system over finite intervals of time after an appropriate scaling. The presentation below is based on Chapter 11 of [EK86].

1.3.3.1 Scaling limits of density-dependent population processes

Let $\mathcal{D} = \{e_i : i \in \llbracket 1, n \rrbracket\} \cup \{-e_i : i \in \llbracket 1, n \rrbracket\} \cup \{e_i - e_j : (i, j) \in \mathcal{I}\}$ denote the set of directions in which our processes will be allowed to jump.

Let us assume that for any $N \geq 0$, X^N is a pure Markov jump process on \mathbb{Z}_+^n such that the rate $q_{k, k+l}^N$ at which X^N jumps from state $k \in \mathbb{Z}_+^n$ to state $k+l \in \mathbb{Z}_+^n$ satisfies

$$q_{k, k+l}^N = \begin{cases} N\beta_l\left(\frac{k}{N}\right) & \text{if } l \in \mathcal{D} \\ 0 & \text{otherwise} \end{cases}$$

where the β_l are nonnegative locally Lipschitz-continuous functions on \mathbb{R}_+^n independent from N .

We assume that the dynamical system defined by

$$\dot{x} = \sum_{l \in \mathcal{D}} l\beta_l(x) \tag{1.12}$$

admits a unique *global* solution for any initial condition $x(0) \in \mathbb{R}_+^n$. Then the following result holds:

THEOREM 1.3.32 (Scaling limit of a density-dependent population process ([EK86] p.456, Theorem 2.1)). — *If $\lim_{N \rightarrow +\infty} X^N(0) = x(0) \in \mathbb{R}_+^n$ and if x is the global solution of (1.12) with initial condition $x(0)$, then for all $t \geq 0$:*

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{s \leq t} \left\| \frac{X^N}{N}(s) - x(s) \right\|_\infty = 0 \right) = 1$$

Approximating the scaled process $\frac{X^N}{N}$ by the deterministic process x relies on comparing a scaled version of unit Poisson processes to the process of their mean value ($t \mapsto t$) using a law of large numbers argument. The central limit theorem, through Donsker's theorem, makes it possible to derive a diffusive limit for the process $\sqrt{N}(X^N/N - x)$ as N tends to infinity under mild regularity assumptions on the β_l functions (see [EK86] p.457 and onwards). These approximations have been used in epidemic modeling to study the finite-time behavior of epidemic processes for a given value of N , and to derive information on their extinction time from the behavior of an appropriate diffusion process [VHG95, VH97, AB00a, Nâ99]. In the framework of the present thesis, we will be interested in macroscopic deviations from a deterministic equilibrium by scaled processes on long, N -dependent time scales. This is the topic of Section 1.3.4 below.

1.3.3.2 Scaling limits of population and epidemic processes

A direct application of Theorem 1.3.32 to the branching population processes yields Proposition 2.2.2 of Section 2.3, which is the following:

PROPOSITION 1.3.33 (Scaling limit of a branching population process). — *Let $(X^N)_{N \geq 1}$ be the sequence of branching population processes defined in Subsection 1.2.2. We denote by x the solution of the Cauchy problem $x' = Ax + B$ with initial condition $x(0)$, that is,*

$$\begin{aligned} x: \mathbb{R} &\longrightarrow \mathbb{R}^n \\ t &\longmapsto e^{tA}(A^{-1}B + x(0)) - A^{-1}B \end{aligned} \quad .$$

Then for any $T \geq 0$,

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{t \in [0, T]} \left\| \frac{X^N(t)}{N} - x(t) \right\|_{\infty} = 0 \right) = 1.$$

Let us now consider the dynamical system on $(\mathbb{R}_+^n)^3$ defined by:

$$\left. \begin{aligned} \dot{s}_j &= p_j B_j + b_j(s_j + i_j + r_j) - d_j s_j + \sum_{k \neq j} \theta_{k,j} s_k - \sum_{k \neq j} \theta_{j,k} s_j - \beta_j i_j \frac{s_j}{s_j + i_j + r_j} \\ \dot{i}_j &= q_j B_j + \beta_j i_j \frac{s_j}{s_j + i_j + r_j} - d_j i_j - \gamma_j i_j + \sum_{k \neq j} \theta_{k,j} i_k - \sum_{k \neq j} \theta_{j,k} i_j \\ \dot{r}_j &= r_j B_j + \gamma_j i_j - d_j r_j + \sum_{k \neq j} \theta_{k,j} r_k - \sum_{k \neq j} \theta_{j,k} r_j \end{aligned} \right\} \quad (\mathcal{S}_{\text{epi}})$$

for all $j \in \llbracket 1, n \rrbracket$. Then we get the following, that is Proposition 3.2.8 of Subsection 3.2.1:

PROPOSITION 1.3.34 (Scaling limit of a branching-driven SIR process). — *Let $((S^N, I^N, R^N))_{N \geq 1}$ be the sequence of branching-driven SIR processes defined in Subsection 1.2.3. Assume that $N^{-1}(S^N(0), I^N(0), R^N(0))$ tends to $(s(0), i(0), r(0)) \in \mathbb{R}_+^3$ as N tends to $+\infty$. Denoting (s, i, r) the solution of $(\mathcal{S}_{\text{epi}})$ with initial condition $(s(0), i(0), r(0))$, we have for any $T \geq 0$:*

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{t \in [0, T]} \left\| \frac{(S^N(t), I^N(t), R^N(t))}{N} - (s, i, r)(t) \right\|_{\infty} = 0 \right) = 1.$$

Similar results hold for the logistic population process and the logistic-driven SIR process. Let us introduce the system on \mathbb{R}_+^n defined by

$$\dot{z}_i = (B_i + b_i z_i)(K_i - z_i)_+ - d_i z_i + \sum_{j \neq i} \theta_{j,i} z_j (K_i - z_i)_+ - \sum_{j \neq i} \theta_{i,j} z_i (K_j - z_j)_+ \quad (\mathcal{S}'_{\text{pop}})$$

for all $i \in \llbracket 1, n \rrbracket$. It can be shown (see Section 2.3) that this system admits an equilibrium in $\prod_{i=1}^n (0, K_i)$ (not necessarily unique), that we will denote z^* .

We further consider the system on $(\mathbb{R}_+^n)^3 = \{(s, i, r) \in (\mathbb{R}_+^n)^3\}$ defined by:

$$\left. \begin{aligned} \dot{s}_j &= (p_j B_j + b_j z_j)(K_j - z_j^*)_+ - d_j s_j - \beta_j i_j \frac{s_j}{z_j^*} \\ &\quad + \sum_{k \neq j} \theta_{k,j} s_k (K_j - z_j^*)_+ - \sum_{k \neq j} \theta_{j,k} s_j (K_k - z_k^*)_+ \\ \dot{i}_j &= q_j B_j (K_j - z_j^*)_+ + \beta_j i_j \frac{s_j}{z_j^*} - d_j i_j - \gamma_j i_j \\ &\quad + \sum_{k \neq j} \theta_{k,j} i_k (K_j - z_j^*)_+ - \sum_{k \neq j} \theta_{j,k} i_j (K_k - z_k^*)_+ \\ \dot{r}_j &= r_j B_j (K_j - z_j^*)_+ + \gamma_j i_j - d_j r_j + \sum_{k \neq j} \theta_{k,j} r_k (K_j - z_j^*)_+ - \sum_{k \neq j} \theta_{j,k} r_j (K_k - z_k^*)_+ \end{aligned} \right\} (\mathcal{S}'_{\text{epi}})$$

for all $j \in \llbracket 1, n \rrbracket$. The following results are analogous to Propositions 1.3.33 and 1.3.34 above in the logistic case. They are respectively Propositions 2.3.2 and 3.2.17 of the present work.

PROPOSITION 1.3.35 (Scaling limit of a logistic population process). — *Let $(X^N)_{N \geq 1}$ be the sequence of logistic population processes defined in Subsection 7.2.2. We denote by z the solution of the dynamical system $(\mathcal{S}'_{\text{pop}})$ with initial value $z(0)$. Then for any $T \geq 0$,*

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{t \in [0, T]} \left\| \frac{X^N(t)}{N} - z(t) \right\|_{\infty} = 0 \right) = 1.$$

PROPOSITION 1.3.36 (Scaling limit of a logistic-driven SIR process). — *Let $((S^N, I^N, R^N))_{N \geq 1}$ be the sequence of logistic-driven SIR processes defined in Subsection 1.2.3. Assume that $z(0) = z^*$ and that $N^{-1}(S^N(0), I^N(0), R^N(0))$ tends to $(s(0), i(0), r(0)) \in \mathbb{R}_+^3$ as N tends to $+\infty$. Denoting (s, i, r) the solution of $(\mathcal{S}'_{\text{epi}})$ with initial condition $(s(0), i(0), r(0))$, we have for any $T \geq 0$:*

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{t \in [0, T]} \left\| \frac{(S^N(t), I^N(t), R^N(t))}{N} - (s, i, r)(t) \right\|_{\infty} = 0 \right) = 1.$$

1.3.4 Metastability for scaled Markov jump processes

Theorem 1.3.32 states the convergence of a scaled sequence of jump processes to a deterministic process over a finite time interval. However, this deterministic approximation of a stochastic jump process fails to hold in general over long time scales. The scaled process can, in some cases, reach a set of absorbing states that the deterministic process does not. This happens for instance for the logistic birth and death process (see Chapter 2 of [BM15]) or some epidemic processes with endemicity without immigration of infectives (see [Bar56, N 99, AB00b]). In these two cases, extinction (of the population or the epidemic process) occurs because of random fluctuations of the scaled stochastic process around the deterministic curve, after it has spent a long time around an equilibrium point for the dynamical system, referred to as *metastable* (see [VO05, Bov06] for a thorough introduction to metastability).

Deviations from a deterministic equilibrium by a Brownian perturbation of a deterministic process have been studied by Freidlin and Wentzell (see [FW84, VO05, Bov06]). Their results

predict both after which scale of time the stochastic process will, with high probability, exit a domain around the metastable equilibrium, and from which part of the domain this exiting is most likely to occur. More recently, similar results have been derived for density-dependent Poisson-driven jump processes [KP18, BP18, PSK17]. The next subsection is built on this theory.

1.3.4.1 Exit time from a domain for a scaled Markov jump process

As in Section 1.3.3, we assume that for any $N \geq 1$, X^N is a pure Markov jump process on \mathbb{Z}_+^n such that the rate $q_{k,k+l}^N$ at which X^N jumps from state $k \in \mathbb{Z}_+^n$ to state $k+l \in \mathbb{Z}_+^n$ satisfies

$$q_{k,k+l}^N = \begin{cases} N\beta_l\left(\frac{k}{N}\right) & \text{if } l \in \mathcal{D} \\ 0 & \text{otherwise} \end{cases}$$

where β_l a nonnegative locally Lipschitz-continuous functions on \mathbb{R}_+^n independent from N . We also assume that for all $x \in \mathbb{R}_+^n$ and all $N \geq 1$, $X^N(0) = \lfloor Nx \rfloor$ under \mathbb{P}_x .

We make the additional assumptions of the rate functions β_l :

ASSUMPTION A (On the rate functions). —

1. The β_l vanish out of a compact, convex subset A of \mathbb{R}_+^n with nonempty interior \mathring{A} .
2. For any l , either $\beta_l \equiv 0$, either β_l takes positive values on \mathring{A} .
3. There exist $z_0 \in \mathring{A}$ and two positive constants λ_1, λ_2 such that whenever $z \in A$ is such that $0 < \beta_j(z) < \lambda_1$, then $\beta_j(az_0 + (1-a)z) > \beta_j(z)$ for all $a \in]0, \lambda_2[$.
4. There exists $\nu \in (0, 1/2)$ such that

$$\lim_{a \rightarrow 0} a^\nu \log \left(\inf_{j: \beta_j \neq 0} \inf_{\text{dist}(z, \partial A) \geq a} \beta_j(z) \right) = 0$$

where $\text{dist}(z, \partial A)$ stands for the Euclidean distance between z and the boundary of A .

In the population and epidemic models we will consider, rate functions β_l do not necessarily vanish outside of a compact subset. Yet, we will focus on the exit time of our various processes from a small ball lying on the basin of attraction of some metastable equilibrium. It will therefore prove sufficient to provide a coupling with processes defined with tweaked versions of the rate functions that vanish quickly outside of this ball.

Let us define $L: \mathbb{R}_+^n \times \mathbb{R}^n \rightarrow \mathbb{R}_+$ by

$$L(x, \gamma) := \max_{u \in \mathbb{R}^n} \left[\gamma \cdot u - \sum_l \beta_l(x) (e^{\langle l, u \rangle} - 1) \right].$$

For any $x \in (\mathbb{R}_+^*)^n$ and any $\varepsilon > 0$ lower than $\min_i x_i$, we define

$$\bar{V}_\varepsilon(x) := \inf_{\|x' - x\|_2 = \varepsilon} \inf_{\int_{T_1}^{T_2} L(\phi(t), \dot{\phi}(t)) dt} \quad (1.13)$$

where the second infimum is taken over the set of $\mathcal{B}_2(x, \varepsilon)$ -valued absolutely continuous functions ϕ on some $[T_1, T_2]$ (with $-\infty \leq T_1 < T_2 \leq +\infty$) such that $\phi(T_1) = x$ and $\phi(T_2) = x'$.

The quantity $\inf_{T_1}^{T_2} \int_{T_1}^{T_2} L(\phi(t), \dot{\phi}(t)) dt$ is called the *quasipotential* of x' with respect to x for the Poisson perturbation $(X^N)_N$ of the dynamical system (1.12). Its analogous for Brownian perturbations of a deterministic process is a core notion in the Freidlin-Wentzell theory of large deviations. The latter predicts that the exit of the stochastic process from a domain around a metastable equilibrium by a stochastic process will occur through paths ϕ that minimize the quasipotential. As such, the $\bar{V}_\varepsilon(x)$ can be seen as the "exit cost" from the domain $\mathcal{B}_2(x, \varepsilon)$ starting at point x . The exiting time from this domain is therefore expected to get longer as $\bar{V}_\varepsilon(x)$ grows. This intuition is confirmed by the following theorem, that is a consequence of Theorem 6 of [PSK17]:

THEOREM 1.3.37 (Time of exit from a ball around an attractive equilibrium). — *If $x^* \in (\mathbb{R}_+^*)^n$ is a locally attractive equilibrium for the dynamical process defined by (1.12), then for $\varepsilon > 0$ small enough, and for all $\alpha > 0$, denoting by τ_ε^N the time of exit from $\mathcal{B}_2(x^*, \varepsilon)$ by X^N/N , we have:*

$$\forall x \in \mathcal{B}_2(x^*, \varepsilon), \quad \lim_{N \rightarrow +\infty} \mathbb{P}_x \left(e^{(\bar{V}_\varepsilon(x^*) - \alpha)N} < \tau_\varepsilon^N < e^{(\bar{V}_\varepsilon(x^*) + \alpha)N} \right) = 1.$$

1.3.4.2 Large deviations of the processes under study

A first application of Theorem 1.3.37 above consists in quantifying the time range over which a scaled branching population process stays in a neighborhood of its equilibrium value once it reaches it (see Proposition 2.2.3):

PROPOSITION 1.3.38 (Exit time of a branching population process). — *Let $(X^N)_{N \geq 1}$ be the sequence of branching population processes and let $x^* = -A^{-1}B$. For any $\varepsilon \in (0, \|x^*\|_2)$, denote by τ_ε^N the exit time of the ball $\mathcal{B}_2(x^*, \varepsilon)$ by X^N/N . Then for ε small enough, there exists $\bar{V}_\varepsilon(x^*) > 0$ such that whenever $x(0) \in \mathcal{B}_2(x^*, \varepsilon)$, for any $\alpha > 0$:*

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(e^{(\bar{V}_\varepsilon(x^*) - \alpha)N} < \tau_\varepsilon^N < e^{(\bar{V}_\varepsilon(x^*) + \alpha)N} \right) = 1.$$

If we assume that $p = 1$, we recall from Subsection 1.3.2.3 that we define the *extinction time* of the epidemic as the (almost surely finite) hitting time of $\mathbb{Z}_+^n \times \{0\}^n \times \mathbb{Z}_+^n$ by the epidemic process, and the *total size of the epidemic* as the total number of individuals infected during the course of the epidemic. The following result shows that in this case, the existence of a globally asymptotically stable endemic equilibrium for system $(\mathcal{S}_{\text{epi}})$ defined in Subsection 1.3.3.2 yields an exponential lower bound for the extinction time and the total size of a branching-driven epidemic. Its proof is based on the fact that in the case of a major outbreak, the scaled epidemic process approaches the endemic equilibrium with high probability, and stays within its neighborhood for a time that is exponential in N before undergoing fluctuations that eventually cause the extinction of the epidemic.

THEOREM 1.3.39 (Outcome of a branching-driven epidemic). — Assume that $p = 1$, that $x(0) = x^*$, that $R_0 > 1$ and that the dynamical system $(\mathcal{S}_{\text{epi}})$ restricted to $\mathbb{R}_+^n \times (\mathbb{R}_+^n \setminus \{0\}) \times \mathbb{R}_+^n$ admits a globally asymptotically stable endemic equilibrium (s^*, i^*, r^*) . Consider the sequence of branching-driven epidemic processes $((S^N, I^N, R^N))_{N \geq 1}$ given by Theorem 1.3.29, with $I^N(0) = I(0) \in \mathbb{Z}_+^n$, $S^N(0) = \lfloor Nx(0) \rfloor - I(0)$ and $R^N(0) = 0$. Then, if τ^N denotes the extinction time of the epidemic and Z^N its final size, there exists $V > 0$ such that:

$$\lim_{N \rightarrow +\infty} \mathbb{P}(\tau^N > e^{VN} | Z^N = +\infty) = 1 \quad (1.14)$$

and

$$\lim_{N \rightarrow +\infty} \mathbb{P}(Z^N > e^{VN} | Z^N = +\infty) = 1. \quad (1.15)$$

When immigration of infectives is allowed, that is, when $q \neq 0$ a simple consequence of Theorem 1.3.37 (Proposition 3.2.9) is that the scaled epidemic process spends most of its time in a neighborhood of an equilibrium value of $(\mathcal{S}_{\text{epi}})$ provided the latter is attractive:

PROPOSITION 1.3.40 (Time spent in a neighborhood of the equilibrium of $(\mathcal{S}_{\text{epi}}^1)$). — Assume that at least one q_i is positive and that $(\mathcal{S}_{\text{epi}})$ admits a globally asymptotically stable equilibrium (s^*, i^*, r^*) . Let $((S^N, I^N, R^N))_{N \geq 1}$ be the sequence of branching-driven epidemic processes. Then $i_j^* > 0$ for all $j \in \llbracket 1, n \rrbracket$, and for every $\varepsilon > 0$ there exist $T > 0$ and $V > 0$ such that

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(\int_0^{T+e^{VN}} \mathbf{1}_{\frac{(S^N(t), I^N(t), R^N(t))}{N} \in \mathcal{B}_2((s^*, i^*, r^*), \varepsilon)} dt > e^{VN} \right) = 1.$$

Once again, the results above transpose to the logistic case:

THEOREM 1.3.41 (Outcome of a logistic-driven epidemic). — The conclusions of Theorem 1.3.39 and Proposition 1.3.40 are true for logistic-driven SIR processes, replacing $(\mathcal{S}_{\text{epi}})$ by $(\mathcal{S}'_{\text{epi}})$ and $x(0) = x^*$ by $z(0) = z^*$.

1.4

The tau-leaping simulation method

Simulating efficiently Markov jump processes with a high number of jump directions and a high sum of jumping rates is a topic of interest in many fields. It was initially raised in chemical physics, that study chemically reacting systems with a high number of molecular species, with small typical quantities of each species making the use of diffusive models irrelevant [MA97, ARM98]. The simulation of stochastic population and epidemic models involving large numbers of individuals is of course another relevant domain of application [KPSK15].

An exact and straightforward numerical simulation method for Markov jump processes is the so-called Gillespie's stochastic simulation (SSA) algorithm [Gil76, Gil77], that in reality was first introduced by Doob [Doo42, Doo45] and implemented by Kendall [Ken50]. The algorithm consists in drawing at each step the time before the next jump of the system from an exponential distribution, then drawing the direction of this jump with a probability given by the relative weight of the corresponding jump rate relatively to the sum of the rates in all directions.

More formally, when simulating a stochastic process with rates given by the following chart:

$$\begin{array}{ll} \text{Transition} & \text{Rate at state } x \in \mathbb{Z}_+^n \\ x \rightarrow x + l & \beta_l(x) \end{array} \quad (1.16)$$

for all $l \in \mathcal{D}$, and denoting $\beta(x) = \sum_{l \in \mathcal{D}} \beta_l(x)$ for all $x \in \mathbb{Z}_+^n$, the SSA algorithm consists in the following:

ALGORITHM 1.4.1 (SSA algorithm for Markov \mathcal{D} -directional jump processes). —

1. Start the process at a chosen value $X(0)$ and set $T = 0$.
2. If the process is at state x , draw an exponential variable S with mean $\beta(x)^{-1}$ (if $\beta(x) > 0$) then draw a vector l out of \mathcal{D} as a random variable with point probability $\beta_l(x)\beta(x)^{-1}$.
3. Define the next jump time of the process as $T + S$ and its direction as l , so $X(T + S) = x + l$.
4. Change T for $T + S$.
5. Repeat Steps 2 to 4 until some final time or condition is reached.

This algorithm requires updating jump rates at each timestep. Therefore, it may prove impractical to deal with high-dimensional jump processes — typically when n is of the order or several thousands as in the cases we will consider in Chapter 4. The τ -leaping method introduced in [Gil01] is a stochastic counterpart to Euler's method for simulating ordinary differential equations. It attempts at speeding up stochastic simulation by examining how many times each jump direction l is taken on average during a fixed time interval $[t, t + \tau[$ to be determined, assuming that the process is constant at state x during this time interval. This allows rates $\beta_l(x)$ not

to be computed again every time a jump occurs. It is well-known that under this assumption, the number of jumps in direction l during a timestep τ is a random variable Z_l with Poisson distribution of mean $\tau\beta_l(x)$, and that the variables Z_l are independent from each other. This leads to the following algorithm:

ALGORITHM 1.4.2 (Tau-leaping algorithm for Markov \mathcal{D} -directional jump processes). —

1. Start the process at a chosen value $X(0)$ and set $T = 0$.
2. If the process is at state x , draw independent Poisson variables Z_l such that for each $l \in \mathcal{D}$, Z_l has mean $\tau\beta_l(x)$.
3. Define $X(T + \tau)$ as $x + \sum_{l \in \mathcal{D}} Z_l l$.
4. Change T for $T + \tau$.
5. Repeat steps 2 to 4 until some final time or condition is reached.

If jump rates do not vary much locally and if τ is small enough, we can expect the resulting simulated process to be close to an actual realization of the process we could obtain through the SSA algorithm. Besides, the computational cost of a simulation obviously increases in inverse proportion of τ ; it is therefore of great interest to select the value of τ carefully. Gillespie and Petzold [GP03] originally proposed to calibrate τ at each step of the algorithm in order to bound the estimated changes in β_j during a leap by a relatively small fraction of the sum of the β_j . Yet, this procedure would allow for a relatively great variation of smaller rate values, which violate the assumption that all rates are almost constant during a leap. Alternative step selection methods are proposed in [CGP06], among which a computationally efficient method ensuring the approximate bounding of all *relative* jump rates variations during a leap.

Moreover, algorithm 1.4.2 above has to be modified to not allow for negative populations to be simulated (and therefore fall outside of the domain of definition of the β_j), which could occur with positive probability when applying algorithm 1.4.2 because of the unboundedness of Poisson variables.

Authors of [CGP06] put forward a new τ -selection procedure addressing these requirements, that proves to provide with simulations that are very close to the SSA while being much faster to execute. This is our choice algorithm for simulating population and epidemic processes (see Chapter 4):

ALGORITHM 1.4.3 (Modified tau-leaping algorithm for Markov \mathcal{D} -directional jump processes). — After choosing a fraction $\varepsilon > 0$ and a criticality threshold $n_c > 0$:

1. Start the process at a chosen value $X(0)$ and set $T = 0$.
2. If the process is at state x , identify the indices i such that $x_i < n_c$, that we should refer to as *critical*, and denote the set of noncritical indices by J_{ncr} .
3. If $J_{ncr} = \emptyset$, take $\tau' = +\infty$ and go to Step 5.

ALGORITHM 1.4.3 (continued). —

4. For all $l \in \mathcal{D}$ and $k \in J_{ncr}$, compute

$$\begin{aligned}
 f_{l,k}(x) &= \frac{\partial \beta_l}{\partial x_k}(x), \\
 \mu_l(x) &= \sum_{k=1}^n f_{l,k}(x) \beta_{e_k}(x) - \sum_{k \in J_{ncr}} f_{l,k}(x) \beta_{-e_k}(x) \\
 &\quad + \sum_{k \in J_{ncr}} \sum_{j=1}^n (f_{l,j}(x) - f_{l,k}(x)) \beta_{e_j - e_k}(x) + \sum_{k=1}^n \sum_{j \in J_{ncr}} (f_{l,k}(x) - f_{l,j}(x)) \beta_{e_k - e_j}(x), \\
 \sigma_l^2(x) &= \sum_{k=1}^n f_{l,k}^2(x) \beta_{e_k}(x) + \sum_{k \in J_{ncr}} f_{l,k}^2(x) \beta_{-e_k}(x) \\
 &\quad + \sum_{k \in J_{ncr}} \sum_{j=1}^n (f_{l,j}(x) - f_{l,k}(x))^2 \beta_{e_j - e_k}(x) + \sum_{k=1}^n \sum_{j \in J_{ncr}} (f_{l,k}(x) - f_{l,j}(x))^2 \beta_{e_k - e_j}(x)
 \end{aligned}$$

and a first candidate for τ :

$$\tau' = \min_{l \in \mathcal{D}} \left\{ \frac{\varepsilon \beta(x)}{|\mu_l(x)|}, \frac{(\varepsilon \beta(x))^2}{\sigma_l^2(x)} \right\}.$$

5. If $\tau' < 10/\beta(x)$, abandon tau-leaping temporarily, simulate 100 jumps of the process with the SSA Algorithm 1.4.1 and go back to Step 2. Otherwise, proceed to Step 6.

6. Set

$$m = \sum_{k \notin J_{ncr}} \left(\beta_{-e_k}(x) + \sum_{j=1}^n \beta_{e_j - e_k}(x) \right)$$

and generate a second candidate for τ as a sample τ'' of the exponential random variable with mean m .

7. Set $\tau = \min(\tau', \tau'')$.

8. For any l that is not a $-e_k$ or a $e_j - e_k$ with k critical, draw a Poisson variable Z_l with mean $\tau \beta_l(x)$. The Z_l have to be drawn independent from each other. If $\tau'' \leq \tau'$, draw l among $\{-e_k : k \text{ critical}\} \cup \{e_j - e_k : j \in \llbracket 1, n \rrbracket, k \text{ critical}\}$, with point probabilities $\beta_l(x)/m_c$, then set $Z_l = 1$.

9. For any l that has not been assigned a Z_l yet, set $Z_l = 0$.

10. If there is a negative component in $x + \sum_{l \in \mathcal{D}} l Z_l$, replace τ' by $\tau'/2$ and return to Step 5. If not, define $X(T + \tau)$ as $x + \sum_{l \in \mathcal{D}} Z_l l$ and proceed to next step.

11. Change T for $T + \tau$.

12. Repeat Steps 2 to 11 until some final time or condition is reached.

In this algorithm, ε stands for the relative variation of rates allowed during a leap. It is gener-

ally said to be taken equal to 0.03 [GP03, CGP06] and we shall follow this usage. Populations with low values (below n_c) are identified as critical, and jump directions that would lead to lowering these populations, that we will also say to be critical, are deactivated. Instead, the algorithm allows only one jump in only one of the critical directions to happen at each iteration (step 8), which insures that critical jump never drive populations below zero.

The time τ' is the largest permissible timestep allowing for a small enough relative variation of the jump rate for the noncritical reactions, while τ'' estimates the time to the next critical jump. This explains Step 7 and why a critical jump is triggered whenever $\tau'' \leq \tau'$.

Critical jumps are those most likely to drive a population below zero, but some noncritical jumps may do so with positive probability due to the unboundedness of Poisson variables. Step 10 of the algorithm makes up for this problem by discarding increments that would result in one population becoming negative and by reducing the chosen timestep to generate smaller Poisson variables. When the timestep τ' is too low for the tau-leaping simulation to be computationally efficient as compared to the SSA, the latter method takes over until the process reaches a state allowing for a larger timestep (Step 5).

Comparisons between the computation time of simulated trajectories for an SIS (Susceptible — Infected — Susceptible) epidemic model with Algorithms 1.4.1 (SSA) and 1.4.3 (modified tau-leaping) can be found in [KPSK15]. It appears that the tau-leaping method results in spectacularly smaller computation times for high values of the scaling parameter N . These times are even decreasing with N , possibly due to less frequent uses of SSA steps (see Step 5 of Algorithm 1.4.3) when N is large.

2

The population model

In the next sections, we provide a formal definition of the population models introduced heuristically in Section 1.2. In Section 2.1, we give sufficient conditions for the stability of metapopulation PDMP in a general framework that encompasses the multiplicative uniform and unitary power settings defined in Subsection 1.2.1. Then we turn to the metapopulation jump processes introduced in Subsection 1.2.2. We derive ergodicity results, exhibit deterministic scaling limits and study the time of deviation of the scaled process from an equilibrium of the associated dynamical system (Section 2.2 and Section 2.3).

2.1

Piecewise deterministic Markovian metapopulation processes

The work presented in this section stems mostly from an article first submitted on April 19, 2017 to *Stochastic Processes and their Applications* [Mon19a], submitted again in a revised form on July 10, 2018 and still under review after revision at the time of writing this manuscript.

2.1.1 Introductory remarks

Although most metapopulations models have been dealing with fully deterministic or fully stochastic population dynamics, network-organized systems with deterministic intra-nodal dynamics and stochastic inter-nodal transfers naturally appear as relevant to describe metapopulations with low local stochasticity (e.g. because of large population sizes) and random population transfers between patches.

Besides the application we have in mind, network-organized systems with deterministic intra-nodal dynamics and stochastic inter-nodal transfers naturally appear in a large range of applicative fields. As we saw in the Introduction, they are relevant to describe metapopulation dynamics within a Levins setting with stochastic migration (see [Lev69] and Figure 2.1). Other possible fields of application range from open Jackson networks [Jac57, MD94, Dai95] with deterministic inputs and outputs to communication networks based on TCP-type processes [HL01, BCG⁺13, CMP10], storage [HR76] on a network, neuronal stimulation [DO16,

DGLO16] and more generally a large class of stochastic hybrid systems on graphs [CL07] with low stochasticity in autonomous dynamics.

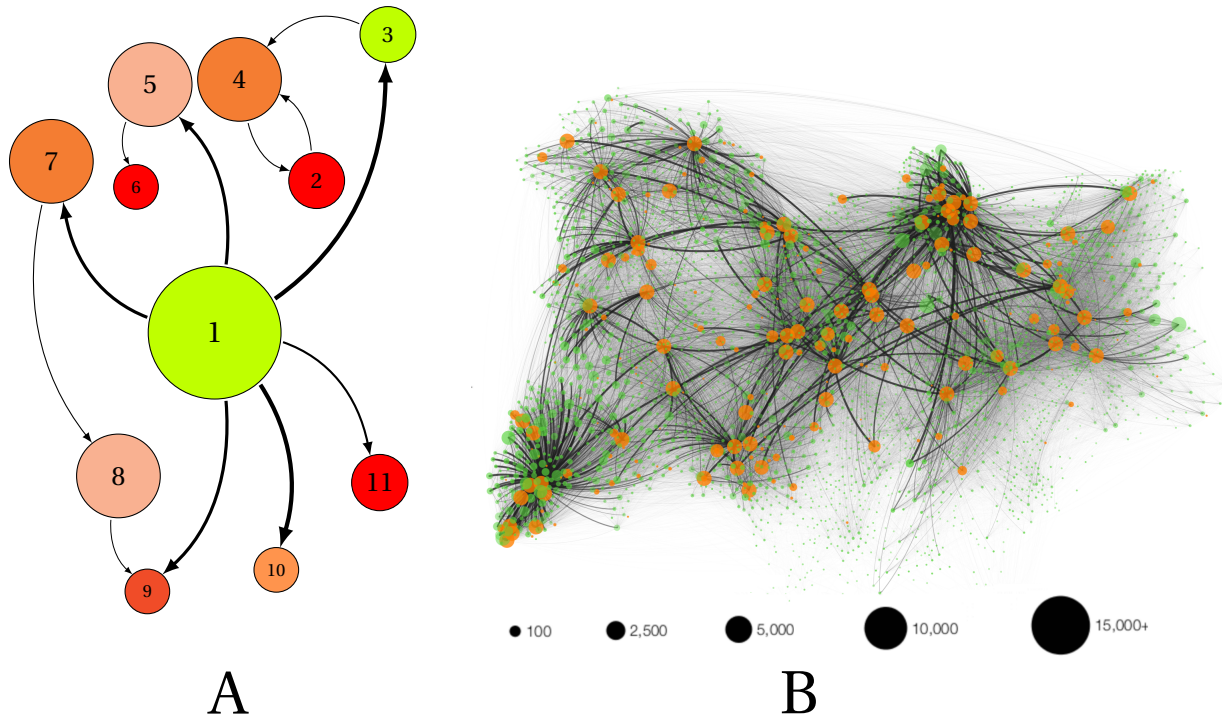


Figure 2.1: Two population networks. Panel A: stochastic "mainland-islands" Levins model [Lev69, MW67] with unitary transfers. Edge thickness corresponds to transfer rates, while colors denote the sign of autonomous growth functions (red tones being associated to negative growth functions, green tones to positive ones). Panel B: 2008 cattle trade network in the French Auvergne-Rhône-Alpes area, densely populated with cattle (courtesy of G. Beaunée). Edge thickness corresponds to the overall volume of cattle transfers within the period and colors stand for holding types (green for farms and orange for commercial operators). Coordinates of farms and commercial operators are randomly distributed over the corresponding commune area.

There is, to our knowledge, little literature on general stability criteria for \mathbb{R}^n -valued piecewise deterministic Markov processes. Meaningful results on the stability of Jackson networks have been derived that are deeply rooted on considerations about the graph structure [WV80]. We wish to obtain similar statements in our semi-deterministic framework while allowing for state-dependent jump intensities and possibly large transfers. The total population of the system is here preserved by jumps and behaves as a non-Markovian randomly switched process [LM01, Mal90]. That is why we expect the process boundedness to arise from conditions on the deterministic inter-jump flow and the process ability to reach population-decreasing states in short times.

As stated in the Introduction (see Subsection 1.2.1), we will associate the population of each patch i with an autonomous growth function ϕ_i (meaning that $dX_i(t) = \phi_i(X(t))dt$ between jumps), and an instantaneous transfer from patch i to patch j at population x occurs at state-dependent rate $\theta_{i,j}(x)$, its amplitude being drawn according to a $[0, x_i]$ -supported law $\mu_{i,j}(x, \cdot)$.

We also recall from Section 1.2.1 the following definition of constant-growth multiplicative uniform and unitary power settings. If $\mathcal{G} = ([1, n], \mathcal{A})$ is a strongly connected directed graph on $[1, n]$, define $(c_1, \dots, c_n) \in \mathbb{R}^n \setminus \{0\}$ and consider the constant-growth settings defined by:

Multiplicative uniform setting

$$\phi_i(x) = \begin{cases} c_i & \text{if } c_i \geq 0 \\ c_i 1_{x_i > 0} & \text{if } c_i < 0 \end{cases} \quad \text{and} \quad \begin{cases} \theta_{i,j}(x) = \theta_{i,j} \\ \mu_{i,j}(x, \cdot) = \mathcal{U}([0, x_i]) \end{cases} \quad (1.1)$$

with $\theta_{i,j} > 0$ if $(i, j) \in \mathcal{A}$ and $\theta_{i,j} = 0$ otherwise, or:

Unitary power setting

$$\phi_i(x) = \begin{cases} c_i & \text{if } c_i \geq 0 \\ c_i 1_{x_i > 0} & \text{if } c_i < 0 \end{cases} \quad \text{and} \quad \begin{cases} \theta_{i,j}(x) = (1 \vee x_i)^\alpha \\ \mu_{i,j}(x, \cdot) = \delta_{1 \wedge x_i} \end{cases} \quad (1.2)$$

for some $\alpha \in (0, 1]$.

Theorems 2.1.2 and 2.1.5 below imply that in any of the two cases above, the process is positive Harris recurrent if and only if

$$\sum_{i=1}^n c_i < 0, \quad (2.1)$$

in which case it is also F-ergodic for some exponential function $F: \mathbb{R}_+^n \rightarrow \mathbb{R}_+$ (statement of Theorem 1.3.22). Note that equation (2.1) is reminiscent of the usual traffic condition for queues networks (see Equation (1.9) of [Dai95]) but does not involve any term related to inter-patch transfers. This stems from the fact that transfers along \mathcal{G} happen and spread the total population among all patches, thus letting the flow on $(\mathbb{R}_+^*)^n$ bring X back towards lower population states. We will see that such a mechanism prevails in more general settings whenever jumps are large or frequent enough; in this case, a simple condition on the autonomous growth functions is required to ensure the process stability.

The rest of this section is organized as follows. We first give a formal definition of the general piecewise deterministic metapopulation process (Subsection 2.1.2). We highlight two instances of interest referred to as the *multiplicative* and *unitary* frameworks (Subsection 2.1.3), that encompass respectively the multiplicative uniform and the unitary power settings, and we state stability results for these models. We then give Meyn-Tweedie inspired criteria for boundedness (Subsection 2.1.4.1), petiteness (Subsection 2.1.4.2) and ergodicity (Subsection 2.1.4.3) in the general case. In Subsections 2.1.5 and 2.1.6, we apply the criteria from Subsection 2.1.4 to prove the results of Subsection 2.1.3. Finally, Subsections 2.1.5 and 2.1.6 contain proofs of Theorem 2.1.2 and Theorem 2.1.5 respectively.

2.1.2 Definition of the metapopulation PDMP

For all $i \in \llbracket 1, n \rrbracket$, let $\phi_i : \mathbb{R}_+^n \rightarrow \mathbb{R}$ be a measurable and bounded function. Assume that $\phi = (\phi_1, \dots, \phi_n)$ is such that the flow Φ associated to the vector field ϕ is well-defined on \mathbb{R}_+^n , that is, that for any $x \in \mathbb{R}_+^n$ there exists a unique continuous function $\Phi(x, \cdot) : \mathbb{R}_+ \rightarrow \mathbb{R}_+^n$ such that $\Phi(x, t) = x + \int_0^t \phi(x(u)) du$ for all $t \geq 0$. This condition is for instance fulfilled if ϕ is \mathcal{C}^1 .

We remind that $\mathcal{I} = \{(i, j) \in \llbracket 1, n \rrbracket^2 : i \neq j\}$. For all $(i, j) \in \mathcal{I}$, let $\theta_{i,j} : \mathbb{R}_+^n \rightarrow \mathbb{R}$ be a positive measurable, locally bounded function. We assume that there exists a directed graph $\mathcal{G} = (\llbracket 1, n \rrbracket, \mathcal{E})$, with $\mathcal{E} \subset \mathcal{I}$, such that for all $(i, j) \in \mathcal{E}$, $\theta_{i,j}(x) > 0$ whenever $x_i > 0$. We call \mathcal{G} the *active graph* of the model.

For all $(i, j) \in \mathcal{I}$ and all $x \in \mathbb{R}_+^n$, finally define a probability measure $\mu_{i,j}(x, \cdot)$ on $[0, x_i]$, and for all $\xi \in [0, 1]$, set

$$q_{i,j}(x, \xi) = \inf \{u \in [0, x_i] : \mu_{i,j}(x, [0, u]) \geq \xi\}$$

and assume that the $q_{i,j} : \mathbb{R}_+^n \times [0, 1] \rightarrow \mathbb{R}_+$ are Borel-measurable.

Our object of interest is the family of processes solution of the following stochastic differential equation:

$$\boxed{dX(t) = \phi(X(t))dt + \sum_{(i,j) \in \mathcal{I}} \int_{\mathbb{R}_+ \times [0,1]} q_{i,j}(X(t^-), \xi) (e_j - e_i) \mathbf{1}_{z < \theta_{i,j}(X(t^-))} N_{i,j}(dt, dz, d\xi)} \quad (2.2)$$

where $(N_{i,j})_{(i,j) \in \mathcal{I}}$ is a collection of independent homogeneous Poisson point measures on $\mathbb{R}_+ \times \mathbb{R}_+ \times [0, 1]$ with intensity $dt dz d\xi$ defined on $(\Omega, \mathcal{A}, \mathbb{P})$.

If $x \in \mathbb{R}_+^n$, the existence of a strong solution $X^x = (X^x(t))_{t \geq 0}$ to (2.2) with initial value x follows from the explicit construction by Davis ([Dav93] p.55). Pathwise uniqueness and uniqueness in law also hold since such solutions can naturally be expressed as deterministic functions of the atoms of the $N_{i,j}$ random measures. Moreover, we see at once that the X^x processes are non-explosive and well-defined on \mathbb{R}_+ because the $\theta_{i,j}$ and ϕ_i are bounded on compacts and because jumps conserve the total population. By Theorem 25.5 of [Dav93] (slightly adapted to allow for zero-amplitude jumps), the strong Markov property holds for $(X^x)_{x \in \mathbb{R}_+^n}$.

We assume that there exists a Markov family $(X, (\mathbb{P}_x)_{x \in \mathbb{R}_+^n})$ on (Ω, \mathcal{A}) such that for any $x \in \mathbb{R}_+^n$, the law of X under \mathbb{P}_x is the law of X^x under \mathbb{P} . We will mostly use this homogeneous and lighter notation.

We will denote by $(T_k)_{k \geq 1}$ and $(U_k)_{k \geq 1}$ the sequences of jump times and jump quantiles of X , the second and third coordinates t and ξ of atoms of any $N_{i,j}$, ordered according to the values of t . More formally, $(T_k)_{k \geq 1}$ is the sequence of jump times of the counting process

$$(Z_t)_{t \geq 0} = \left(\sum_{(i,j) \in \mathcal{I}} \int_{[0,t] \times \mathbb{R}_+} \mathbf{1}_{z < \theta_{i,j}(X(u^-))} N_{i,j}(du, dz, [0, 1]) \right)_{t \geq 0},$$

so T_k it is the time of the k -th (potentially null) transfer between patches of $\llbracket 1, n \rrbracket$ commanded

by the $N_{i,j}$ processes. The jump quantiles sequence $(U_k)_{k \in \mathbb{Z}_+}$ is defined as follows:

$$\forall k \geq 1, \quad U_k = \int_0^1 \xi \sum_{(i,j) \in \mathcal{J}} N_{i,j}(T_k, \mathbb{R}_+, d\xi),$$

so the U_k are independent and uniformly distributed on $[0, 1]$, and the amplitude of the population transfer at time T_k is given by $\sum_{(i,j) \in \mathcal{J}} N_{i,j}(T_k, \mathbb{R}_+, U_k) q_{i,j}(X(T_k^-), U_k)$.

It stems from equation (26.15) of [Dav93] that the infinitesimal generator \mathfrak{A} of $(X, \mathbb{P}_x, x \in \mathbb{R}_+^n)$ is given by

$$\mathfrak{A}f(x) = \sum_{k=1}^n \frac{\partial f}{\partial x_k}(x) \phi_k(x) + \sum_{(i,j) \in \mathcal{J}} \theta_{i,j}(x) \int \left(f(x + y \cdot (e_j - e_i)) - f(x) \right) \mu_{i,j}(x, dy) \quad (2.3)$$

for every \mathcal{C}^1 function $f: \mathbb{R}_+^n \rightarrow \mathbb{R}$. This equation is of well-known interest in studying invariant measures for X , as we illustrate in Appendix A.

2.1.3 Multiplicative and unitary models

We now turn to two particular classes of metapopulation PDMP models for which we will state simple stability results, each of them being representative of a typical feature that our graph-based model may exhibit. The first one corresponds to constant jump rates and multiplicative transfers (as in Equation (1.1)). The second one, symmetrically, is defined by coercive jump rates and unitary transfers (as in Equation (1.2)). Let us begin by stating additional assumptions that are common to both frameworks.

2.1.3.1 Additional assumptions

Let $m \in \llbracket 1, n \rrbracket$ and $d \in \llbracket 1, m \rrbracket$. We set $V^+ = \llbracket 1, d \rrbracket$, $V^0 = \llbracket d + 1, m \rrbracket$ and $V^- = \llbracket m + 1, n \rrbracket$. Patches in V^+ , V^0 and V^- will respectively be called *sources*, *neutral patches* and *sinks* following the terminology of [Pul88].

We consider the following set of assumptions:

ASSUMPTION B (On autonomous growth functions). —

(a) For all $i \in \llbracket 1, n \rrbracket$ and all $x \in \mathbb{R}_+^n$, $\phi_i(x) = \phi_i(x_i)$ only depends on x_i .

(b) For all $i \in \llbracket 1, n \rrbracket$:

- $\phi_i > 0$ if $i \in V^+$
- $\phi_i = 0$ if $i \in V^0$
- $\phi_i \leq 0$, $\phi_i(0) = 0$ and $\phi_i(y) < 0$ as soon as $y > 0$ if $i \in V^-$

(c) For all $i \in V^+$, ϕ_i is continuous and piecewise \mathcal{C}^1 .

(d) For all compact subset $K \subset \mathbb{R}_+^n$ there exists $T > 0$ such that $\Phi_i(x, T) = 0$ for any $x \in K$ if $i \in V^-$.

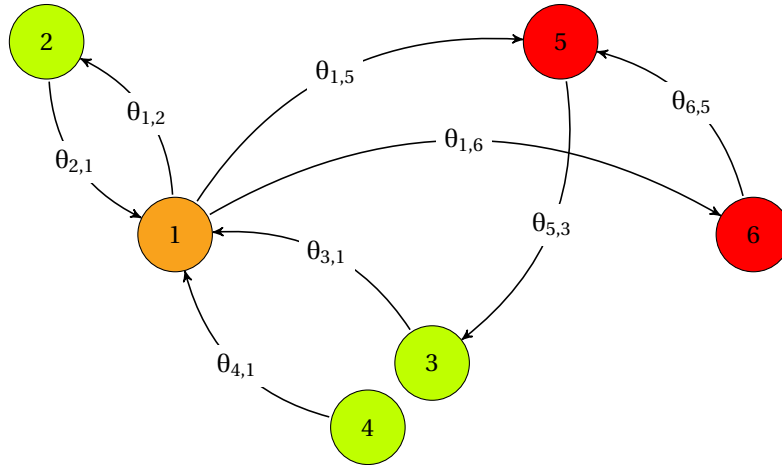


Figure 2.2: Graph structure complying with Assumption C. The edges in the figure are the elements of \mathcal{E} ; sources, neutral patches and sinks are respectively green, orange and red. Note that the graph represented is not strongly connected since no edge leads to node 4.

This first set of assumptions makes it possible to monitor the response of a given trajectory to small variations of jump times and transfer quantiles, with minor concern for the local behavior of Φ , and to describe simple trajectories leading to the emptying of the system. Note that the constant growth setting, defined by

$$\phi_i(x) = \begin{cases} c_i & \text{if } c_i \geq 0 \\ c_i 1_{x_i > 0} & \text{if } c_i < 0 \end{cases} \quad (2.4)$$

and involved in the multiplicative uniform and the unitary power setting, obviously satisfies these conditions.

We then require a strong condition on the graph structure of the active graph \mathcal{G} to hold:

ASSUMPTION C (On the topology of \mathcal{G}). —

- (a) Any $j \in V^-$ can be reached from any $i \in \llbracket 1, n \rrbracket$ by a path in \mathcal{G} .
- (b) Any $j \in V^0$ can be reached from some $i \in V^+$ by a path in \mathcal{G} .

The latter assumption is quite restrictive but will prove crucial in discussing both the boundedness of the process and the petiteness of compact subsets of \mathbb{R}_+^n . It allows to describe paths along which the system empties without having to discuss complex connectivity properties, while still being weaker than plain connectivity (see Figure 2.2).

2.1.3.2 Multiplicative models

We first introduce multiplicative models:

DEFINITION 2.1.1 (Multiplicative setting). — *A metapopulation PDMP model is said to be multiplicative if the following hold:*

1. *Assumptions B and C are fulfilled.*
2. *For all $(i, j) \in \mathcal{I}$, $\theta_{i,j}$ is constant.*
3. *For all $(i, j) \in \mathcal{I}$, there exists a probability distribution $\bar{\mu}_{i,j}$ on $[0, 1]$, the restriction of which to some non-punctual interval $I_{i,j} \subset [0, 1]$ admits a piecewise continuous and positive density with respect to the Lebesgue measure, such that:*

$$\forall x \in \mathbb{R}_+^n, \quad \forall A \in \mathcal{B}([0, 1]), \quad \mu_{i,j}(x, x_i A) = \bar{\mu}_{i,j}(A)$$

The "multiplicative" denomination refers to the fact that the relative population moving from patch i to patch j is drawn according to a distribution $\bar{\mu}_{i,j}$ which is independent from x . The process therefore goes through macroscopic jumps, but the assumption on the $\theta_{i,j}$ implies that these cannot be too frequent, which results in long, uninterrupted emptying periods under suitable assumptions. Note that we required the $\theta_{i,j}$ to be constant for the sake of simplicity, but all of the results we will present hold if the $\theta_{i,j}$ take values in a compact interval of \mathbb{R}_+^* .

Multiplicative models encompass the introductory multiplicative uniform setting defined by (1.1) as well as a large class of *additive increase multiplicative decrease* (AIMD) models that are absolutely continuous counterparts to those studied in [DGR02] and [HL01].

Our main stability result for the multiplicative setting is the following:

THEOREM 2.1.2 (Stability of multiplicative models). — *If the model is multiplicative and*

$$\limsup_{\min_i x_i \rightarrow +\infty} \sum_{i=1}^n \phi_i(x) < 0 \tag{2.5}$$

then X is positive Harris recurrent and there exists $\eta > 0$ such that X is F-ergodic with

$$F : \begin{cases} \mathbb{R}_+^n \rightarrow [1, +\infty[\\ (x_1, \dots, x_n) \mapsto e^{\eta \sqrt{\sum_{i=1}^n x_i}} \end{cases} .$$

EXAMPLE 1. A multiplicative uniform model defined by (1.1) is Harris-recurrent positive if and only if $\sum_{i=1}^n c_i < 0$ and transient otherwise (remind that we assumed that $V^+ \neq \emptyset$).

EXAMPLE 2. The multiplicative uniform model represented on the left of Figure 2.3 corresponds to an ergodic setting, while the model on the right does not.

Subsection 2.1.5 is devoted to the proof of this theorem, that stems from Theorem 2.1.9 stated below. Let us give the main thrust of this proof, that will be developed in a more general

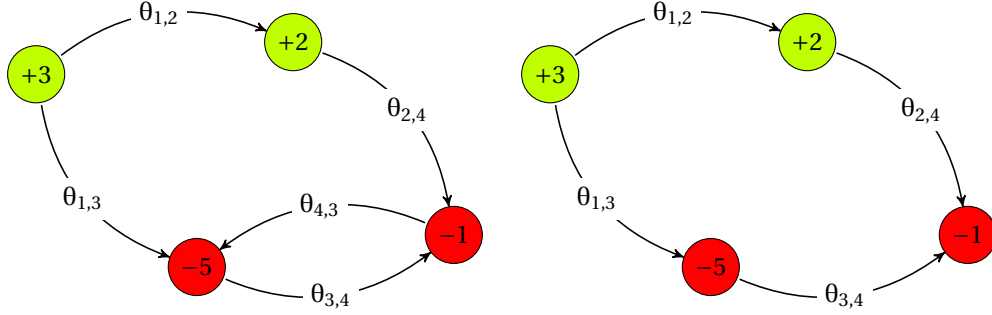


Figure 2.3: The importance of connectivity: if (1.1) is fulfilled, then the process corresponding to the graph configuration on the left is ergodic (according to Theorem 2.1.2) and that on the right is transient (consider the population on the subgraph formed by the two right patches). Coefficients within patches are the c_i and all $\theta_{i,j}$ represented here are strictly positive.

framework in Subsection 2.1.4. Our reasoning is based on the conceptual framework by Meyn and Tweedie [MT93a, MT93b, DMT95] and presented in Section 1.3.1. It consists in showing that X is brought back quickly enough to some compact subset of \mathbb{R}_+^n (a *boundedness* property) and that its various trajectories scan some Borel subset of \mathbb{R}_+^n (a so-called *petiteness* property). The condition on the ϕ_i entails the existence of some \mathbb{R}_+^n area (namely $\{x \in \mathbb{R}_+^n : \min_i x_i \geq R\}$ for R large enough) on which the flow commands a steady decrease of the system total population. The assumptions on the $\theta_{i,j}$ and the $\mu_{i,j}(x, \cdot)$ imply that with lower-bounded probability, the process reaches this zone quickly enough and stays in it long enough for the total population of the system to be brought back below a given threshold after some time, which yields the boundedness property. On the other hand, small variations of jump quantiles along a given path induce locally one-to-one changes of its point of arrival, which implies the petiteness property.

In the transient case, the stability of transfer laws and the existence of macroscopic jumps make scaled multiplicative processes easy to describe. If the model is multiplicative with all $I_{i,j} = [0, 1]$ and if X is transient, then $\|X\|_1$ goes to infinity almost surely and for any $x \in \mathcal{S} = \{x \in \mathbb{R}_+^n : \|x\|_1 = 1\}$:

$$\mathbb{E}_{R^x} \left[\sup_{t \in [0, R]} \left\| \frac{X(t)}{\|X(t)\|_1} - S(t) \right\|_\infty \right] \xrightarrow{R \rightarrow +\infty} 0 \quad (2.6)$$

where S is a \mathcal{S} -valued pure jump process which is a weak solution of the following SDE:

$$\forall (i, j) \in \mathcal{I}, \quad dS_i(t) = \sum_{j \neq i} \int_0^1 \xi S_j(t) N'_{j,i}(dt, d\xi) - \sum_{j \neq i} \int_0^1 \xi S_i(t) N'_{i,j}(dt, d\xi)$$

with initial value x under the \mathbb{P}_{R^x} probability measure, and the $N'_{i,j}$ are independent Poisson point processes with intensity $dt \mu_{i,j}(d\xi)$. Studying the stability of S only requires petiteness analysis, and (2.6) makes it possible to infer the behavior of $\frac{X}{\|X\|_1}$ (which may not be a Markov process) from that of S . As an example, we prove the following result.

PROPOSITION 2.1.3 (Transient multiplicative uniform case when $n = 2$). — *In the two-patch multiplicative uniform model with $c_1 + c_2 \geq 0$, $\frac{X_1(t)}{X_1(t)+X_2(t)}$ converges in distribution to a Beta distribution with parameters $\left(\frac{\theta_{2,1}}{\lambda}, \frac{\theta_{1,2}}{\lambda}\right)$ as t goes to infinity, where $\lambda = \theta_{1,2} + \theta_{2,1}$.*

Proof of Proposition 2.1.3.— We remind that the Beta distribution with parameters $a, b \in \mathbb{R}_+^*$, denoted $\beta(a, b)$, is the probability measure on \mathbb{R} with density

$$f_{a,b} : t \mapsto 1_{]0,1[}(t) \frac{t^{a-1}(1-t)^{b-1}}{B(a,b)}$$

with respect to the Lebesgue measure, where $B(a, b) := \int_0^1 t^{a-1}(1-t)^{b-1} dt$.

Set $x \in \mathcal{S}$ and let S be a weak solution of

$$dS_1(t) = \int_0^1 \xi S_2(t) N'_{2,1}(dt, d\xi) - \int_0^1 \xi S_1(t) N'_{1,2}(dt, d\xi)$$

with initial value $\frac{x}{\|x\|_1}$ and such that $S_1 + S_2 = 1$. Here $\bar{\mu}_{1,2} = \bar{\mu}_{2,1}$ is the uniform distribution on $[0, 1]$, so $N_{1,2}$ and $N_{2,1}$ have intensity $dt d\xi$. Our aim is to show that $S_1(t)$ weakly converges to a $\beta\left(\frac{\theta_{2,1}}{\lambda}, \frac{\theta_{1,2}}{\lambda}\right)$ distribution as t tends to infinity. It is easy to see that S_1 fulfills the requirements of Theorem 1.3.21, all compact subsets of \mathbb{R} being petite for this process, so we only need to characterize its invariant (and limiting) probability distribution π . It is clear that the support of π lies within $[0, 1]$ and that if $f : [0, 1] \rightarrow \mathbb{R}$ is continuous, then for all $t > 0$ the following holds:

$$\int_0^1 \mathfrak{A}' f(s) d\pi(s) = 0$$

where \mathfrak{A}' is the infinitesimal generator of S_1 , that is:

$$\int_0^1 \left[\theta_{1,2} \int_0^1 (f(\xi s) - f(s)) d\xi + \theta_{2,1} \int_0^1 (f(\xi s + (1-\xi)) - f(s)) d\xi \right] d\pi(s) = 0.$$

Applying this equation to power functions $f : x \mapsto x^k$ we get the following recursive formula for the moments of π :

$$\forall k \geq 1, \quad \int_0^1 s^k d\pi(s) = \frac{\theta_{2,1}}{k\lambda} \sum_{i=0}^{k-1} \int_0^1 s^i d\pi(s)$$

which yields, for all $k \geq 1$:

$$\int_0^1 s^k d\pi(s) = \frac{1}{k!} \left[\prod_{i=0}^{k-1} \left(i + \frac{\theta_{2,1}}{\lambda} \right) \right]. \quad (2.7)$$

Now π can be characterized by its moments among Borel probability measures on $[0, 1]$ since $[0, 1]$ is a compact subset of \mathbb{R} . It is therefore sufficient to compute the moments of the $\beta\left(\frac{\theta_{2,1}}{\lambda}, \frac{\theta_{1,2}}{\lambda}\right)$ distribution by using the classical formula

$$B(a, b) = \frac{\Gamma(a)\Gamma(b)}{\Gamma(a+b)}$$

holding for all positive a and b , and see that these moments coincide with these given by Equation 2.7. \square

2.1.3.3 Unitary models

We define unitary models as follows:

DEFINITION 2.1.4 (Unitary setting). — *The PDMP metapopulation model is said to be unitary if the following hold:*

1. Assumptions B and C are fulfilled.
2. There exists an increasing and subadditive function $\Theta : \mathbb{R}_+ \rightarrow \mathbb{R}_+^*$ with $\lim_{y \rightarrow +\infty} \Theta(y) = +\infty$ and $\alpha > 1$ such that for any $x \in \mathbb{R}_+^n$:
 - For all $(i, j) \in \mathcal{E}$, $\Theta(x_i) \leq \theta_{i,j}(x)$.
 - For all $(i, j) \in \mathcal{J}$, $\theta_{i,j}(x) \leq \alpha \Theta(x_i)$.
3. For all $x \in \mathbb{R}_+^n$ and all $(i, j) \in \mathcal{E}$, $\mu_{i,j}(x, \cdot) = \delta_{1 \wedge x_i}$.

The unitary setting is typically fit for applications to large animals trade or human transportation observed over short time steps. A simple example is given by our introductory model defined by (1.2).

Our main stability result on unitary models is the following:

THEOREM 2.1.5 (Stability of unitary models). — *If the model is unitary and if either*

$$\limsup_{\min_{i \in V^-} x_i \rightarrow +\infty} \sum_{i=1}^n \phi_i(x) < 0 \quad (2.8)$$

or

$$\mathcal{G} \text{ is strongly connected and } \limsup_{\min_i x_i \rightarrow +\infty} \sum_{i=1}^n \phi_i(x) < 0 \quad (2.9)$$

then there exists $\eta > 0$ such that X is positive Harris recurrent and F-ergodic with

$$F : \begin{cases} \mathbb{R}_+^n \rightarrow [1, +\infty[\\ (x_1, \dots, x_n) \mapsto e^{\eta \sqrt{\sum_{i=1}^n x_i}} \end{cases} .$$

EXAMPLE 3. The following setting corresponds to an unitary metapopulation model with logistic autonomous growth in sources and jump rates taking into account the carrying capacity of target patches:

$$\begin{cases} \forall i \in V^+, \quad \phi_i(x) = b_i x_i (K_i - x_i)_+ + c_i \\ \forall j \in V^-, \quad \phi_j(x) = -\frac{c_j x_j}{\alpha_j + x_j} \\ \forall i \in V^+, \forall j \in V^-, \quad \theta_{i,j}(x) = \gamma_{i,j} x_i \frac{\varepsilon_{i,j} + x_j}{1 + x_j} \quad \text{and} \quad \theta_{j,i} \equiv 0 \\ \forall (i, j) \notin \mathcal{E}, \quad \theta_{i,j} \equiv 0 \\ \forall (i, j) \in \mathcal{E}, \quad \mu_{i,j}(x, \cdot) = \delta_{1 \wedge x_i} \end{cases} \quad (2.10)$$

where the b_i , K_i , $\gamma_{i,j}$ and $\varepsilon_{i,j}$ are positive constants and the c_i are such that $c_i > 0$ if $i \in V^+$ and $c_i < 0$ if $i \in V^-$. Theorem 2.1.5 implies the ergodicity of the process in this setting as soon as $\sum_{i=1}^n c_i < 0$ if \mathcal{G} is strongly connected.

EXAMPLE 4. A power unitary model defined by (1.2) is ergodic if and only if $\sum_{i=1}^n c_i < 0$ and transient otherwise (remind that we assumed that $V^+ \neq \emptyset$).

The proof of Theorem 2.1.5, presented in Subsection 2.1.6, is based on arguments that only slightly differ from those put forward in the multiplicative case. If \mathcal{G} is strongly connected, boundedness is shown as in the proof of Theorem 2.1.2. If this is not the case but (2.8) holds, we show that X satisfies Assumption 1 for any value of T , which entails that Assumption 3 holds as well. In both cases, we then consider small variations of jump times (and not jump quantiles anymore) to check for the petiteness of compacts for the resolvent chain of X .

2.1.4 Stability criteria for the metapopulation PDMP

We now present Meyn-Tweedie inspired criteria for boundedness, petiteness and ergodicity for the general model defined in Subsection 2.1.2. We will see that their application requires proof strategies that are dependent from the model specification and the system's active graph structure. However, it is easy to adapt the proofs of Theorems 2.1.2 and 2.1.5 in a discretionary way to a large range of frameworks, which is why we endeavored to state their general philosophy. In particular, these criteria will apply to both multiplicative and unitary settings, yielding Theorems 2.1.2 and 2.1.5.

It is not difficult to see that if the $q_{i,j}$ are continuous and if $t \mapsto \mathbb{E}_x(\phi(X_i(t)))$ is right continuous for any $i \in \llbracket 1, n \rrbracket$ and any $x \in \mathbb{R}_+^n$, then the $t \mapsto \mathbb{E}_x(X_i(t))$ are continuous and right differentiable, and the following holds:

$$\forall t \geq 0, \forall i \in \llbracket 1, n \rrbracket, \quad \frac{d^+ \mathbb{E}_x(X_i(t))}{dt} = \mathbb{E}_x[\phi_i(X(t))] + \mathbb{E}_x \left[\sum_{j \neq i} (d_{j,i} - d_{i,j})(X(t)) \right] \quad (2.11)$$

where $d_{i,j}(x) = \theta_{i,j}(x) \int_0^{x_i} \xi_{\mu_{i,j}}(x, d\xi)$ is the *average debit from patch i to patch j at state x* , and

$$\forall t \geq 0, \quad \frac{d^+ \sum_{i=1}^n X_i(t)}{dt} = \sum_{i=1}^n \phi_i(X(t)) \quad (2.12)$$

Depending on the specification, we may partly describe the asymptotic behavior of X by studying these equations. Yet, characterizing the stability of X does not boil down to studying a dynamical system defined by (2.11) for two main reasons. First, terms in the right hand side of (2.11) and (2.12) may prove difficultly tractable, as a simple glance at our introductory constant growth models should suggest. A second, more fundamental obstruction stems from the fact that X and $(\mathbb{E}_x(X_i(t)))_{t \geq 0}$ do not necessarily have similar stability properties. Indeed, while Fatou's lemma does imply that $(\mathbb{E}_x(X_i(t)))_{t \geq 0}$ not going to infinity with t results \mathbb{P}_x -a.s. in the same property for $(X_i(t))_{t \geq 0}$, it is not difficult to build an example showing that the converse is not true.

2.1.4.1 Criterion for boundedness

We first want to state a sufficient condition for X to be *bounded in probability on average*. Remind from Subsection 1.3.1 that this property means that for all $x \in \mathbb{R}_+^n$ and all $\varepsilon > 0$ there exists a compact subset $C \subset \mathbb{R}_+^n$ such that

$$\liminf_{t \rightarrow +\infty} \frac{1}{t} \int_0^t \mathbb{P}_x(X(s) \in C) ds \geq 1 - \varepsilon.$$

We first want to describe a Borel subset S of \mathbb{R}_+^n corresponding to population configurations on which the local deterministic dynamics cause the system to empty. For instance, in the constant growth setting defined by (2.4) and under condition (2.1), S may be defined as any Borel set lying in $\{x \in \mathbb{R}_+^n : \forall i \in V^-, x_i > 0\}$.

Let therefore S be a Borel subset of \mathbb{R}_+^n . Our first assumption implies that the flow on S drives the process at a steady rate towards the origin:

ASSUMPTION D (Existence of a steady population decrease zone). — *There exists $c > 0$ such that:*

$$\forall x \in S, \quad \sum_{i=1}^n \phi_i(x) \leq -c$$

It is worth mentioning a simple case with straightforward consequences. If Assumption D holds with $S = K^c$ for some compact subset K of \mathbb{R}_+^n , it is a simple matter to show that X is bounded in probability on average using, for instance, Fatou's Lemma. In this case, $\sum \phi_i$ may play the role of a Lyapunov function for X , and it is possible to derive results on recurrence and ergodicity provided all compacts are petite for X (see Theorem 1.3.21). However, it is not always the case that $S = K^c$ for some compact K . In particular, it is not under Assumption B since S cannot contain any x such that $x_i = 0$ for all $i \in V^-$.

Under Assumption D, it is natural to think that X will be bounded in probability on average if it quickly goes back to S and stays within S for a long time whenever it reaches it. This is why we put forward the following conditions:

ASSUMPTION E (Bounds for the hitting time of S' and the exit time from S). — *There exist a Borel subset S' of S as well as $\delta, \varepsilon, T, T' \in \mathbb{R}_+^*$ and $R \geq 0$ such that:*

1. *For any $x \notin S'$ with $\|x\|_1 \geq R$:*

$$\mathbb{P}_x(\exists s \in [0, T], X(s) \in S') \geq \delta$$

2. *For any $x \in S'$ with $\|x\|_1 \geq R$:*

$$\mathbb{P}_x(\forall s \in [0, T'], X(s) \in S) \geq \varepsilon$$

3. *The following holds:*

$$\varepsilon T' c > \frac{T}{\delta} \sup_{\mathbb{R}_+^n} \sum_{i=1}^n \phi_i$$

Note that Assumption E.2 may be void since we do not assume that $S' \cap \{\|x\|_1 \geq R\}$ is not empty.

One can see that under Assumptions D, E.1 and E.2 and starting from a point in S with high enough total population, then with probability of at least ε , X does not leave S before time T' , and the mean total population increase during an excursion of the process outside of S is at most $\frac{T}{\delta} \sup_{\mathbb{R}_+^n} \sum_i \phi_i$. Assumption E.3 is therefore sufficient for the visits of S by X to bring the population process back to some compact set of \mathbb{R}_+^n regardless of its original position.

The expected result follows.

THEOREM 2.1.6 (Boundedness criterion). — *Under Assumptions D and E, X is bounded in probability on average.*

Proof of Theorem 2.1.6.— The proof of Theorem 2.1.6 consists in a comparison with a random walk on \mathbb{R} . It may easily adapt to some models that do not necessarily fulfill Assumptions D and E by considering suitable \mathbb{R} -valued Markov chains.

We write

$$M := \sup_{\mathbb{R}_+^n} \sum_{i=1}^n |\phi_i| < +\infty.$$

For any Borel subset $E \subset \mathbb{R}_+^n$, we denote by $(\tau_E^k)_{k \geq 1}$ the sequence of successive hitting times of E by X (with $\tau_E^1 = 0$ \mathbb{P}_x -a.s. if $x \in E$), so $\tau_E = \tau_E^1$.

Step 1: study of a random walk

Assume that Assumptions D and E hold and let $y \in \mathbb{R}$. Consider a \mathbb{R} -valued random walk $Y = (Y_k)_{k \geq 1}$ with i.i.d. increments defined on $(\Omega, \mathcal{A}, \mathbb{P})$ in such a way that the following equality in distribution holds:

$$Y_1 = y \quad \text{and} \quad \forall k \geq 1, \quad Y_{k+1} - Y_k \stackrel{d}{=} -BcT' + \Gamma \cdot TM \quad (2.13)$$

where B and Γ are independent random variables with respective distributions Bernoulli $\mathcal{B}(1, \varepsilon)$ and shifted geometric $\mathcal{G}(\delta)$ (that is, such that $\mathbb{P}(\Gamma = k) = \delta(1-\delta)^{k-1}$ for all $k \geq 1$). We first observe that

$$\mathbb{E}(-BcT' + \Gamma \cdot TM) = -\varepsilon cT' + \frac{T}{\delta} M < 0$$

which entails that the hitting time σ_R of $(-\infty, R]$ by Y is almost surely finite by the law of large numbers. Moreover, there exists $r > 0$ independent from the choice of $y \in \mathbb{R}$ such that:

$$\mathbb{E}(e^{\gamma(r)\sigma_R}) \leq e^{r(-cT' - R + y)}.$$

Indeed, straightforward computations show that if $r > 0$ is such that $r < \frac{|\log(1-\delta)|}{TM}$, and if we set

$$\gamma(r) = -\log\left(\frac{\delta}{e^{-rTM} - (1-\delta)} + \varepsilon e^{-rcT'}\right)$$

then $(\exp(rY_k + \gamma(r)(k-1)))_{k \geq 1}$ is a positive martingale with respect to its natural filtration. Using Fatou's lemma then yields the expected inequality since $\gamma(r) > 0$.

Step 2: exponential moment of the hitting time of a compact subset

Let $C = \{x \in \mathbb{R}_+^n : \|x\|_1 \leq R\}$. We now prove that there exists $\beta > 0$ such that $x \mapsto \mathbb{E}_x(\exp(\beta\sqrt{\tau_C}))$ is locally bounded on \mathbb{R}_+^n . Let us first assume that $x \in S^c \cap C^c$, set $\bar{\tau}_{S^c}^1 = \tau_{S^c}^1 = 0$, and for all $k \geq 1$:

$$\bar{\tau}_{S'}^k = \inf \{t \geq \bar{\tau}_{S^c}^k : X(t) \in S'\} \quad \text{and} \quad \bar{\tau}_{S^c}^{k+1} = \inf \{t \geq \bar{\tau}_{S'}^k : X(t) \in S^c\}.$$

Then, \mathbb{P}_x -a.s.:

$$\begin{aligned} \tau_C &= \bar{\tau}_{S'}^1 \wedge \tau_C + \sum_{k=1}^{+\infty} \left(\bar{\tau}_{S'}^{k+1} \wedge \tau_C - \bar{\tau}_{S'}^k \wedge \tau_C \right) \\ &= \bar{\tau}_{S'}^1 \wedge \tau_C + \sum_{k=1}^{+\infty} \left(\bar{\tau}_{S'}^{k+1} \wedge \tau_C - \bar{\tau}_{S^c}^{k+1} \wedge \tau_C + \bar{\tau}_{S^c}^{k+1} \wedge \tau_C - \bar{\tau}_{S'}^k \wedge \tau_C \right) \\ &\leq \sum_{k=0}^{+\infty} 1_{\bar{\tau}_{S^c}^{k+1} < \tau_C} \left(\bar{\tau}_{S'}^{k+1} - \bar{\tau}_{S^c}^{k+1} \right) + \sum_{k=1}^{+\infty} 1_{\bar{\tau}_{S'}^k < \tau_C} \frac{\|X(\bar{\tau}_{S'}^k)\|_1 - R}{c} \end{aligned}$$

since the decrease of the flow on $S' \subset S$ is at least c . For $\beta > 0$, we thus get:

$$\begin{aligned} &(\mathbb{E}_x[\exp(\beta\sqrt{\tau_C})])^2 \\ &\leq \mathbb{E}_x \left[\exp \left(2\beta \sqrt{\sum_{k=1}^{+\infty} 1_{\bar{\tau}_{S^c}^k < \tau_C} (\bar{\tau}_{S'}^k - \bar{\tau}_{S^c}^k)} \right) \right] \mathbb{E}_x \left[\exp \left(2\beta \sqrt{\sum_{k=1}^{+\infty} 1_{\bar{\tau}_{S'}^k < \tau_C} \frac{\|X(\bar{\tau}_{S'}^k)\|_1 - R}{c}} \right) \right] \end{aligned} \quad (2.14)$$

\mathbb{P}_x -a.s. using the inequality $\sqrt{a+b} \leq \sqrt{a} + \sqrt{b}$ for $(a, b) \in \mathbb{R}_+^2$ and the Cauchy-Schwarz inequality. Yet Assumption E entails that the increment of the total system population between two successive $\bar{\tau}_{S'}^k$ before τ_C is dominated by $-BcT' + \Gamma \cdot TM$. Applying the strong Markov property to the sequences of stopping times $(\bar{\tau}_{S'}^k \wedge \tau_C)_{k \geq 1}$ and $((\bar{\tau}_{S^c}^k + pT) \wedge \bar{\tau}_{S'}^{k+1} \wedge \tau_C)_{k \geq 1, p \geq 0}$ ensures that there exists $(Y_k)_{k \geq 1}$ on $(\Omega, \mathcal{A}, \mathbb{P}_x)$ satisfying (2.13) with $y = \|x\|_1$ such that \mathbb{P}_x -a.s.:

$$\forall k \geq 1, \quad 1_{\bar{\tau}_{S^c}^k < \tau_C} (\bar{\tau}_{S'}^k - \bar{\tau}_{S^c}^k) \leq 1_{k < \sigma_R} \left(\frac{Y_{k+1} - Y_k + cT'}{M} \right) \quad (2.15)$$

and

$$\forall k \geq 1, \quad \|X(\bar{\tau}_{S'}^k \wedge \tau_C)\|_1 \leq Y_{k \wedge \sigma_R}. \quad (2.16)$$

For any $\beta > 0$, (2.15) yields

$$\mathbb{E}_x \left[\exp \left(2\beta \sqrt{\sum_{k=1}^{+\infty} 1_{\bar{\tau}_{S^c}^k < \tau_C} (\bar{\tau}_{S'}^k - \bar{\tau}_{S^c}^k)} \right) \right] \leq \mathbb{E} \left[\exp \left(2\beta \sqrt{\sum_{k=1}^{\sigma_R-1} \left(\frac{Y_{k+1} - Y_k + cT'}{M} \right)} \right) \right]$$

so

$$\mathbb{E}_x \left[\exp \left(2\beta \sqrt{\sum_{k=1}^{+\infty} 1_{\bar{\tau}_{S^c}^k < \tau_C} (\bar{\tau}_{S'}^k - \bar{\tau}_{S^c}^k)} \right) \right] \leq \mathbb{E} \left[\exp \left(2\beta \sqrt{\frac{R - \|x\|_1 + cT'\sigma_R}{M}} \right) \right]. \quad (2.17)$$

Now (2.16) entails:

$$\mathbb{E}_x \left[\exp \left(2\beta \sqrt{\sum_{k=1}^{+\infty} 1_{\bar{\tau}_{S'}^k < \tau_C} \frac{\|X(\bar{\tau}_{S'}^k)\|_1 - R}{c}} \right) \right] \leq \mathbb{E} \left[\exp \left(2\beta \sqrt{\sum_{k=1}^{\sigma_R-1} \frac{Y_k - R}{c}} \right) \right].$$

The increments of the Y chain are greater than $-cT'$ and the value of Y at time σ_R is at most R , so we can write

$$\sum_{k=1}^{\sigma_R-1} (Y_k - R) \leq \sum_{k=1}^{\sigma_R-1} \sigma_R c T' \leq \sigma_R^2 c T'$$

from which we deduce that

$$\mathbb{E}_x \left[\exp \left(2\beta \sqrt{\sum_{k=1}^{+\infty} \mathbf{1}_{\bar{\tau}_{S'}^k < \tau_C} \frac{\|X(\bar{\tau}_{S'}^k)\|_1 - R}{c}} \right) \right] \leq \mathbb{E} \left[\exp \left(2\beta \sqrt{T'} \sigma_R \right) \right]. \quad (2.18)$$

Inequality (2.14) combined with (2.17) and (2.18) finally yields:

$$\left(\mathbb{E}_x \left[e^{\beta \sqrt{\tau_C}} \right] \right)^2 \leq \mathbb{E} \left[\exp \left(2\beta \sqrt{\frac{R - |x|_1 + cT' \sigma_R}{M}} \right) \right] \mathbb{E} \left[\exp \left(2\beta \sqrt{T'} \sigma_R \right) \right]. \quad (2.19)$$

Obviously $\sigma_R \leq \sigma_R^2$, so there exists $\alpha_1 \in \mathbb{R}_+^*$ independent from our choice of x in $S^c \cap C^c$ such that

$$\left(\mathbb{E}_x \left(e^{\beta \sqrt{\tau_C}} \right) \right)^2 \leq \mathbb{E} \left[\exp \left(2\beta \alpha_1 \sigma_R \right) \right] \mathbb{E} \left[\exp \left(2\beta \sqrt{T'} \sigma_R \right) \right]$$

and therefore

$$\mathbb{E}_x \left(e^{\beta \sqrt{\tau_C}} \right) \leq \mathbb{E} \left[\exp \left(2\beta (\alpha_1 \vee \sqrt{T'}) \sigma_R \right) \right].$$

If $x \in S \cap C^c$, we derive a similar inequality by letting the process reach S^c and using the strong Markov property, and the case $x \in C$ is trivial. Step 1 ensures that if $\beta > 0$ is small enough, then the function $x \mapsto \mathbb{E}_x \left(e^{\beta \sqrt{\tau_C}} \right)$ is locally bounded on \mathbb{R}_+^n . We will use this result when proving the ergodicity of X in section 2.1.4.3; for our present purpose, it is sufficient to know that $x \mapsto \mathbb{E}_x \left[(\tau_C)^2 \right]$ is locally bounded on \mathbb{R}_+^n .

Step 3: boundedness in probability on average

If $p \geq 3$ is an integer, then for all $t > 0$ and $x \in \mathbb{R}_+^n$:

$$\frac{1}{t} \int_0^t \mathbf{1}_{X(s) \notin pC} ds \leq \frac{1}{t} \left[\tau_C + \sum_{j \geq 1, k \geq 1} \mathbf{1}_{\tau_C^k < \tau_{(2C)^c}^j < \tau_C^{k+1}} \mathbf{1}_{\tau_{(2C)^c}^j < t} \int_{\tau_{(2C)^c}^j}^{\tau_C^{k+1}} \mathbf{1}_{X(s) \notin pC} ds \right]$$

since $(pC)^c \subset (2C)^c$, so that

$$\mathbb{E}_x \left[\frac{1}{t} \int_0^t \mathbf{1}_{X(s) \notin pC} ds \right] \leq \frac{1}{t} \mathbb{E}_x \left[\tau_C + \sum_{j, k \in \mathbb{Z}_+^*} \mathbf{1}_{\tau_C^k < \tau_{(2C)^c}^j < \tau_C^{k+1}} \mathbf{1}_{\tau_{(2C)^c}^j < t} \left(\tau_C^{k+1} - \tau_{(2C)^c}^j \right) \mathbf{1}_{\tau_C^{k+1} - \tau_{(2C)^c}^j \geq \frac{(p-2)R}{M}} \right]$$

because the process needs at least $\frac{(p-2)R}{M}$ units of time to reach pC from a state with total population $2R$. From this we deduce

$$\mathbb{E}_x \left[\frac{1}{t} \int_0^t \mathbf{1}_{X(s) \notin pC} ds \right] \leq \frac{1}{t} \mathbb{E}_x \left[\tau_C + \sum_{j, k \in \mathbb{Z}_+^*} \mathbf{1}_{\tau_C^k < \tau_{(2C)^c}^j < \tau_C^{k+1}} \mathbf{1}_{\tau_{(2C)^c}^j < t} \mathbb{E}_{X_{\tau_{(2C)^c}^j}} \left(\tau_C \mathbf{1}_{\tau_C \geq \frac{(p-2)R}{M}} \right) \right]$$

using the strong Markov property, and, setting $\zeta = \sup_{y \in \mathbb{R}_+^n, \|y\|_1 \leq 2C} \mathbb{E}_y [(\tau_C)^2]$ (which is finite according to Step 2) and writing that $\tau_C 1_{\tau_C \geq \frac{(p-2)R}{M}} \leq \frac{M}{(p-2)R} (\tau_C)^2$,

$$\mathbb{E}_x \left[\frac{1}{t} \int_0^t 1_{X(s) \notin pC} ds \right] \leq \frac{1}{t} \left(\zeta + \mathbb{E}_x \left[\sum_{j,k \in \mathbb{Z}_+^*} 1_{\tau_C^k < \tau_{(2C)^c}^j} < \tau_C^{k+1} 1_{\tau_{(2C)^c}^j < t} \zeta \sqrt{\frac{M}{(p-2)R}} \right] \right)$$

by the Cauchy-Schwarz inequality. Thus, for any integer $p \geq 3$, any $t > 0$ and any $x \in \mathbb{R}_+^n$:

$$\mathbb{E}_x \left[\frac{1}{t} \int_0^t 1_{X(s) \notin pC} ds \right] \leq \frac{1}{t} \left(\zeta + \frac{t}{MR} \zeta \sqrt{\frac{M}{(p-2)R}} \right)$$

as the process cannot go through more than $\frac{t}{MR}$ times the full way between C and $(2C)^c$ within time t . Finally,

$$\limsup_{t \rightarrow +\infty} \mathbb{E}_x \left[\frac{1}{t} \int_0^t 1_{X(s) \notin pC} ds \right] \leq \frac{\zeta}{\sqrt{MR}^{3/2}} \sqrt{\frac{1}{p-2}}.$$

Choosing p arbitrarily large shows that X is bounded in probability on average. \square

Alternate criteria for boundedness may be derived using Theorem 2.1 of [MT94] under irreducibility assumptions. In particular, Theorem 3.1 of [Dai95] holds in our setting whenever compact subsets of \mathbb{R}_+^n are petite. Yet, as we will see in Section 2.1.4.3, Assumptions D and E yield an upper bound for expected exponential functionals of return times, which implies strong ergodicity results.

2.1.4.2 Criterion for petiteness

Let us now consider a compact set $C \subset \mathbb{R}_+^n$. We remind from Subsection 1.3.1 that C being *petite* for some sampled chain $(X(A_n))_{n \geq 0}$ of X means that there exists a non-trivial Borel measure ν on \mathbb{R}_+^n such that $\mathbb{P}_x(X(A_1) \in \cdot) \geq \nu(\cdot)$ for all $x \in C$, and that C is just said to be *petite* if it is petite for some $(A_n)_{n \geq 0}$.

Proving that C is petite relies on framework-specific strategies. The criterion for petiteness we will derive in this section applies to a broad range of settings, but it is worth keeping in mind that it may prove unnecessarily technical in some cases. In particular, it can be easier to identify sampled chains that dominate \mathbb{R}_+^n -valued Dirac measures — provided, of course, that such chains exist.

In most non-pathological specifications, the distribution of inter-jump times exhibits an absolutely continuous component with respect to the Lebesgue measure. This observation drives us to look for subsets of \mathbb{R}_+^n on which the Lebesgue measure is dominated by the semigroup for the resolvent chain $(R_n)_{n \in \mathbb{Z}_+}$ defined by:

$$\forall n \in \mathbb{Z}_+, \quad R_n = X(S_n)$$

where $(S_n)_{n \in \mathbb{Z}_+}$ is the sequence of jump times of a Poisson process with density 1 independent from X .

With this aim in mind, let us first define tracking functions that return the position of our process from its inter-jump times t_k , the edges κ_k along which the transfers occur and the values

of its jump distributions quantiles ξ_k . For all $x \in \mathbb{R}_+^n$, all $(i, j) \in \mathcal{I}$ and all $\xi \in [0, 1]$, set

$$g_{i,j}(x, \xi) = x + q_{i,j}(x, \xi)(e_j - e_i).$$

For all $x \in \mathbb{R}_+^n$, let us define recursively the sequence of functions $(h_x^k)_{k \geq 1}$ by

$$h_x^1 : \begin{cases} \bigcup_{l \geq 1} (\mathbb{R}_+^l \times [0, 1]^{l-1} \times \mathcal{I}^{l-1}) \rightarrow \mathbb{R}^n \\ (t, \xi, \kappa) \mapsto \Phi(x, t_1) \end{cases}$$

and for all $k \in \mathbb{N}$,

$$h_x^{k+1} : \begin{cases} \bigcup_{l \geq k+1} (\mathbb{R}_+^l \times [0, 1]^{l-1} \times \mathcal{I}^{l-1}) \rightarrow \mathbb{R}^n \\ (t, \xi, \kappa) \mapsto \Phi(g_{\kappa_k}(h_x^k(t, \xi, \kappa), \xi_k), t_{k+1}) \end{cases}$$

where $\kappa = (\kappa_1, \dots, \kappa_{j-1})$ denotes the generic element of \mathcal{I}^{j-1} . The vector $h_x^k(t, \xi, \kappa)$ is the state occupied by the process initiated at x after it has followed the flow for time t_1 , undergone a transfer along edge κ_1 with amplitude given by the quantile of order ξ_1 of the appropriate $\mu_{i,j}(x, \cdot)$ law, followed the flow again for time t_2 , and so on until $k-1$ transfers occurred and the process followed the flow for time t_k after its last jump.

Our strategy is to look for a subset V of an affine subspace of \mathbb{R}_+^n such that we can provide a lower bound for the Lebesgue measure of the pre-image by some h_x^k of any Borel subset of V . We therefore introduce the following assumption:

ASSUMPTION F (Likely paths scanning a Borel subset). — *There are $M > 0$, $\bar{N} \in \mathbb{N}$, $\bar{T} \geq 1$, $p \in [1, n]$, a p -dimensional affine subspace V of \mathbb{R}^n , a Borel subset \mathcal{P} of V with non-zero Lebesgue measure in V , and for any $x \in C$ there are $N(x) \in [1, \bar{N}]$ with $q(x) = 2N(x) - 1 - p \geq 0$, a vector of edges $\kappa_x \in \mathcal{I}^{N(x)-1}$, a $\mathbb{R}^{2N(x)-1}$ -coordinates permutation σ_x and open subsets $U_1^x \subset [0, \bar{T}]^p$ and $U_2^x \subset [0, \bar{T}]^{q(x)}$ such that setting*

$$\Psi_{z_2}^x : \begin{cases} U_1^x \rightarrow V \\ z_1 \mapsto h_x^{N(x)}(\sigma_x(z_1, z_2), \kappa_x) \end{cases}$$

the following hold:

1. For all $z_2 \in U_2^x$, $\Psi_{z_2}^x$ is a \mathcal{C}^1 -diffeomorphism with Jacobian determinant bounded by M on U_1^x .

2. For all $z_2 \in U_2^x$,

$$\mathcal{P} \subset \Psi_{z_2}^x(U_1^x).$$

3. Defining

$$\theta_0 = \inf_{x \in C} \left[\lambda_{q(x)}(U_2^x) \inf_{\substack{z_1 \in U_1^x \\ z_2 \in U_2^x}} \prod_{i=1}^{N(x)-1} \theta_{\kappa_i(x)} \left(h_x^k(\sigma_x(z_1, z_2), \kappa_x) \right) \right],$$

with $\lambda_{q(x)}$ denoting the Lebesgue measure on $\mathbb{R}^{q(x)}$, we have that $\theta_0 > 0$.

Note that Proposition 2.1.7 below still holds if we replace p -dimensional affine subspaces by p -dimensional manifolds in the condition above. Assumption F.3 states that trajectories that lead X to Borel subsets of V correspond to sequences of jump times or jump quantiles with a likelihood bounded below.

A change of variables argument then yields the following proposition:

PROPOSITION 2.1.7 (Petiteness criterion). — *If Assumption F is met, then C is petite.*

Proof of Proposition 2.1.7.— Let us suppose that Assumption F is met and recall that we denote the resolvent of X by $(R_n)_{n \in \mathbb{N}}$. For all $x \in C$ and all $B \in \mathcal{B}(\mathcal{P})$, we can write:

$$\begin{aligned} \mathbb{P}_x(R_1 \in B) &= \int_0^{+\infty} \mathbb{P}_x(X(u) \in B) e^{-u} du \\ &\geq e^{-N(x)\bar{T}} \int_0^{\bar{T}} \mathbb{P}_x[h_x^{N(x)}(S_u^{N(x)}, (U_1, \dots, U_{N(x)-1}), \kappa_x) \in B] du \end{aligned}$$

where $S_u^{N(x)} = (T_1, T_2 - T_1, \dots, T_{N(x)-1} - T_{N(x)-2}, u)$.

Computing the joint density of the inter-jump times and the U_k and considering a common upper bound θ for the $\theta_{i,j}$ on $\{x' \in \mathbb{R}_+^n : \forall y \in C, \|x' - y\|_1 \leq N(x)\bar{T}M\}$ yields, for all $x \in C$ and all $B \in \mathcal{B}(\mathcal{P})$:

$$\mathbb{P}_x(R_1 \in B) \geq e^{-(1+\bar{\theta}n(n-1))N(x)\bar{T}} \int_{[0, \bar{T}]^{N(x)}} \int_{[0, 1]^{N(x)-1}} \left[\prod_{i=1}^{N(x)-1} \theta_{\kappa_i(x)} \left(h_x^i(t, \xi, \kappa_x) \right) \right] 1_{h_x^{N(x)}(t, \xi, \kappa_x) \in B} d\xi dt,$$

and therefore

$$\mathbb{P}_x(R_1 \in B) \geq e^{-(1+\bar{\theta}n(n-1))N(x)\bar{T}} \int_{U_2^x} \int_{U_1^x} \left[\prod_{i=1}^{N(x)-1} \theta_{\kappa_i(x)} \left(h_x^i(\sigma_x(z_1, z_2), \kappa_x) \right) \right] 1_{h_x^{N(x)}(\sigma_x(z_1, z_2), \kappa_x) \in B} dz_1 dz_2$$

by the change of variables formula. Applying this formula again using Assumption F.1 and recalling Assumption F.3 yields

$$\mathbb{P}_x(R_1 \in B) \geq e^{-(1+\bar{\theta}n(n-1))N(x)\bar{T}} \frac{\theta_0}{\lambda_{q(x)}(U_1^x)} \int_{U_2^x} \frac{1}{M} \int_{\Psi_{z_2}^x(U_2^x)} 1_{y \in B} dy dz_2.$$

Using Assumption F.2, we may thus write:

$$\mathbb{P}_x(R_1 \in B) \geq e^{-(1+\bar{\theta}n(n-1))N(x)\bar{T}} \frac{\theta_0}{M} \cdot \lambda_p(B)$$

for any $B \in \mathcal{B}(\mathcal{P})$, which entails that C is petite for $(R_n)_{n \in \mathbb{N}}$, then petite for X . \square

Most of the technicity in applying this proposition lies on proving that Assumption F.1 holds. Indeed, this requires describing paths of the process that lead to a given area of the state space as well as monitoring their response to small variations of jump times and jump quantiles. In general, this can be made simpler by the following straightforward but useful result allowing for localization of the starting point of such paths, which is Lemma 3.1 from [MT92b].

PROPOSITION 2.1.8 (Petiteness transitivity). — *If C' is a Borel subset of \mathbb{R}_+^n and if there exists $A > 0$ such that*

$$\inf_{x \in C'} \mathbb{P}_x(\tau_{C'} < A) > 0,$$

then if C' is a petite set for the resolvent of X , so is C .

2.1.4.3 Criterion for ergodicity

Theorem 1.3.17 along with present Theorem 2.1.6 and Proposition 2.1.7 imply that X is positive Harris recurrent as soon as Assumptions D and E are met and all compact subsets of \mathbb{R}_+^n are petite. We are now looking for an additional condition to ensure *F-ergodicity* for some measurable $F : \mathbb{R}_+ \rightarrow [1, +\infty)$. Remind from Subsection 1.3.1 that this property writes:

$$\forall x \in \mathbb{R}_+^n, \quad \lim_{t \rightarrow +\infty} \sup_{\substack{g : \mathbb{R}_+^n \rightarrow \mathbb{R}_+ \\ g \text{ measurable} \\ g \leq F}} |\mathbb{E}_x(g(X(t))) - \pi(g)| = 0$$

where π denotes the invariant probability of X .

Our result is the following:

THEOREM 2.1.9 (Ergodicity criterion). — *If Assumptions D and E hold, if all compact subsets of \mathbb{R}_+^n are petite and if X admits an irreducible skeleton chain, then there exists $\eta > 0$ such that X is *F-ergodic* for*

$$F : \begin{cases} \mathbb{R}_+^n \rightarrow \mathbb{R}_+ \\ x \mapsto e^{\eta \sqrt{\sum_{i=1}^n x_i}} \end{cases} \quad (2.20)$$

Proof of Theorem 2.1.9.— From Theorem 1.3.19, it is sufficient for *F-ergodicity* to hold to prove that there are $\delta > 0$ and a compact set $C \subset \mathbb{R}_+^n$ such that

$$\sup_{x \in C} \mathbb{E}_x \left[\int_0^{\tau_C(\delta)} F(X(t)) dt \right] < +\infty \quad (2.21)$$

where $\tau_C(\delta) := \inf\{t \geq \delta : X(t) \in C\}$, and that:

$$\forall x \in \mathbb{R}_+^n, \quad \mathbb{E}_x \left[\int_0^{\tau_C(0)} F(X(t)) dt \right] < +\infty. \quad (2.22)$$

Most of the work we need to provide in order to prove that the assumptions we stated in Section 2.1.4.1 entail (2.21) and (2.22) has already been done in the process of proving Theorem 2.1.6, where we showed that the hitting time τ_C of any compact subset $C = \{x \in \mathbb{R}_+^n : \|x\|_1 \leq R\}$ was such that $x \mapsto \mathbb{E}_x[\exp(\beta\sqrt{\tau_C})] < +\infty$ was finite-valued and locally bounded on \mathbb{R}_+^n for some $\beta > 0$.

We now show that there exists $\eta \in \mathbb{R}_+^*$ such that defining F by (2.20),

$$x \mapsto \mathbb{E}_x \left[\int_0^{\tau_C(1)} F(X(t)) dt \right]$$

is locally bounded on \mathbb{R}_+^n . This will end the proof of Theorem 2.1.9.

Using the notations of the proof of Theorem 2.1.6, we set $\eta_0 = \frac{\beta}{\sqrt{M}}$ and

$$F_0 : \begin{cases} \mathbb{R}_+ \rightarrow \mathbb{R}_+ \\ y \mapsto 1_{y > \frac{1}{\eta_0}} \frac{e^{\eta_0 \sqrt{y}}}{\sqrt{y}} \end{cases}$$

For any $x \in \mathbb{R}_+^n$, we observe that

$$\mathbb{E}_x \left[\int_0^{\tau_C(1)} F_0 \left(\sum_{i=1}^n X_i(t) \right) dt \right] \leq \mathbb{E}_x \left[\int_0^1 F_0 \left(\sum_{i=1}^n X_i(t) \right) dt + \mathbb{E}_{X(1)} \left[\int_0^{\tau_C} F_0 \left(\sum_{i=1}^n X_i(t) \right) dt \right] \right] \quad (2.23)$$

by the Markov property and that for any X -stopping time τ and any $z \in \mathbb{R}_+^n$:

$$\begin{aligned} \mathbb{E}_z \left[\int_0^\tau F_0 \left(\sum_{i=1}^n X_i(t) \right) dt \right] &\leq \mathbb{E}_z \left[\int_0^\tau F_0 \left(\sum_{i=1}^n z_i + tM \right) dt \right] = \mathbb{E}_z \left[\frac{2}{\eta_0} \left(e^{\eta_0 \sqrt{\sum_{i=1}^n z_i + \tau M}} - e \right)_+ \right] \\ &\leq \mathbb{E}_z \left[\frac{2}{\eta_0} e^{\eta_0 \sqrt{\sum_{i=1}^n z_i + \tau M}} \right] \leq \frac{2}{\eta_0} e^{\eta_0 \sqrt{\sum_{i=1}^n z_i}} \mathbb{E}_z \left[e^{\eta_0 \sqrt{\tau M}} \right] \end{aligned}$$

since F_0 is nondecreasing and $\sqrt{a+b} \leq \sqrt{a} + \sqrt{b}$ for all $(a, b) \in \mathbb{R}_+^2$.

We know from Step 2 of the proof of Theorem 2.1.6 that $z \mapsto \mathbb{E}_z \left[e^{\eta_0 \sqrt{\tau_C M}} \right] = \mathbb{E}_z \left[e^{\beta \sqrt{\tau_C}} \right]$ is locally bounded on \mathbb{R}_+^n . So are therefore $z \mapsto \mathbb{E}_z \left[\int_0^{\tau_C} F_0 \left(\sum_{i=1}^n X_i(t) \right) dt \right]$ and, consequently, $z \mapsto \mathbb{E}_z \left[\int_0^{\tau_C(1)} F_0 \left(\sum_{i=1}^n X_i(t) \right) dt \right]$ by (2.23) since $\|X_1\|_1 \leq \|x\|_1 + M$ holds \mathbb{P}_x -almost surely for all $x \in \mathbb{R}_+^n$. We easily find $\alpha_0, \beta_0, \gamma \in \mathbb{R}_+^*$ such that $e^{\gamma \sqrt{y}} \leq \alpha_0 + \beta_0 F_0(y)$ for all $y \in \mathbb{R}_+$, which entails:

$$\forall x \in \mathbb{R}_+^n, \quad \mathbb{E}_x \left[\int_0^{\tau_C(1)} e^{\gamma \sqrt{\sum_{i=1}^n X_i(t)}} dt \right] \leq \alpha_0 \mathbb{E}_x(\tau_C(1)) + \beta_0 \mathbb{E}_x \left[\int_0^{\tau_C(1)} F_0 \left(\sum_{i=1}^n X_i(t) \right) dt \right].$$

This yields the expected result since $x \mapsto \mathbb{E}_x[\tau_C(1)]$ is locally bounded on \mathbb{R}_+^n . \square

Theorems 2.1.2 and 2.1.5 are corollaries of the latter result, as is detailed in Subsections 2.1.5 and 2.1.6.

In some cases, it is possible to prove a still stronger result and establish exponential uniform ergodicity for X using a Lyapunov function. Indeed, if all compact subsets of \mathbb{R}_+^n are petite, if X admits an irreducible skeleton chain and if there exists a \mathcal{C}^1 function $f : \mathbb{R}_+^n \rightarrow [1, +\infty)$ such that

$$\mathcal{A}f \leq -cf + b1_C \quad (2.24)$$

for a compact set $C \subset \mathbb{R}_+^n$ and some positive real numbers b and c , then Theorem 1.3.21 entails that X is f -(exponentially) uniformly ergodic, in the sense that:

$$\forall t \in \mathbb{R}_+, \quad \sup_{\substack{g : \mathbb{R}_+^n \rightarrow \mathbb{R}_+ \\ g \text{ measurable} \\ g \leq F}} \left| \mathbb{E}_x(g(X(t))) - \pi(g) \right| \leq Mf(x)\rho^t$$

for some $M \geq 0$ and $\rho \in [0, 1)$. An elementary example of such a Lyapunov function can be given in the two-patch uniform constant growth setting with $c_2 < 0 < c_1$, $c_1 + c_2 < 0$ and $\theta_{2,1}c_1 < \theta_{1,2}|c_1 + c_2|$. Under these conditions, it is a simple matter to see that there are $\alpha, \beta \in \mathbb{R}_+^*$ such that (2.24) holds with $f : (x_1, x_2) \mapsto 1 + (\alpha x_1 + x_2) e^{\beta(x_1 + x_2)}$.

2.1.5 Proof of stability Theorem 2.1.2

We now consider that Assumptions B and C hold and set some further notation.

First let $\gamma = (\gamma_1, \dots, \gamma_r) \in \mathcal{E}^r$ be a cycle of \mathcal{G} that visits all sinks. Then, for all $l \in \llbracket 1, n \rrbracket$, let $d_-(l)$ be the \mathcal{G} -graph distance from patch l to V^- . Given Assumption C, there exists a vector $\kappa = (\kappa_1, \dots, \kappa_m) \in \mathcal{E}^m$, such that, writing $\kappa_k = (i_k, j_k)$ for all $k \in \llbracket 1, m \rrbracket = V^+ \cup V^0$:

- For all $k \in V^+ \cup V^0$, $d_-(i_k) > d_-(j_k)$ (edges in κ are "directed towards the exit of the system", that is, towards sinks).
- For all $l \in V^+ \cup V^0$, there is a $k(l) \in V^+$ such that $i_{k(l)} = l$ (each source or neutral patch is the origin and one and only one edge in κ).

This choice of κ corresponds to an ordered collection of edges along which the population in every patch of the system "reaches the exit by the shortest path". A possible choice of κ when \mathcal{G} is the graph in Figure 2.2 is $\kappa = ((2, 1), (3, 1), (4, 1), (1, 5))$; if \mathcal{G} is the first graph of Figure 2.3, then we may choose $\kappa = ((1, 3), (2, 4))$.

Recalling Proposition 2.1.7 and Theorem 2.1.9, it is sufficient to prove the following:

PROPOSITION 2.1.10. — *Assume that the model is multiplicative and (2.5) holds. Then:*

- (i) *There exists $S \subset \mathbb{R}_+^n$ such that X fits Assumptions D and E.*
- (ii) *X fits Assumption F.*
- (iii) *X admits an irreducible skeleton chain.*

Proof of Proposition 2.1.10.(i).— Let $q > 0$ and $a > 0$ be such that $\mu_{i,j}([a, 1-a]) > q$ for all $(i, j) \in \mathcal{I}$. Using (2.5), we may choose $R > 0$ such that Assumption D holds for $S = \{x \in \mathbb{R}_+^n : \min_i x_i \geq R\}$. Let us now set $Z_0 = 2na^{-(m+r)}(M+R)$, $M_0 = \inf_{i \in V^+} \inf_{[0, Z_0]} \phi_i$, $\underline{\theta} = \min_{(i,j) \in \mathcal{E}} \theta_{i,j}$, $\bar{\theta} = \max_{(i,j) \in \mathcal{E}} \theta_{i,j}$ and

$$S' = \left\{ x \in \mathbb{R}_+^n : \min_{i \in \llbracket 1, n \rrbracket} x_i \geq 2R \right\}.$$

We will show that S' meets Assumption E.1 by considering suitable paths of X defined by transfers along the edges of κ and γ .

It is an easy matter to see that with probability at least $\exp\left(-|\mathcal{E}|\left(\frac{Z_0}{M_0} + 2\right)\bar{\theta}\right)\underline{\theta}^{m+r}q^{m+r}\frac{1}{m^m r^r}$, the following holds for the path of X stemmed from any $x \in \mathbb{R}_+^n$:

- No transfer occurs before time $\frac{Z_0}{M_0}$.
- m successive transfers occur along edges $\kappa_1, \kappa_2, \dots$ and κ_m between times $\frac{Z_0}{M_0}$ and $\frac{Z_0}{M_0} + 1$. Each of these transfers, if originated from patch i and directed towards patch j , has an amplitude between z and $(1-a)z$.
- r successive transfers happen along edges of γ between times $\frac{Z_0}{M_0} + 1$ and $\frac{Z_0}{M_0} + 2$, the first of which is undertaken from the edge of V^- with the largest population. Each of these transfers, if originated from patch i with population z and directed towards patch j , has an amplitude between az et $(1-a)z$.

- No other transfer than those just described occurs before time $\frac{Z_0}{M_0} + 2$.

By construction, on such event one has $X_i(1) \geq \frac{Z_0}{n} a^{m+r} - 2M = 2R$ for all $i \in \llbracket 1, n \rrbracket$ so $X(1) \in S'$, which entails that Assumption E.1 holds.

Besides, Assumption E.2 is met for any choice of $\varepsilon \in (0, 1)$ and $T' > 0$ if R is large enough. Indeed, if we define

$$A_{i,j}^{\varepsilon'}(T') = \bigcup_{\substack{k \geq 1 \\ T_k < T'}} (q_{i,j}(X(T_k^-), U_k) \leq (1 - \varepsilon')X_i(T_k^-))$$

for any $T' > 0$, $(i, j) \in \mathcal{I}$ and $\varepsilon' > 0$, $A_{i,j}^{\varepsilon'}(T')$ being the event that all $i \rightarrow j$ transfers before time T' are of relative amplitude less than $1 - \varepsilon'$, one can write that for any $T' > 0$,

$$\mathbb{P}_x \left(A_{i,j}^{\varepsilon'}(T') \right) \xrightarrow{\varepsilon' \rightarrow 0} 1$$

uniformly in x since the $\mu_{i,j}$ assign mass 0 to $\{1\}$. Now the ϕ_i and $\theta_{i,j}$ being bounded implies that for all $T' > 0$:

$$\liminf_{\substack{\|x\|_1 \rightarrow +\infty \\ x \in S'}} \mathbb{P}_x(\forall s \in [0, T'], X(s) \in S) \geq \liminf_{\substack{\|x\|_1 \rightarrow +\infty \\ x \in S'}} \mathbb{P}_x \left(\bigcap_{(i,j) \in \mathcal{E}} A_{i,j}^{\varepsilon'}(T') \right)$$

for all $\varepsilon' \in (0, 1)$, hence the result as ε' tends to 0. Assumption E.3 is then true if T' is large enough (which is possible as soon as R is), which completes our proof of Proposition 2.1.10.(i).

Proof of Proposition 2.1.10.(ii).— Using Proposition 2.1.8, we will consider the behavior of our process starting from a small ball centered on a state that corresponds to positive population levels for sources and neutral patches, and use the change of variables formula to check for Assumption F.1.

It is clear that we may assume that $C = \{x \in \mathbb{R}_+^n : \|x\|_1 \leq R\}$ for some $R > 0$.

Step 1: reachability of the $\overline{\mathcal{B}}_\infty(x^*, \delta)$ for some x^*

For any $x \in \mathbb{R}_+^m \times \{0\}^{n-m}$ and $\delta > 0$, we denote the closed ball of $\mathbb{R}_+^m \times \{0\}^{n-m}$ for the infinite norm by $\overline{\mathcal{B}}_\infty(x, \delta)$. We will show that there exists $x^* \in (\mathbb{R}_+^m)^m \times \{0\}^{n-m}$ such that any $\overline{\mathcal{B}}_\infty(x^*, \delta)$ fulfills the requirement of Proposition 2.1.8.

Let us first assume that $V^0 = \emptyset$. By assumption on Φ , there exists $T > 0$ such that $\Phi_i(x, T) = 0$ for all $x \in \mathbb{R}_+^n$ with $\|x\|_1 \leq R + M$ and all $i \in V^-$. Let $x^* = \Phi(0, T)$ and first note that $x^* = \Phi(z, T)$ for all $z \in \mathbb{R}_+^n$ such that $\|z\|_1 \leq R + M$ and $z_i = 0$ for all $i \in V^0 \cup V^-$. Now consider $\delta > 0$. (Φ_1, \dots, Φ_m) is uniformly continuous on $C \times [T, T + 1]$ since the non-negative ϕ_i are \mathcal{C}^1 , so there are $\delta' \in (0, M]$ and $t_0 \in (0, 1]$ such that $\|\Phi(x, u) - x^*\|_\infty \leq \delta$ for all $x \in \mathbb{R}_+^n$ with $x_1 + \dots + x_m \leq \delta'$ and all $u \in [T, T + t_0]$. Set $\varepsilon \in (0, 1)$ and $\eta \in (0, 1)$ such that:

$$\forall (i, j) \in \mathcal{I}, \quad \bar{\mu}_{i,j}([0, \varepsilon]) < \eta \tag{2.25}$$

and denote by N the smallest positive integer such that $(1 - \varepsilon)^N R < \frac{\delta'}{2}$.

It is easy to see that setting $\kappa^0 = (\kappa, \dots, \kappa) \in \mathcal{S}^{mN}$, we have:

$$\forall x \in \mathbb{C}, \quad \forall t \in \left[0, \frac{\delta'}{2mNM}\right]^{mN} \times [T, T + t_0], \quad \forall \xi \in (\eta, 1]^{mN}, \quad h_x^{mN+1}(t, \xi, \kappa^0) \in \overline{\mathcal{B}}_\infty(x^*, \delta).$$

Considering the joint density of the T_k and the U_k as in the proof of Proposition 2.1.10.(i) finally yields, for all $x \in \mathbb{C}$:

$$\mathbb{P}_x \left(\forall t \in \left[T, T + \frac{\delta'}{2M} + t_0\right], X(t) \in \overline{\mathcal{B}}_\infty(x^*, \delta) \right) \geq \exp \left(-|\mathcal{E}| \left(\frac{\delta'}{2M} + t_0 \right) \bar{\theta} \right) \left(\frac{\theta \delta'}{2mNM} \right)^{mN} (1 - \eta)^{mN} \quad (2.26)$$

which, in turn, implies the expected property.

The proof relies on the same reasoning if $V^0 \neq \emptyset$, using paths along which a sequence of transfers results in all neutral patches having a positive population, then the flow brings the population of sinks to zero.

Step 2: petiteness of a $\overline{\mathcal{B}}_\infty(x^*, \delta)$ for some δ

According to Proposition 2.1.8 and Step 1 hereabove, Proposition 2.1.10.(ii) will be proved if we show that there exists some $\delta > 0$ such that $\overline{\mathcal{B}}_\infty(x^*, \delta)$ is petite for the resolvent of X , which can be done by way of checking Assumption F.

Let us thus set some $\delta \in (0, \min_{i \in V^+ \cup V^0} x_i^*)$ that we may have to take smaller later on, and let $\underline{x} = \min_{i \in V^+ \cup V^0} x_i^* - \delta$.

For simplicity reasons, we will assume that all ϕ_i associated with sources are \mathcal{C}^1 functions (rather than merely piecewise \mathcal{C}^1) on \mathbb{R}_+ and that $\bar{\mu}_{i,j}$ measures admit continuous density functions $f_{i,j}$ on $[0, 1]$ (instead of just admitting an absolutely continuous component on a subinterval of $[0, 1]$). The general case only requires reducing the domain over which it is possible to consider our paths of interest, which induces an unnecessary notational inflation.

Even if it means considering a larger T in Step 1, we may assume that $\Phi(x, T) \in \mathbb{R}_+^m \times \{0\}^{n-m}$ for all $x \in \overline{\mathcal{B}}_\infty(x^*, \delta)$. As in Step 1, we define ε and η such that (2.25) holds.

Let us begin by proving the following inequality:

$$\forall i \in V^+, \forall y > 0, \forall u > 0, \quad \frac{\min_{[0, y+Mu]} \Phi_i}{M} \leq \frac{\partial \Phi_i}{\partial y}(y, u) \leq \frac{M}{\min_{[0, y+Mu]} \Phi_i}. \quad (2.27)$$

If $i \in V^+$, $0 < y < y + h$ and $u > 0$, the mean value inequality entails that $\Phi_i \left(y, \frac{h}{M} \right) \leq y + h$, from which we deduce

$$\frac{\min_{[\Phi_i(y, u), \Phi_i(y, u) + h]} \Phi_i}{M} h \leq \Phi_i \left(y, u + \frac{h}{M} \right) - \Phi_i(y, u) \leq \Phi_i(y + h, u) - \Phi_i(y, u)$$

using the mean value theorem, hence the left hand side of (2.27) by letting h go to 0. Proving the right-side inequality of (2.27) relies on the very same argument and is left to the reader. Moreover, it is clear that

$$\forall i \in V^0, \forall y > 0, \forall u > 0, \quad \frac{\partial \Phi_i}{\partial y}(y, u) = 1. \quad (2.28)$$

We now show that for any $x \in \overline{\mathcal{B}}_\infty(x^*, \delta)$ and $t \in (0, 1)^m \times (T, T + 1)$, then

$$\Psi_t^x : \begin{cases} (0, a)^m \rightarrow \mathbb{R}^m \times \{0\}^{n-m} \\ \xi \mapsto h_x^{m+1}(t, \xi, \kappa) \end{cases}$$

is a \mathcal{C}^1 -diffeomorphism of $(0, \eta)^m$ onto its image. For fixed x and t , indeed, a simple calculation shows that

$$\frac{\partial \Psi_t^x}{\partial \xi_m}(t, \xi, \kappa) = \partial_1 \Phi(g_{\kappa_m}(h_x^m, \xi_m), t_{m+1}) \cdot \partial_2 g_{\kappa_m}(h_x^m, \xi_m) \quad (2.29)$$

and that for any $i \in \llbracket 1, m-1 \rrbracket$:

$$\frac{\partial \Psi_t^x}{\partial \xi_i}(t, \xi, \kappa) = \left[\prod_{k=m}^{i+1} \partial_1 \Phi(g_{\kappa_k}(h_x^k, \xi_k), t_{k+1}) \cdot \partial_1 g_{\kappa_k}(h_x^k, \xi_k) \right] \cdot \partial_1 \Phi(g_{\kappa_i}(h_x^i, \xi_i), t_{i+1}) \cdot \partial_2 g_{\kappa_i}(h_x^i, \xi_i). \quad (2.30)$$

where we wrote h_x^k as a short for $h_x^k(t, \xi, \kappa)$, defined

$$\partial_1 g_{i,j}(y, \zeta) = I_m + F_{\mu_{i,j}}^{-1}(\zeta) \cdot (1_{j \leq m} E_{j,i} - E_{i,i})$$

with $(E_{i,j})_{i,j \in \llbracket 1, m \rrbracket}$ the canonical basis of $\mathcal{M}_m(\mathbb{R})$, as well as

$$\partial_1 \Phi(y, u) = \begin{pmatrix} \frac{\partial \Phi_1(y, u)}{\partial y_1} & 0 & \dots & 0 \\ 0 & \ddots & \ddots & \vdots \\ \vdots & \ddots & \ddots & 0 \\ 0 & \dots & 0 & \frac{\partial \Phi_m(y, u)}{\partial y_m} \end{pmatrix}$$

and

$$\partial_2 g_{i,j}(y, \xi) = \frac{y_i}{f_{i,j}(F_{\mu_{i,j}}^{-1}(\xi))} (1_{j \leq m} \tilde{e}_j - \tilde{e}_i)$$

where $(\tilde{e}_1, \dots, \tilde{e}_m)$ is the canonical basis of \mathbb{R}^m .

Recalling the fact that every $i \in V^+$ is the origin of one only edge κ_i , (2.27) and (2.28) then imply that for all $t \in (0, 1)^m \times (T, T + 1)$ and all $\xi \in (0, \eta)$, the Jacobian matrix of Ψ_t^x at (t, ξ, κ) is a continuous function of ξ and is an invertible matrix with determinant $J(t, \xi, \kappa)$ such that

$$0 < J(t, \xi, \kappa) \leq \left(\frac{M}{\min_{i \in V^+} \min_{[0, x_i + (m+T+1)M]} \Phi_i} \right)^{\frac{m(m+1)}{2}} \frac{(\|x\|_1 + \delta + (m+T+1)M)^m}{\prod_{i=1}^m \min_{[0,1]} f_{\kappa_i}} < +\infty. \quad (2.31)$$

Now Ψ_t^x is injective over $(0, \eta)^m$ for fixed t and x ; this stems from the fact that the cumulative distribution functions of the μ_{κ_k} are strictly increasing, so knowing $\langle \Psi_t^x(t, \xi, \kappa), e_{i_1} \rangle$ makes it possible to determine ξ_1 , knowing ξ_1 and $\langle \Psi_t^x(t, \xi, \kappa), e_{i_2} \rangle$ yields ξ_2 and so on. This proves our claim that Ψ_t^x is a \mathcal{C}^1 -diffeomorphism.

We therefore only need to check that Assumption F.2 holds to conclude. Take $x \in \overline{\mathcal{B}}_\infty(x^*, \delta)$ and for all $t \in [0, 1]^m$, set $I_t = \Psi_t^x(t, (0, \eta)^m, \kappa)$. Considering the possible value of the population of patches 1 to m after a series of jumps along the edges of κ such that the k -th transfer

has amplitude between 0 and $k\frac{\varepsilon}{m}\underline{x}$, it is fairly easy to check that for a given $t = (t_1, \dots, t_m)$ in $\left(0, \left(\frac{\varepsilon}{Mm^2}\underline{x}\right) \wedge 1\right)^m \times (T, T+1)$:

$$\prod_{i=1}^m \left[\Phi_i \left(x_i - \frac{\varepsilon}{m} + (t_1 + \dots + t_i)M, t_{i+1} + \dots + t_{m+1} \right), \Phi_i(x_i, t_1 + \dots + t_{m+1}) \right] \subset I_t$$

and then, by (2.27), (2.28) and the mean value theorem for the $\Phi_i(\cdot, t)$:

$$\prod_{i=1}^m [\Phi_i(x_i, t_{i+1} + \dots + t_{m+1}) - \varepsilon_0, \Phi_i(x_i, t_1 + \dots + t_{m+1})] \subset I_t$$

for some positive ε_0 independent from the choice of x within $\overline{\mathcal{B}}_\infty(x^*, \delta)$. For small enough values of δ , there are $T^0 \in \left(0, \left(\frac{\varepsilon}{Mm^2}\underline{x}\right) \wedge 1\right)$ and an orthotope $\mathcal{P} \subset \mathbb{R}_+^m \times \{0\}^{n-m}$ with non-zero Lebesgue measure, both independent from the choice of x within $\overline{\mathcal{B}}_\infty(x^*, \delta)$, such that $\mathcal{P} \subset I_t$ for all $t \in (0, T^0)^m \times (T, T+T^0)$. This entails that Assumption F.2 holds. Proposition 2.1.7 then implies that $\overline{\mathcal{B}}_\infty(x^*, \delta)$ is petite for the resolvent of X , which ends the proof of Proposition 2.1.10.(ii), and therefore of Theorem 2.1.2. \square

Note that if the $t \mapsto h_x^m(t, \xi, \kappa)$ are diffeomorphisms for suitable values of ξ (which typically is the case in a multiplicative model with constant growth!), we may want to monitor the effect of small variations of t (rather than of ξ) on $h_x^m(t, \xi, \kappa)$. This would allow to relax the absolute continuity assumptions on the $\mu_{i,j}$, since it would then be sufficient to assume that $\bar{\mu}_{i,j}(\{0\}) < 1$ and $\bar{\mu}_{i,j}(\{1\}) = 0$ for petiteness to hold.

Proof of Proposition 2.1.10.(iii).— We keep all notations from the proof of Proposition 2.1.10.(ii) above. First set $\Delta_0 = \frac{\delta'}{2M} + t_0$. If π denotes the invariant probability of X , we may assume that $\pi(C) > 0$, which entails by Birkhoff's ergodic theorem (Theorem 1.3.8) that τ_C is \mathbb{P}_x -a.s. finite for all $x \in \mathbb{R}_+^n$. Inequality (2.26) then yields:

$$\inf_{x \in \mathbb{R}_+^n} \mathbb{P}_x \left(\forall t \in [\tau_C + T, \tau_C + T + \Delta_0], X(t) \in \overline{\mathcal{B}}_\infty(x^*, \delta) \right) > 0.$$

Thus, according to the strong Markov property, it is sufficient to show that there exists $\Delta \in (0, \Delta_0]$ such that:

$$\forall x \in \mathcal{B}(x^*, \delta), \forall B \in \mathcal{B}(\mathcal{P}), \quad \lambda_m(B) > 0 \Rightarrow \mathbb{P}_x(\exists k \geq 1, X(k\Delta) \in B) > 0.$$

Set $\Delta = \Delta_0 \wedge T$ and $k \in \mathbb{Z}_+$ such that $mT^0 \leq k\Delta < mT^0 + T$, and let $x \in \overline{\mathcal{B}}_\infty(x^*, \delta)$. Then for any Borel subset B of \mathcal{P} , the change of variables formula yields:

$$\begin{aligned} \mathbb{P}_x(X(k\Delta) \in B) &\geq \mathbb{P}_x[(T_m < k\Delta < T_{m+1}) \cap (\Phi(X(T_m), k\Delta - T_m) \in B)] \\ &\geq e^{-\bar{\theta}n(n-1)k\Delta} \int_{(0, T^0)^m} \int_{(0, \eta)^m} \left[\prod_{i=1}^m \theta_{\kappa_i(x)}(h_x^i) \right] \mathbb{1}_{\Phi(h_x^m, k\Delta - \sum_{j=1}^m t_j) \in B} d\xi dt \\ &\geq e^{-\bar{\theta}n(n-1)k\Delta} \underline{\theta}^m \int_{(0, T^0)^m} \int_{(0, \eta)^m} \mathbb{1}_{\Phi(h_x^m, k\Delta - \sum_{j=1}^m t_j) \in B} d\xi dt \\ &\geq e^{-\bar{\theta}n(n-1)k\Delta} \underline{\theta}^m \int_{(0, T^0)^m} \int_{(0, \eta)^m} \mathbb{1}_{h_x^{m+1}((t, k\Delta - \sum_{j=1}^m t_j), \xi, \kappa) \in B} d\xi dt \\ &\geq \frac{1}{\alpha} e^{-\bar{\theta}n(n-1)k\Delta} \underline{\theta}^m \int_{(0, T^0)^m} \mathbb{1}_{k\Delta - \sum_{j=1}^m t_j \in [T, T+T^0]} \left(\int_{\mathcal{P}} \mathbb{1}_{y \in B} dy \right) dt \\ &\geq \frac{1}{\alpha} e^{-\bar{\theta}n(n-1)k\Delta} \underline{\theta}^m \lambda_m(S) \lambda_m(B) \end{aligned}$$

where h_x^i stands for $h_x^i(t, \xi, \kappa)$, α is the upper bound of $J(t, \xi, \kappa)$ defined by (2.31) and

$$S = \left\{ t \in (0, T^0)^m, \sum_{j=1}^m t_j \in [k\Delta - T - T^0, k\Delta - T] \right\}.$$

Now $\lambda_m(S) > 0$, which ends the proof. □

2.1.6 Proof of stability Theorem 2.1.5

We keep considering γ and κ as defined in the proof of Theorem 2.1.2. We will show the following, which is sufficient to conclude thanks to Proposition 2.1.7 and Theorem 2.1.9.

PROPOSITION 2.1.11. — *Assume that the model is unitary and that either (2.8) holds, or \mathcal{G} is strongly connected and (2.9) holds. Then:*

- (i) *There exists $S \subset \mathbb{R}_+^n$ such that X fits Assumptions D and E.*
- (ii) *X fits Assumption F.*
- (iii) *X admits an irreducible skeleton chain.*

Proof of Proposition 2.1.11.(i).— Let us first assume that (2.8) holds. Let $R \geq 2$ be an integer such that Assumption D holds with

$$S = \left\{ x \in \mathbb{R}_+^n : \min_{i \in V^-} x_i \geq R \right\}$$

and set

$$S' = \left\{ x \in \mathbb{R}_+^n : \min_{i \in V^-} x_i \geq 2R \right\}.$$

In order to verify that Assumption E.1 holds, we consider $x \in \mathbb{R}_+^n$ as well as $T \in (0, 1]$ and argue as in the proof of Proposition 2.1.10.(i). On the event we consider, transfers along edges $\kappa_1, \dots, \kappa_m$ occur before time T and result in the total population of sinks being at least $2(n-m)R + TM$, and transfers along γ occur between time T and time $2T$ and result in the population of each sink at time $2T$ reaching at least $2R$. For corresponding paths, $X(2T) \in S'$, and it is easy to show using the assumptions on Θ that the probability under \mathbb{P}_x of observing such paths for a fixed T goes to 1 as $\|x\|_1$ goes to $+\infty$. As a result, T may be taken arbitrarily small in Assumption E.1 for any fixed value of δ . Assumption E.3 will thus be automatically fulfilled for some value of T provided that Assumption E.2 holds. Showing the latter relies on the observation that as a sink gives up its charge, the temporal intensity of subsequent transfers from this patch is upper bounded. Simple calculations then show that the probability for a sink with original population above $2R'$ to have a population lower than R' before time $\frac{R'}{M}$ is lower than some constant in $[0, 1)$, which ends our proof.

The argument is similar in the connected case with (2.9) except that it is now possible to define S and S' as in the proof of Proposition 2.1.10.(i). The connectivity assumption then entails that the process returns to S' arbitrarily fast with a given probability when the total population in the system is high enough, and we may conclude just as before.

Proof of Proposition 2.1.11.(ii).— Without loss of generality, we may assume that C writes $\{x \in \mathbb{R}_+^n : \|x\|_1 \leq R\}$ for some $R \in \mathbb{Z}_+^*$. Let $T > 0$ be such that $\Phi_i(x, T) = 0$ for all $i \in V^-$ and all $x \in \mathbb{R}_+^n$ with $\|x\|_1 \leq R + 1$ and define

$$\kappa' = (\kappa_1, \dots, \kappa_1, \kappa_2, \dots, \kappa_2, \dots, \kappa_m, \dots, \kappa_m) \in \mathcal{J}^{m(R+1)}$$

as the vector of edges made of $R + 1$ successive repetitions of each of κ 's edges.

For all $t \in \left[0, \frac{1}{mM(R+1)}\right)^{m(R+1)} \times (T, T + 1)$ and all $\xi \in (0, 1)^{m(R+1)}$, we may write:

$$\forall i \in V^+, \quad (h_x(t, \xi, \kappa'))_i = \Phi_i(0, t_{(i+1)(R+1)} + t_{(i+2)(R+1)} + \dots + t_{m(R+1)} + t_{m(R+1)+1})$$

and

$$\forall i \in V^0 \cup V^-, \quad (h_x(t, \xi, \kappa'))_i = 0.$$

For $t' = (t_1, \dots, t_R, t_{R+2}, \dots, t_{2(R+1)-1}, t_{2(R+1)+1}, \dots, t_{m(R+1)-1}, t_{m(R+1)+1}) \in \left[0, \frac{1}{mM(R+1)}\right)^{mR} \times (T, T + 1)$ and $\xi \in (0, 1)^{mR}$, we easily see that

$$\Psi_{t'}^x : \begin{cases} \left(0, \frac{1}{mM(R+1)}\right)^m \rightarrow \mathbb{R}^d \times \mathbb{R}^{n-d} \\ (t_{R+1}, t_{2(R+1)}, \dots, t_{m(R+1)}) \mapsto h_x^{m(R+1)+1}(t, \xi, \kappa) \end{cases}$$

is a \mathcal{C}^1 -diffeomorphism of $\left(0, \frac{1}{mM(R+1)}\right)^m$ onto its image. It is independent from the choice of x in C and has its Jacobian determinant upper bounded by $\alpha = \prod_{i=1}^d \max_{[0, R+1+(T+1)M]} \Phi_i$. It is then possible to define, as in the proof of Proposition 2.1.10.(ii), $T^0 \in \left(0, \frac{1}{mM(R+1)}\right)$ and an orthotope $\mathcal{P} \subset \mathbb{R}_+^d \times \{0\}^{n-d}$ with non-zero Lebesgue measure, independently from the choice of $x \in C$, such that \mathcal{P} be included in the image of $(0, T^0)^m$ by $\Psi_{t'}^x$ for all $t' \in (0, T^0)^{mR} \times (T, T + T^0)$. Assumption F.3 is also met since Θ is lower bounded by a positive real number, and Proposition 2.1.7 therefore implies that C is petite.

Proof of Proposition 2.1.11.(iii).— We use the notations of the proof of Proposition 2.1.11.(ii) above. It is sufficient to prove the irreducibility property for initial conditions within C because of the same argument as in the proof of Proposition 2.1.10.(iii). Even if it means considering smaller T^0 and \mathcal{P} , one may assume that:

$$\forall t' \in \left(0, \frac{T^0}{2m(R+1)}\right)^{mR} \times (0, T^0), \quad \mathcal{P} \subset \Psi_{t'}^x \left(0, \frac{T^0}{2m(R+1)}\right)^m.$$

Let us consider $\Delta \in \left(0, \frac{T^0}{2}\right)$ and $k \geq 1$ such that $k\Delta \in \left(T + \frac{T^0}{2}, T + T^0\right)$. Reproducing the calculations of the proof of Proposition 2.1.10.(iii) yields for any $x \in C$ and any $B \in \mathcal{B}(\mathcal{P})$:

$$\begin{aligned} \mathbb{P}_x(X_{k\Delta} \in B) &\geq e^{-k\Delta\bar{\theta}} \Theta(0)^{m(R+1)} \int_{(0, T^0)^{m(R+1)}} \mathbf{1}_{h_x^{m(R+1)}((t, k\Delta - T - \sum_{j=1}^{m(R+1)} t_j), \xi, \kappa') \in B} dt \\ &\geq \frac{1}{\alpha} e^{-k\Delta\bar{\theta}} \Theta(0)^{m(R+1)} \int_{(0, T^0)^{m(R+1)}} \int_{\left(0, \frac{T^0}{2m(R+1)}\right)^{mR}} \lambda_d(\mathcal{P} \cap B) dt' \\ &\geq \frac{1}{\alpha} e^{-k\Delta\bar{\theta}} \Theta(0)^{m(R+1)} \left(\frac{T^0}{2m(R+1)}\right)^{mR} \lambda_d(B) \end{aligned}$$

where $\bar{\theta}$ is a common upper bound for the $\theta_{i,j}$ on $\{y \in \mathbb{R}_+^n : \|y\|_1 \leq R + k\Delta M\}$. Therefore we have $\mathbb{P}_x(X(k\Delta) \in B) > 0$ whenever $\lambda_d(B) > 0$, which ends our proof. \square

2.1.7 Conclusion on metapopulation PDMP

The results presented in this section may be expanded in various ways. First, the multiplicative and unitary frameworks were designed as simple models that allow either for large jumps or large jump rates, but many applications may require designing and studying hybrid models. Criteria from Subsections 2.1.4.1 and 2.1.4.2 will hopefully prove flexible and be useful in such settings.

Besides, some metapopulation settings do not necessarily fit with the additional hypothesis we made on the structure of the active graph \mathcal{G} of the system — that is, on the graph formed by edges along which non-zero transfers occur at non-zero rate. Although the criteria for boundedness and petiteness we stated in Sections 2.1.4.1 and 2.1.4.2 do not refer to this active graph, they cannot be applied without particular sequences of transfers being made explicit, which assumes that one can describe entire paths followed by the population load. Moreover, they require some degree of connectivity so the system, loosely speaking, can "empty" and "mix". Adapting the results above to more general graphs is therefore a topic of further research.

Finally, we chose to model deterministic intra-patch population dynamics. This assumption is only legitimate if the local demographics exhibit little stochasticity, either intrinsically or because quantities observed over a timestep are so large that their aggregate evolution can be approximated by a non-random dynamical system. This condition is not met when considering daily observed cattle movements. This is why we will turn in next section to an all-stochastic framework using jump metapopulation processes, that will also happen to be more tractable and provide a straightforward coupling with epidemic processes. As stated in our Introduction, the downside of modeling population dynamics using jump processes with unitary jumps is not to be able to account for instantaneous macroscopic transfers, as the multiplicative models presented above do. However, in the application we have in mind, the fact that cattle herds are controlled populations with transfers limited by transportation capacities rules out the existence of such transfers.

2.2

The branching population model

The population model presented in this section and the associated epidemic model (see Subsection 3.2.1) have been studied in a paper published in *Journal of Mathematical Biology* in 2019 [Mon19b]. It is a metapopulation multitype branching process with immigration, that we shall henceforth simply refer to as the *branching population model*.

We will define a \mathbb{Z}_+^n -valued population process $(X^N(t))_{t \geq 0}$ modeling the population dynamics (n being the number of nodes in the graph and N a scaling parameter) and impose a condition (Assumption G) ensuring its convergence in distribution, as $t \rightarrow \infty$, to an invariant probability measure at a geometric speed (Proposition 2.2.1). We will then investigate the time for the scaled population process to deviate by any given fixed distance from the corresponding deterministic model, described as the solution of a linear ODE (Propositions 2.2.2 and 2.2.3).

2.2.1 Definition of the branching population model

We model the population dynamics using a \mathbb{Z}_+^n -valued multitype continuous-time branching process with immigration, denoted X^N . At any population state $x = (x_1, \dots, x_n) \in \mathbb{Z}_+^n$, the inflow rate in node i is $NB_i + b_i x_i$ and the death rate in node i is $d_i x_i$ with $b_i, B_i, d_i \in \mathbb{R}_+$. The $b_i x_i$ might be considered as Malthusian birth rates and the NB_i as constant immigration rates.

Data suggest that the temporal rate of transfers between agents also is size-dependent. Moreover, their amplitude is bounded by a few units because of transportation constraints and does not vary much empirically, so we will set it to be unitary and define the transfer rate from node i to node j at population state x as $\theta_{i,j} x_i$ with $\theta_{i,j} \geq 0$.

We will define X^N as the solution of a stochastic differential equation with respect to a point measure, as we did for the metapopulation PDMP studied in Section 2.1. We state this equation under its integral form in order to make its initial condition clearly appear.

Set $x(0) \in \mathbb{R}_+^n$. For all $(i, j) \in \mathcal{I}$, let N_i^B , N_i^b , N_i^d and $N_{i,j}$ be independent Poisson random measures on $\mathbb{R}_+ \times \mathbb{R}_+$ with intensity $ds du$. For all $N \geq 1$, we define the multitype branching process with immigration X^N as the solution of the integral equation

$$\begin{aligned} X_i^N(t) = & \lfloor Nx_i(0) \rfloor + \int_0^t \int_{\mathbb{R}_+} 1_{u \leq NB_i} N_i^B(ds, du) \\ & + \int_0^t \int_{\mathbb{R}_+} 1_{u \leq b_i X_i^N(s^-)} N_i^b(ds, du) - \int_0^t \int_{\mathbb{R}_+} 1_{u \leq d_i X_i^N(s^-)} N_i^d(ds, du) \\ & + \sum_{j \neq i} \left[\int_0^t \int_{\mathbb{R}_+} 1_{u \leq \theta_{j,i} X_j^N(s^-)} N_{j,i}(ds, du) - \int_0^t \int_{\mathbb{R}_+} 1_{u \leq \theta_{i,j} X_i^N(s^-)} N_{i,j}(ds, du) \right] \end{aligned} \quad (2.32)$$

for all $i \in \llbracket 1, n \rrbracket$. The existence and trajectorial uniqueness of solutions to this equation, and of all jump processes defined in a similar way in the rest of this work, are granted by [Dav93] p.55. For any $N \geq 1$, X^N is a \mathbb{Z}_+^n -valued jump process with initial value $X^N(0) = \lfloor Nx(0) \rfloor$ and the following transition rates under \mathbb{P} :

Transition	Rate at state x	
$x \rightarrow x + e_i$	$NB_i + b_i x_i$	(1.3)
$x \rightarrow x - e_i$	$d_i x_i$	
$x \rightarrow x - e_i + e_j$	$\theta_{i,j} x_i$	

Table 2.1: Branching population process jump rates chart.

From now on, we assume that the directed graph with vertices set $\llbracket 1, n \rrbracket$ and edges set $\{(i, j) : \theta_{i,j} > 0\}$ is strongly connected, so that for any i and j , any individual born in node i can get to node j with positive probability during its lifetime. We assume that $B = (B_1, \dots, B_n) \neq 0$ in order to rule out pathological cases that would be irrelevant for the application we have in mind.

In our framework, immigration in node i occurs at rate NB_i , and individuals in node i give birth at rate b_i , die at rate d_i and move to node j at rate $\theta_{i,j}$, independently from other individuals in the network. The lineage of a single individual is a branching process with the following transition rates:

Transition	Rate at state x
$x \rightarrow x + e_i$	$b_i x_i$
$x \rightarrow x - e_i$	$d_i x_i$
$x \rightarrow x - e_i + e_j$	$\theta_{i,j} x_i$

Table 2.2: Immigration-free branching population process jump rates chart.

Once they enter the system through immigration, individuals give birth to independent lineages that do not interact. As a superimposition of independent multitype branching processes initiated at constant time rate, X^N is non-explosive, that is, that $X^N(t)$ is almost surely finite for all $t \geq 0$.

We wish to model populations that are stable over time, so it is clear that the branching population process must not tend to infinity with positive probability, that is, we do not want it to be supercritical (see however [BT14] for the study of an epidemic process within a growing population modeled using a supercritical branching process). We impose a slightly stronger condition — subcriticality — to make sure that the first moment of the population process does not go to infinity. From now on, we will therefore assume the following condition to hold:

ASSUMPTION G (Subcriticality of the immigration-free population BP). — *The eigenvalues of*

$$A = \begin{pmatrix} b_1 - d_1 - \sum_{j \neq 1} \theta_{1,j} & \theta_{2,1} & \cdots & \theta_{n,1} \\ \theta_{1,2} & b_2 - d_2 - \sum_{j \neq 2} \theta_{2,j} & \ddots & \vdots \\ \vdots & \ddots & \ddots & \theta_{n,n-1} \\ \theta_{1,n} & \cdots & \theta_{n-1,n} & b_n - d_n - \sum_{j \neq n} \theta_{n,j} \end{pmatrix} \quad (1.4)$$

have negative real parts.

2.2.2 Stability and scaling limit of the branching population process

We may now state our first convergence result for the population process. Although it is a continuous-time version of standard results for discrete-time multitype branching processes with immigration, we could not find the exact same statement in the existing literature.

PROPOSITION 2.2.1 (Ergodicity of the branching population process). — *Let $N \geq 1$. The branching population process X^N is positive recurrent (we denote its limiting probability by π^N) and $(\|\cdot\|_1 + 1)$ -uniformly exponentially ergodic. Moreover, for every $N \geq 1$ and independently of $x(0) \in \mathbb{R}_+^N$,*

$$\lim_{t \rightarrow +\infty} \mathbb{E}(X^N(t)) = \int x d\pi^N(x) = -NA^{-1}B$$

where A is defined by (1.4).

This statement is reminiscent of a classical result on multitype branching processes (see Section 7 of Chapter IV of [AN72] or Theorem 4.2.2 of [Jag78]). However, the definition of such processes slightly differs from the one we chose here: in the classical setting, individuals do not move between nodes but split at death between other individuals of various types. Chapter 4 of [Jag78] considers a unidimensional *general branching process* that allows individuals to give birth at random times of their lives, and his proof could be adapted to fit our framework. One could also consider a time-sampled version of X^N to retrieve a multitype Bienaymé-Galton-Watson process with immigration (see Chapter III.6 of [AN72]) or compare X^N to multitype branching processes with splitting at death. Yet, we need a finer description of the return time to compact subsets of \mathbb{Z}_+^n in order to establish not only positive recurrence but also uniform ergodicity.

Proving Proposition 2.2.1 is easy when $B = 0$, using that $\frac{d}{dt}\mathbb{E}(X^N(t)) = A\mathbb{E}(X^N(t))$ and a generalized eigendecomposition of A (in this particular case $\pi = \delta_0$), so we now assume that $B \neq 0$. We first show the following lemma.

LEMMA 1 (Existence of a Lyapunov function for X^N). — There exist $v \in \mathbb{R}^n$ with positive coordinates, $c > 0$ and $R \geq 0$ such that

$$v \cdot (Ax + B) < -c(v \cdot x + 1)$$

for any $x \in \mathbb{R}_+^n$ such that $\|x\|_1 \geq R$.

Proof of Lemma 1.— Recall that the transpose tA of A is invertible because of Assumption G and set $u = -{}^tA^{-1}B$. Quick calculations show that u is the limit value of solutions of the n -dimensional linear ODE

$$x' = {}^tAx + B \tag{2.33}$$

since tA 's eigenvalues have negative real parts. Let us consider a solution of (2.33) such that y_0 has positive coordinates. Writing (2.33) as

$$\forall i \in \llbracket 1, n \rrbracket, \quad y_i' = \left[b_i - d_i - \sum_{j \neq i} \theta_{i,j} \right] y_i + \sum_{j \neq i} \theta_{i,j} y_j + B_i$$

and using that the graph with vertices set $\llbracket 1, n \rrbracket$ and with edges set $\{(i, j) : \theta_{i,j} > 0\}$ is strongly connected (so that all $\theta_{i,j}$ cannot be zero), we see that no y_i ever reaches 0 in finite time. As a result, u has nonnegative coordinates. Similarly, if $u_i = 0$ then $u_j = 0$ for any j such that $\theta_{i,j} > 0$, hence $u = 0$ by induction because of the graph connectivity, which contradicts the fact that $B \neq 0$. All components of u are therefore positive. Now ${}^tAu = -B$, B has nonnegative components and tA is invertible, so for any $x \in \mathbb{R}_+^n$ one may find v in a neighborhood of u and C in a neighborhood of B such that both v and C have positive components and such that ${}^tAv = -C$. This rewrites ${}^t vA = -{}^tC$, so

$$v \cdot (Ax + B) = -C \cdot x + v \cdot B.$$

Defining

$$c = \frac{\min_i C_i}{2 \max_i v_i} > 0$$

and

$$R = \frac{1}{\min_i v_i} \left(1 + \frac{v \cdot B}{c} \right)$$

then yields the result.

Proof of Proposition 2.2.1.— Lemma 1 shows that $f : x \mapsto 1 + v \cdot x$ satisfies Condition (CD2) from [MT93b] with $V = f$, $C = \{x \in \mathbb{Z}_+^n : \|x\|_1 \leq R\}$ and $d = \max_i v_i R$ since the infinitesimal generator of \mathcal{A} of X^N is such that $\mathcal{A}f(x) = v \cdot (Ax + B)$ for any $x \in \mathbb{Z}_+^n$. Moreover, it is not difficult to see that all compact sets of \mathbb{Z}_+^n are δ_0 -petite for any skeleton chain of X^N by considering sequences of appropriate transfers and death events — recalling that Assumption G implies that at least one of the d_i is positive. Theorem 1.3.21 then yields the expected result. The proposition on the first moment of π comes from the fact that $\int (Ax + B) d\pi(x) = 0$ since $x \mapsto Ax + B$ is the value of the generator of X^N applied to Id. \square

Just as expected, the limiting average population size $-NA^{-1}B$ is proportional to the scaling factor N . Additional results on the limiting probability π^N can be found in Appendix B.

We are interested in the behavior of our process over finite time intervals as N tends to infinity. The mean equilibrium value $z^* = -A^{-1}B$ of X^N/N does not depend on N , and as N grows we expect the scaled superimposition of independent lineages to get smoother (see Figure 2.4, where the parameter values are chosen arbitrarily to make the figure easy to read and assimilate). This intuition is confirmed by the following law of large numbers, which is a direct consequence of Theorem 1.3.32:

PROPOSITION 2.2.2. — Define x as the solution of the Cauchy problem $x' = Ax + B$ with initial value $x(0)$, that is,

$$\begin{aligned} x : \mathbb{R} &\longrightarrow \mathbb{R}^n \\ t &\longmapsto e^{tA}(A^{-1}B + x(0)) - A^{-1}B \end{aligned} .$$

For any $T \geq 0$,

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{t \in [0, T]} \left\| \frac{X^N(t)}{N} - x(t) \right\|_\infty = 0 \right) = 1.$$

The deterministic process $x = (x(t))_{t \geq 0}$ converges to its equilibrium value $x^* := -A^{-1}B$ at an exponential rate. When coupling further dynamics with the population process, it is therefore common to consider that the latter starts from some point close to x^* . The following result provides bounds for population fluctuations over very large time intervals for such initial conditions. It will prove of great interest when coupling these population dynamics with SIR processes in Chapter 3, that will almost behave on finite time intervals as if the population of each node were constant. It directly stems from the Freidlin-Wentzell-type results on large deviations from a deterministic system adapted to Poisson perturbations, and more precisely from Theorem 1.3.37.

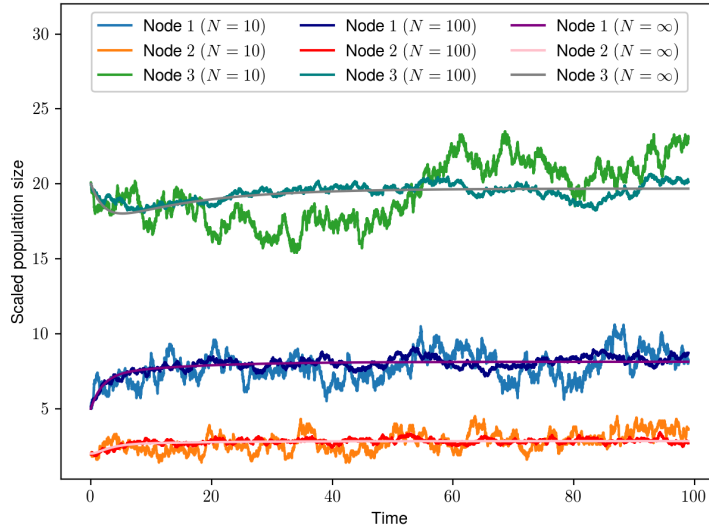


Figure 2.4: Simulated values of $X^N(t)/N$ ($t \in [0, 100]$) for $N = 10$ and $N = 100$ and limiting deterministic process with arbitrary parameter values $n = 3$, $\tilde{x}_0 = (5, 2, 20)$, $\tilde{B} = (1, .5, .5)$, $d = (.1, .2, .1)$, $b = (.1, .05, .02)$, $\theta_{1,2} = \theta_{1,3} = .2$, $\theta_{2,1} = .1$, $\theta_{2,3} = .5$, $\theta_{3,1} = .1$ and $\theta_{3,2} = 0$. The time unit is arbitrary.

PROPOSITION 2.2.3 (Exit time of a branching population process). — *Recall that for all $N \geq 0$, $X^N(0) = \lfloor Nx(0) \rfloor$. For any $\varepsilon \in (0, \|x^*\|_2)$, denote by τ_ε^N the exit time of the ball $\mathcal{B}_2(x^*, \varepsilon)$ by X^N/N . Then for ε small enough, there exists $\bar{V}_\varepsilon(x^*) > 0$ such that whenever $x(0) \in \mathcal{B}_2(x^*, \varepsilon)$, for any $\alpha > 0$:*

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(e^{(\bar{V}_\varepsilon(x^*) - \alpha)N} < \tau_\varepsilon^N < e^{(\bar{V}_\varepsilon(x^*) + \alpha)N} \right) = 1.$$

The constant $\bar{V}_\varepsilon(x^*)$ above is the *exit cost* from $\mathcal{B}_2(x^*, \varepsilon)$ starting from x^* for the dynamical system $x' = Ax + B$ and the Poisson perturbation considered, as introduced in Subsection 1.3.4.

Proof of Proposition 2.2.3.— This Proposition is Theorem 1.3.37 applied to a modified version of X^N/N with rates vanishing outside of $\mathcal{B}_2(x^*, 2\varepsilon)$, for instance the scaled process \tilde{X}^N/N where \tilde{X}^N is defined from the same Poisson processes and with the same initial condition as X^N with all rates in (1.7) multiplied by

$$\sigma(x/N) = 1_{\|x/N - x^*\|_2 \leq \varepsilon} + 1_{\varepsilon < \|x/N - x^*\|_2 \leq 2\varepsilon} \left(2 - \frac{\|x/N - x^*\|_2}{\varepsilon} \right).$$

The trajectories of \tilde{X}^N/N are the same as those of X^N/N until τ_ε^N , so it is sufficient to apply Theorem 1.3.37 to \tilde{X}^N/N . Note that $\mathcal{B}_2(x^*, \varepsilon)$ lies in the domain of attraction of x^* for the dynamical system $x' = \sigma(x)Ax + B$ since A is negative definite. It is an easy matter to check Assumption A of

Subsection 1.3.4. What remains to be shown is that $\bar{V}_\varepsilon(x^*) := \min_{y \in \partial \mathcal{B}_2(x^*, \varepsilon)} V(x^*, y)$ is positive, $V(x^*, \cdot)$ denoting the quasipotential introduced in Subsection 1.3.4.

It follows from A having only eigenvalues with negative real parts that there exist ε' and η in $(0, \frac{\varepsilon}{2}]$ such that for any absolutely continuous function $\phi : \mathbb{R} \rightarrow \mathbb{R}^n$, if $\varepsilon' < \|\phi(t) - x^*\| < \varepsilon$ then $\frac{d}{dt} \|\phi(t) - x^*\|_2^2 < 0$ whenever $\|\dot{\phi}(t) - (A\phi(t) + B)\|_2 < \eta$. The definition of the quasipotential $V(x^*, \dots)$ implies that

$$\bar{V}_\varepsilon(x^*) \geq \inf_{y \in \partial \mathcal{B}_2(x^*, \varepsilon)} \inf_{y' \in \partial \mathcal{B}_2(x^*, \varepsilon')} \inf_{\int_{T_1}^{T_2} L(\phi(t), \dot{\phi}(t)) dt}, \quad (2.34)$$

where the third infimum is taken over the set of $\{z \in \mathbb{R}^n : \varepsilon' \leq \|z - x^*\|_2 \leq \varepsilon\}$ -valued absolutely continuous functions ϕ on some $[T_1, T_2]$ (with $-\infty \leq T_1 < T_2 \leq +\infty$) such that $\phi(T_1) = y'$ and $\phi(T_2) = y$, and L is defined by

$$L(z, \beta) := \max_{u \in \mathbb{R}^n} \left[\beta \cdot u - \sum_i (e^{u_i} - 1)(B_i + b_i z_i) - \sum_i (e^{-u_i} - 1) d_i z_i - \sum_{i \neq j} (e^{u_j - u_i} - 1) \theta_{i,j} z_i \right] \quad (2.35)$$

for all $z \in \mathbb{R}_+^n$ and all $\beta \in \mathbb{R}^n$. Now take $y \in \partial \mathcal{B}_2(x^*, \varepsilon)$ and $y' \in \partial \mathcal{B}_2(x^*, \varepsilon')$ and assume that $\inf_{\int_{T_1}^{T_2} L(\phi(t), \dot{\phi}(t)) dt} = 0$, with the infimum defined as before. For any choice of ϕ it follows from the definition of ε' and η that:

$$\begin{aligned} \varepsilon^2 - \varepsilon'^2 &\leq \|y - x^*\|_2^2 - \|y' - x^*\|_2^2 \\ &\leq \int_{t: \|\dot{\phi}(t) - (A\phi(t) + B)\|_2 > \eta} \frac{d}{dt} \|\phi(t) - x^*\|_2^2 dt \\ &= 2 \int_{t: \|\dot{\phi}(t) - (A\phi(t) + B)\|_2 > \eta} \langle \phi(t) - x^*, \dot{\phi}(t) \rangle dt \\ &\leq 2\varepsilon \int_{t: \|\dot{\phi}(t) - (A\phi(t) + B)\|_2 > \eta} \|\dot{\phi}(t)\|_2 dt, \end{aligned}$$

by the Cauchy-Schwarz inequality, so

$$\int_{t: \|\dot{\phi}(t) - (A\phi(t) + B)\|_2 > \eta} \|\dot{\phi}(t)\|_2 dt \geq \frac{1}{2} \frac{\varepsilon^2 - \varepsilon'^2}{\varepsilon} \geq \frac{3\varepsilon}{8}. \quad (2.36)$$

Now there exists $\delta > 0$ such that for all $z \in \mathcal{B}_2(x^*, \varepsilon)$ and all $\beta \in \mathbb{R}^n$,

$$L(z, \beta) \geq \delta \left(\|\beta - (Az + B)\|_2 - \frac{\eta}{2} \right), \quad (2.37)$$

as seen by considering $u = \delta \frac{\beta - (Az + B)}{\|\beta - (Az + B)\|_2}$ in (2.35) if $Az + B \neq \beta$ and using a Taylor expansion for $\delta \approx 0$ for the function maximized in (2.35), so

$$L(z, \beta) \geq \delta \left(\|\beta\|_2 - \|Az + B\|_2 - \frac{\eta}{2} \right). \quad (2.38)$$

Let $M > 0$. If ϕ is such that

$$\int_{T_1}^{T_2} L(\phi(t), \dot{\phi}(t)) dt < \frac{\delta \eta}{2M},$$

then the Lebesgue measure of $\{t \in [T_1, T_2] : \|\dot{\phi}(t) - (A\phi(t) + B)\|_2 \geq \eta\}$ has to be lower than $\frac{1}{M}$ because of (2.37). For such a ϕ :

$$\begin{aligned} \int_{T_1}^{T_2} L(\phi(t), \dot{\phi}(t)) dt &\geq \int_{t: \|\dot{\phi}(t) - (A\phi(t) + B)\|_2 > \eta} L(\phi(t), \dot{\phi}(t)) dt \\ &\geq \int_{t: \|\dot{\phi}(t) - (A\phi(t) + B)\|_2 > \eta} \delta \left(\|\dot{\phi}(t)\|_2 - \|A\phi(t) + B\|_2 - \frac{\eta}{2} \right) dt \\ &\geq \delta \left(\frac{3\varepsilon}{8} - \frac{\sup_{z \in \mathcal{B}_2(x^*, \varepsilon)} \|Az + B\|_2 + \frac{\eta}{2}}{M} \right), \end{aligned}$$

using (2.36), which contradicts, for M large enough, the fact that $\int_{T_1}^{T_2} L(\phi(t), \dot{\phi}(t)) dt$ can be made arbitrarily small for some choice of ϕ . This and (2.34) yield $\bar{V}_\varepsilon(x^*) > 0$ since δ does not depend from the choice of y and y' , which ends the proof. \square

Despite its high tractability, the branching process we just considered fails to take into account the fact that populations we deal with in the framework of our cattle trade application are controlled and necessarily bounded above by the carrying capacities of holdings. By considering lineages that do not interact with each other, it allows for the total population of the system to reach an arbitrarily large level with positive probability. Moreover, it assumes that transfers from one holding to another occur at a rate that is proportional to the population of the original patch, regardless of how close the population of the target holding is from the number of animals this holding can *effectively* handle. This leads us to define another population jump model, with more complex jump rates — that entail an increased complexity of the scaling limiting dynamical system — but more realistic logistic dynamics and a finite number of states.

2.3

The logistic population model

In this section, we introduce and study another metapopulation jump process on \mathbb{Z}_+^n , that we will refer to as the *logistic population model*. For every node i , we define a capacity $NK_i > 0$ that intervenes in the logistic rates or importation to node i , its interior population logistic growth rate and the "pseudo-logistic" rates of transfers to node i from any other node. Logistic dynamics, first introduced by Verhulst [Ver38], account for the saturation effect of a population that cannot sustain Malthusian growth because of its *carrying capacity*, that may refer to space, technology or resource constraints.

2.3.1 Definition of the logistic population model

Let $K_i > 0$ for all $i \in \llbracket 1, n \rrbracket$. We take $z(0) \in \prod_{i=1}^n [0, K_i]$, and consider independent Poisson measures $N_i^B, N_i^b, N_i^d, N_{i,j}$ on $\mathbb{R}_+ \times \mathbb{R}_+$ with intensity $ds du$ for any $(i, j) \in \mathcal{I}$. For all $N \geq 1$, we define the logistic population process X^N as the solution of the integral equation

$$\begin{aligned}
 X_i^N(t) = & \lfloor Nz_i(0) \rfloor + \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq B_i(NK_i - X_i^N(s))_+} N_i^B(ds, du) \\
 & + \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \frac{b_i}{N} X_i^N(s^-)(NK_i - X_i^N(s))_+} N_i^b(ds, du) - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq d_i X_i^N(s^-)} N_i^d(ds, du) \\
 & + \sum_{j \neq i} \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \frac{\theta_{j,i}}{N} X_j^N(s^-)(NK_i - X_i^N(s^-))_+} N_{j,i}(ds, du) \\
 & - \sum_{j \neq i} \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \frac{\theta_{i,j}}{N} X_i^N(s^-)(NK_j - X_j^N(s^-))_+} N_{i,j}(ds, du), \quad (2.39)
 \end{aligned}$$

for all $i \in \llbracket 1, n \rrbracket$, where the b_i, d_i and $\theta_{i,j}$ are nonnegative real numbers. For any $N \geq 1$, $(X^N(t))_{t \geq 0}$ is a \mathbb{Z}_+^n -valued jump process with initial value $X^N(0) = \lfloor Nz(0) \rfloor$ and the following transition rates under \mathbb{P} :

Transition	Rate at state x	
$x \rightarrow x + e_i$	$(B_i + \frac{b_i}{N} x_i)(NK_i - x_i)_+$	(1.5)
$x \rightarrow x - e_i$	$d_i x_i$	
$x \rightarrow x - e_i + e_j$	$\frac{\theta_{i,j}}{N} x_i(NK_j - x_j)_+$	

Table 2.3: Logistic population process jump rates chart.

X^N is therefore a $\prod_{i=1}^n \llbracket 0, \lfloor NK_i \rfloor \rrbracket$ -valued Markov jump process. Here the scaling parameter N intervenes in the carrying capacity NK_i of patches, which is quite intuitive since this capacity determines the maximal size of the system. It also appears in the birth coefficients $\frac{b_i}{N}$ and the transfer coefficients $\frac{\theta_{i,j}}{N}$, which is a purely technical condition so scaling limit Theorem 1.3.32 does apply.

Once again, we will assume that the directed graph with vertices set $\llbracket 1, n \rrbracket$ and edges set $\{(i, j) : \theta_{i,j} > 0\}$ is strongly connected, so that for any i and j , any individual born in node i can get to node j with positive probability during its lifetime. We also assume that $B = (B_1, \dots, B_n) \neq 0$, and that $d = (d_1, \dots, d_n) \neq 0$. These last conditions ensure that X^N is irreducible.

2.3.2 Stability and scaling limit of the logistic population process

From the irreducibility of the jump processes X^N with finite state space, we deduce the following straightforward result:

PROPOSITION 2.3.1 (Ergodicity of the logistic population process). — *Let $N \geq 1$. The logistic population process X^N is positive recurrent and exponentially ergodic.*

As in the case of the branching population model, Theorem 1.3.32 applies to yield a scaling limit over finite time intervals for processes X^N . Defining the dynamical system $(\mathcal{S}'_{\text{pop}})$ as

$$\forall i \in \llbracket 1, n \rrbracket, \quad \dot{z}_i = (B_i + b_i z_i)(K_i - z_i)_+ - d_i z_i + \sum_{j \neq i} \theta_{j,i} z_j (K_i - z_i)_+ - \sum_{j \neq i} \theta_{i,j} z_i (K_j - z_j)_+, \quad (\mathcal{S}'_{\text{pop}})$$

we obtain

PROPOSITION 2.3.2 (Scaling limit of a logistic population process). — Let $(X^N)_{N \geq 1}$ be the sequence of logistic population processes. Define z as the solution of the dynamical system $(\mathcal{S}'_{\text{pop}})$ with initial value $z(0)$. Then for any $T \geq 0$,

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{t \in [0, T]} \left\| \frac{X^N(t)}{N} - z(t) \right\|_{\infty} = 0 \right) = 1.$$

The behavior of $(\mathcal{S}'_{\text{pop}})$ is much less straightforward than that of the dynamical system $x' = Ax + B$ seen in the branching case. We derive the existence of an equilibrium for $(\mathcal{S}'_{\text{pop}})$ from Brouwer's fixed point theorem:

PROPOSITION 2.3.3 (Existence of an equilibrium for $(\mathcal{S}'_{\text{pop}})$). — $(\mathcal{S}'_{\text{pop}})$ admits an equilibrium $z^* \in \prod_{i=1}^n [0, K_i]$ (possibly not unique).

Proof of Proposition 2.3.3.— For any fixed $i \in \llbracket 1, n \rrbracket$ and any $z \in \mathbb{R}_+^n$, we denote by \tilde{z}^i the \mathbb{R}_+^{n-1} -vector $(z_1, \dots, z_{i-1}, z_{i+1}, \dots, z_n)$. For any given value of \tilde{z}^i , it is an easy matter to see that there exists a unique nonnegative solution $z_i = \rho_i(\tilde{z}^i)$ to the second-degree polynomial equation

$$(B_i + b_i z_i)(K_i - z_i)_+ - d_i z_i + \sum_{j \neq i} \theta_{j,i} z_j (K_i - z_i)_+ - \sum_{j \neq i} \theta_{i,j} z_i (K_j - z_j)_+ = 0$$

and that this solution lies within $[0, K_i]$. This defines continuous *response functions* $\rho_i : \mathbb{R}_+^{n-1} \rightarrow [0, K_i]$. Our aim is to show that there exists $z \in \prod_{i=1}^n [0, K_i]$ such that $z_i = \rho_i(\tilde{z}^i)$ for all $i \in \llbracket 1, n \rrbracket$, that is, a fixed point of

$$\Phi : \prod_{i=1}^n [0, K_i] \longrightarrow \prod_{i=1}^n [0, K_i] \\ x \longmapsto (\rho_1(\tilde{z}^1), \dots, \rho_n(\tilde{z}^n)) .$$

But Φ is continuous since the ρ_i and the $z \mapsto \tilde{z}^i$ projections are, so Brouwer's fixed point theorem shows that there indeed exists an equilibrium for $(\mathcal{S}'_{\text{pop}})$ in $\prod_{i=1}^n [0, K_i]$. \square

From the irreducibility of Θ and the fact that $d \neq 0$, we can easily see that z^* is necessarily interior to $\prod_{i=1}^n [0, K_i]$, that is, that $0 < z_i^* < K_i$ for all $i \in \llbracket 1, n \rrbracket$.

Numerical approximations of the deterministic population processes following $(\mathcal{S}'_{\text{pop}})$ suggest that z^* could be a unique, globally asymptotically stable equilibrium of $(\mathcal{S}'_{\text{pop}})$ (see Figure 2.5). When defining epidemic models coupled with a logistic population process, we will therefore assume that the population process quickly converges (just as in the branching case) and initiate the population dynamics in a neighborhood of the equilibrium. As a weaker result than Proposition 2.2.3 on population stability over time, the following Proposition will prove useful when studying long-term logistic-driven epidemic dynamics in Chapter 3.

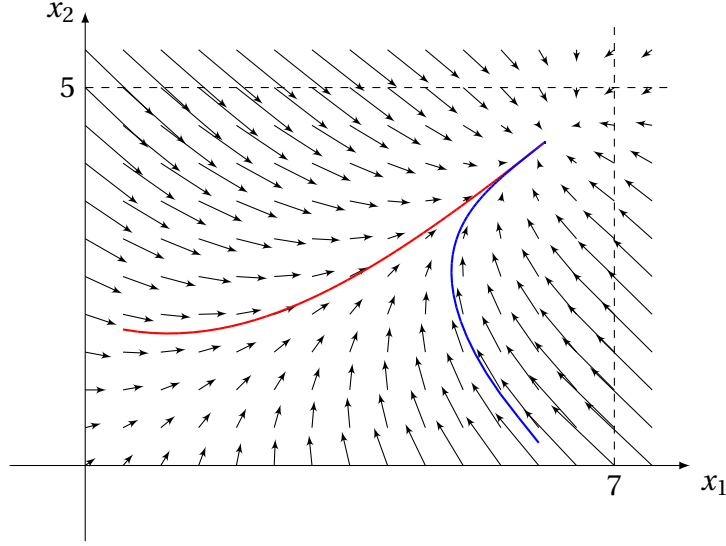


Figure 2.5: Vector field associated with $(\mathcal{S}'_{\text{pop}})$ with $n = 2$, $K_1 = 7$, $K_2 = 5$, $B_1 = B_2 = 1$, $b_1 = b_2 = 1$, $d_1 = d_2 = 1$, $\theta_{1,2} = \theta_{2,1} = 1$. The curve in red is a solution of $(\mathcal{S}'_{\text{pop}})$ with initial condition $x(0) = (.5, 1.8)$, and the curve in blue a solution with initial condition $x(0) = (6, .3)$.

PROPOSITION 2.3.4 (Lower bound for the scaled population). — *There exist positive constants ε and V such that whenever $\min_i z_i(0) \geq \varepsilon$ for every $i \in \llbracket 1, n \rrbracket$*

$$\lim_{N \rightarrow +\infty} \mathbb{P}(\forall t \in [0, e^{NV}], \min_i X_i^N(t) \geq N\varepsilon) = 1$$

It proceeds from Theorem 4 of [PSK17] with the same reasoning as in Section 7 of [KP18] adapted to the case of potentially multiple equilibria, using the fact that the vector field associated to $(\mathcal{S}'_{\text{pop}})$ on the boundary of $K_\varepsilon := \prod_{i=1}^n [\varepsilon, K_i]$ is directed towards the inside of K_ε when ε is small enough (see Figure 2.5 for an illustration in the case $n = 2$).

3

The epidemic model

The branching and the logistic population models defined in Chapter 2 are two ways of representing the evolution over time of cattle populations with local demographics and connected through animal trade. We now proceed to the definition of epidemic SIR processes on a network for which the total population of each node follows either a branching or a logistic population process, and in which animals are submitted to the same demographic dynamics regardless of their sanitary status. Section 3.1 states results for the case $n = 1$ (one single population), that allows for explicit calculations and simple characterizations of the behavior of the epidemic. In Section 3.2, we define two SIR models corresponding to each of the jump processes specifications presented in Chapter 2. Under the assumption that no immigration of infectives is allowed (Subsections 3.2.1.1 and 3.2.2.1), branching approximation results are then derived for both of these models, for which we compute the probability of a major epidemic outbreak and give a lower bound for the total size and extinction time of the epidemic when a stable endemic equilibrium exists. When infectives are allowed to enter the system through immigration (Subsections 3.2.1.2 and 3.2.2.2), we state approximation and stability results describing the persistence of the epidemic at an endemic level over long periods of time.

3.1

The unitype (one-population) case

We start by studying the branching-driven and logistic-driven epidemic models in the case of a single isolated population, that is, when $n = 1$. We will use this unitype case both as an introductory model and as a reference for studying holdings with no outflow in Chapter 4.

A formal definition of the branching-driven and logistic-driven SIR processes using Poisson random measures will be provided in Section 3.2. It is sufficient for the purpose of this preliminary study (Subsections 3.1.1 and 3.1.2) to provide with a more heuristic introduction.

3.1.1 The unitype branching-driven SIR model

We consider for every $N \geq 1$ a \mathbb{Z}_+^3 -valued pure Markovian jump process $(S^N(t), I^N(t), R^N(t))_{t \geq 0}$ defined on (Ω, \mathcal{A}) and described by the following transition rates at state (s, i, r) , where p, q, d, β

and γ are nonnegative real numbers such that $p + q \leq 1$, $B > 0$ and $d - b < 0$, and where $x = s + i + r$:

Transition	Rate	
$(s, i, r) \rightarrow (s + 1, i, r)$	$pNB + bx$	
$(s, i, r) \rightarrow (s, i + 1, r)$	qNB	
$(s, i, r) \rightarrow (s, i, r + 1)$	$(1 - p - q)NB$	
$(s, i, r) \rightarrow (s - 1, i, r)$	ds	(3.1)
$(s, i, r) \rightarrow (s, i - 1, r)$	di	
$(s, i, r) \rightarrow (s, i, r - 1)$	dr	
$(s, i, r) \rightarrow (s - 1, i + 1, r)$	$\beta \frac{is}{x}$	
$(s, i, r) \rightarrow (s, i - 1, r + 1)$	γi	

Table 3.1: Branching-driven SIR process rates chart.

It is easy to see that for any $N \geq 1$, $X^N := S^N + I^N + R^N$ is a unitype branching population jump process with rates as in Section 2.2. $(S^N(t), I^N(t), R^N(t))_{t \geq 0}$ models a population divided into three compartments S (for susceptibles), I (for infectives) and R (for removed) with respective populations $S^N(t)$, $I^N(t)$ and $R^N(t)$ at time t . Each infected individual makes contact are rate β with an individual chosen independently and uniformly from the total population. Contacted individuals that are still susceptible get infected; the their status of non-susceptible contacted individuals does not change. When infected, an individual recovers at rate γ . In addition, all individuals die at rate d and give birth to a new individual in compartment S at rate b (we assume that no vertical transmission of the disease occurs). Immigration occurs in the population at rate B , with a probability p for the new individual to arrive in compartment S, a probability q to arrive in compartment I, and a probability $1 - p - q$ to arrive in compartment R.

3.1.1.1 The case $p = 1$

In this entire subsection, we assume that $p = 1$ and therefore $q = 0$. In this case, only infected individuals that are present in the system at time $t = 0$ can initiate epidemic dynamics. Therefore, our main focus will be on the probability for an epidemic started by one initial infective to cause a major epidemic outbreak, and on the total size of the epidemic in this case, that is, the total number of infection transitions of the type $(s, i, r) \rightarrow (s - 1, i + 1, r)$ occurring before the process is absorbed by $\mathbb{Z}_+ \times \{0\} \times \mathbb{Z}_+$ (which we will refer to as the *extinction* of the epidemic). We therefore assume that $(S^N(0), I^N(0), R^N(0)) = (X^N(0) - I(0), I(0), 0)$ for some $I(0) \in \mathbb{Z}_+$ and for all $N \geq 1$ such that $X^N(0) = \lfloor Nx(0) \rfloor \geq I(0)$. The following results will be proved in the general multitype case in Section 3.2.1:

THEOREM 3.1.1 (Finite-time convergence to a multitype branching process (branching case)). — *It is possible to define the (S^N, I^N, R^N) processes such that there exists a \mathbb{Z}_+^n -valued multitype branching process $(I'(t))_{t \geq 0}$ on $(\Omega, \mathcal{A}, \mathbb{P})$ with $I'(0) = I(0)$ describing a population of individuals giving birth at rate β and dying at rate $d + \gamma$, such that for any time $T \geq 0$,*

\mathbb{P} -almost surely:

$$\exists N_0 \in \mathbb{Z}_+^* : \forall N \geq N_0, \forall u \in [0, T], \quad I^N(u) = I'(u).$$

In particular, if τ^N (resp. Z^N) denotes the extinction time (resp. total size) of the epidemic and τ' (resp. Z') that of the branching process, then

$$\tau^N \xrightarrow{N \rightarrow +\infty} \tau' \quad \text{and} \quad Z^N \xrightarrow{N \rightarrow +\infty} Z' \quad (3.2)$$

\mathbb{P} -almost surely.

We say that the epidemic undergoes a *major outbreak* whenever $Z' = +\infty$ and a *minor outbreak* otherwise. The theorem above indicates that in the case of a major outbreak the total size of the epidemic goes to infinity with N , and that it is bounded in the case of a minor outbreak. The probability of major outbreak $\mathbb{P}(Z' = +\infty)$ is therefore a quantity of paramount interest. It is given by the following result:

PROPOSITION 3.1.2 (Major outbreak probability (unitype branching case)). — *Let W denote the number of offspring of an individual in the branching process I' . Then:*

1. $R_0 := \mathbb{E}(W) = \frac{\beta}{d+\gamma}$.
2. The branching process I' is subcritical if $R_0 < 1$, critical if $R_0 = 1$ and supercritical if $R_0 > 1$.
3. If the branching process I' is subcritical or critical, then the major outbreak probability is 0. If it is supercritical, then this probability is strictly positive and equals $1 - \zeta^{1(0)}$, where ζ is the only fixed point in $[0, 1)$ of the moment generating function

$$G: [0, 1] \longrightarrow [0, 1] \\ s \longmapsto \frac{\gamma+d}{(1-s)\beta+d+\gamma},$$

that is,

$$\zeta = \frac{d+\gamma}{\beta}.$$

Theorem 3.1.1 states that the total size Z^N of the epidemic almost surely goes to infinity with N on the part of the sample space where the approximating branching process I' does not get extinct. A standard result on the unidimensional SIR model without demography states that Z^N satisfies a central limit theorem conditionally on a major outbreak occurring (see Chapter 4 of [AB00a]). In such closed frameworks, major outbreaks are characterized by a positive fraction of the population being affected by the epidemic at some point in time ([Sca90, AB00a], and see [BC93] for a multidimensional generalization) when individuals cannot enter or leave the system. In our open setting, we will see in the study of the general multitype case that on the event of a major outbreak, the maximal number of infectives during the course of the epidemic is *at least* equal to a fraction of N with high probability as N goes to infinity when the

population process starts at its equilibrium value. Although this type of bound is the general rule in closed population models, it happens to be quite bad in cases where susceptible population renewal through demographic mechanisms is strong enough to entail endemicity. This latter phenomenon has been thoroughly investigated for deterministic systems in the single-population case (see the deterministic approximations in [AB00b, Nå99, VHG95, VH97]); in our stochastic framework, we may reasonably expect an increase of N to affect both the typical infective population during the course of the epidemic and the time scale of the endemic period, thus resulting in a more than proportional total size response.

Defining the dynamical system

$$\left. \begin{aligned} \dot{s} &= B + b(s + i + r) - ds - \beta i \frac{s}{s+i+r} \\ \dot{i} &= \beta i \frac{s}{s+i+r} - di - \gamma i \\ \dot{r} &= \gamma i - dr \end{aligned} \right\} (\mathcal{S}_{\text{epi}}^{1,0})$$

we obtain the following:

PROPOSITION 3.1.3 (Equilibrium for $(\mathcal{S}_{\text{epi}}^{1,0})$). — Assume that $\beta > d + \gamma$. Then any solution (s, i, r) of $(\mathcal{S}_{\text{epi}}^{1,0})$ such that $i(0) > 0$ converges to the endemic steady state

$$(s^*, i^*, r^*) = \left(\frac{d+\gamma}{\beta} x^*, dx^* \left(\frac{1}{d+\gamma} - \frac{1}{\beta} \right), \gamma x^* \left(\frac{1}{d+\gamma} - \frac{1}{\beta} \right) \right),$$

where $x^* := \frac{B}{d-b}$.

Proof of Proposition 3.1.3.— It is not difficult to see that $\beta > d + \gamma$ is a necessary and sufficient condition for the existence of an endemic equilibrium for $(\mathcal{S}_{\text{epi}}^{1,0})$ and that the latter is precisely (s^*, i^*, r^*) (see [Nå99] for the study of a similar model). If $s(0) + i(0) + r(0) = x^* := \frac{B}{d-b}$, then the total population is constant and equal to x^* so we can get rid of the third line of $(\mathcal{S}_{\text{epi}}^{1,0})$ and the dynamical system can be seen as a Lotka-Volterra prey-predator model (where preys are susceptibles and predators are infectives, see [Vol28]) with prey immigration. For any initial condition in $\mathbb{R}_+ \times \mathbb{R}_+^* \times \mathbb{R}_+$, standard arguments (see [Vol28]) show that s, i and r are well-defined on \mathbb{R}_+ and positive. Moreover, $s + i + r$ converges to $s^* + i^* + r^* = x^*$, so it is sufficient to show that (s, i) converges to (s^*, i^*) . Setting

$$V(t) = s(t) - s^* \log(s(t)) + i(t) - i^* \log(i(t))$$

for all $t \geq 0$ yields, after a few calculations:

$$\dot{V}(t) = \underbrace{(B + b(s + i + r)(t)) \left(2 - \frac{s^*}{s(t)} - \frac{s(t)}{s^*} \right)}_{\leq 0} + \underbrace{b(x^* - (s + i + r)(t)) \left(1 - \frac{s(t)}{s^*} \right)}_{=O(x^* - (s+i+r)(t)) = O(e^{(b-d)t}}$$

Now, if $s(0) + i(0) + r(0) \leq 2x^*$, V is lower bounded by $-2x^* |\log(4x^*)| > -\infty$, so for any $\eta > 0$ its derivative cannot be lower than $-\eta$ for an infinite amount of time. As a result, for any $\delta > 0$ we

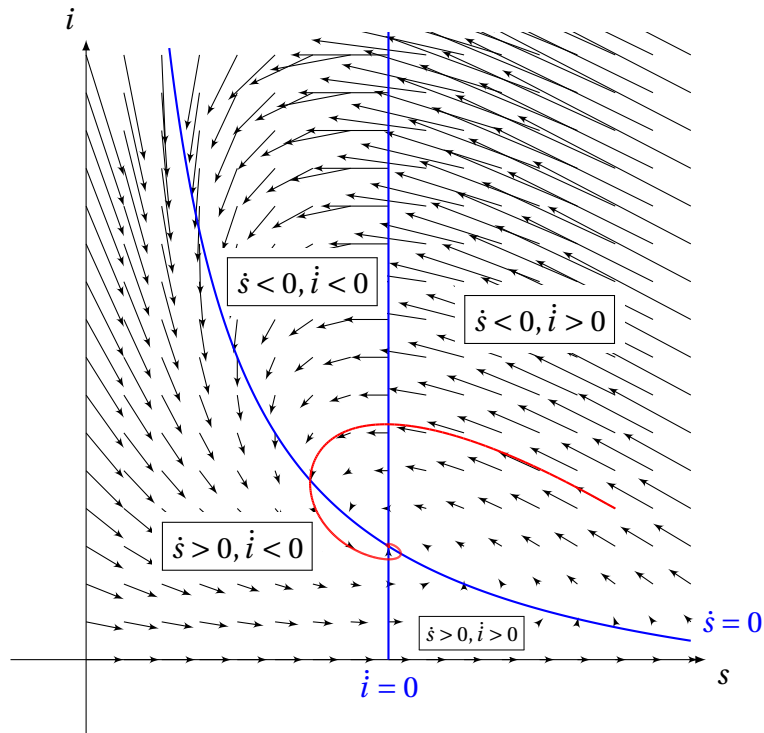


Figure 3.1: Projection on the (s, i) plane of the vector field associated with $(\mathcal{S}_{\text{epi}}^{1,0})$ with constant population $x^* = 10$, $B = 5$, $d = 1$, $b = .5$, $\beta = 1$ and $\gamma = 3$. Blue curves are nullclines for s^* and i^* .

The red curve is the solution of $(\mathcal{S}_{\text{epi}}^{1,0})$ starting from point $(7, 2)$.

may only have $s(t) \notin [s^* - \delta, s^* + \delta]$ for a finite amount of time because $B + b(s + i + r)$ is greater than $B > 0$ and because $\int_0^{+\infty} b(x^* - (s + i + r)(t)) \left(1 - \frac{s(t)}{s^*}\right) dt$ is finite. This entails that s cannot cross $[s^* - 2\delta, s^* - \delta]$ or $[s^* + \delta, s^* + 2\delta]$ an infinite number of times since \dot{s} is bounded because of $(\mathcal{S}_{\text{epi}}^{1,0})$. Therefore $s(t)$ lies in $[s^* - \delta, s^* + \delta]$ for t large enough, so s does converge to s^* . Similar arguments yield the convergence of i towards i^* using the first equation of $(\mathcal{S}_{\text{epi}}^{1,0})$. \square

The vector field associated with $(\mathcal{S}_{\text{epi}}^{1,0})$ is represented in Figure 3.1.

Theorem 1.3.32 states that the scaling limit of (S^N, I^N, R^N) is a solution of $(\mathcal{S}_{\text{epi}}^{1,0})$ when the initial number of infectives is a proportion of N . This is not the case here since we assumed that $I^N(0) = I(0)$ did not depend on N , but knowing that I^N goes above a proportion of N with high probability conditionally on the event of major outbreak makes it possible to conclude. In the case where the epidemics takes off, that is, conditionally to a major outbreak event, the scaled epidemic process $(S^N, I^N, R^N)/N$ observed after the number of infectives reaches this proportion of N converges on finite time intervals to a solution of (s^*, i^*, r^*) , and then approaches the endemic steady state described in Proposition 3.1.3. Metastability results from Section 1.3.4.2 then give an estimation of the time needed for the scaled process to leave a ball centered on this steady state. This entails a lower bound for the extinction time and the final size of the epidemic:

THEOREM 3.1.4 (Outcome of a unitype branching-driven epidemic). — Assume that $\beta > d + \gamma$. Then there exists $V > 0$ such that:

$$\lim_{N \rightarrow +\infty} \mathbb{P}(\tau^N > e^{VN} | Z' = +\infty) = 1 \quad (3.3)$$

and

$$\lim_{N \rightarrow +\infty} \mathbb{P}(Z^N > e^{VN} | Z' = +\infty) = 1. \quad (3.4)$$

3.1.1.2 The case $q > 0$

When $q > 0$, a positive proportion of infectives enter the system through immigration. Studying the major outbreak probability for an epidemic started by a fixed number of individuals is not relevant anymore since the mean number of infectives entering the system through immigration per unit of time is proportional to N . The concepts of epidemic extinction time and total size do not transpose either. However, scaling limit Theorem 1.3.32 shows that if we consider an initial population of infectives that is proportional to N , that is, $I^N(0) = \lfloor NI(0) \rfloor$ for some $I(0) \geq 0$ (possibly zero), the scaled epidemic processes converge almost surely on finite time intervals to a solution of a dynamical system that itself converges to the unique equilibrium point of this system.

More precisely, defining the dynamical system

$$\left. \begin{aligned} \dot{s} &= pB + b(s+i+r) - ds - \beta i \frac{s}{s+i+r} \\ \dot{i} &= qB + \beta i \frac{s}{s+i+r} - di - \gamma i \\ \dot{r} &= (1-p-q)B + \gamma i - dr \end{aligned} \right\} \quad (\mathcal{S}_{\text{epi}}^1)$$

on \mathbb{R}_+^3 (with $\frac{s}{s+i+r} = 0$ when $s = i = r = 0$), we obtain the following:

PROPOSITION 3.1.5 (Equilibrium for $(\mathcal{S}_{\text{epi}}^1)$). — $(\mathcal{S}_{\text{epi}}^1)$ admits a unique equilibrium $(s^*, i^*, r^*) \in \mathbb{R}_+^3$, that is globally asymptotically stable and such that $s^* + i^* + r^* = x^*$ and

$$i^* = \frac{2qBdx^*}{\sqrt{[(\gamma+d)dx^* - \beta((p+q)B + bx^*)]^2 + 4\beta(\gamma+d)qBdx^* + (\gamma+d)dx^* - \beta((p+q)B + bx^*)}}$$

where we recall that $x^* = \frac{B}{d-b}$.

Proof of Proposition 3.1.5.— We first notice that $s+i+r = x$ admits x^* for unique equilibrium value and that any equilibrium (s^*, i^*, r^*) of $(\mathcal{S}_{\text{epi}}^1)$ is such that $i^* > 0$ since $q > 0$. Solving

$$\frac{s}{x^*} = \frac{\gamma+d}{\beta} - \frac{qB}{\beta i} = \frac{pB + bx^*}{dx^* + \beta i}$$

yields both the existence and the unicity of (s^*, i^*, r^*) . To show the convergence of (s, i, r) towards (s^*, i^*, r^*) , we set

$$V(t) = s(t) - s^* \log(s(t)) + i(t) - i^* \log(i(t))$$

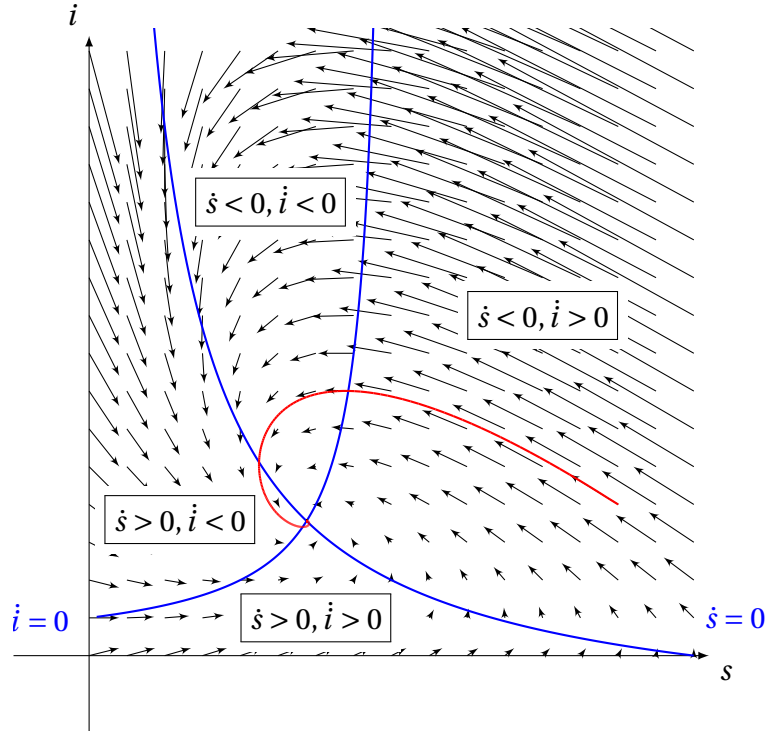


Figure 3.2: Projection on the (s, i) plane of the vector field associated with $(\mathcal{S}_{\text{epi}}^1)$ with constant population $x^* = 10$, $p = .6$, $q = .4$, $B = 5$, $d = 1$, $b = .5$, $\beta = 1$ and $\gamma = 3$. Blue curves are nullclines for s^* and i^* . The red curve is the solution of $(\mathcal{S}_{\text{epi}}^{1,0})$ starting from point $(7, 2)$.

for all $t \geq 0$ as in the proof of Proposition 3.1.3, derive

$$\dot{V}(t) = \underbrace{(B + b(s + i + r)(t)) \left(2 - \frac{s^*}{s(t)} - \frac{s(t)}{s^*} \right) + qB \left(2 - \frac{i^*}{i(t)} - \frac{i(t)}{i^*} \right)}_{\leq 0} + \underbrace{b(x^* - (s + i + r)(t)) \left(1 - \frac{s(t)}{s^*} \right)}_{=O(x^* - (s+i+r)(t))=O(e^{(b-d)t})}$$

and conclude as in the proof of Proposition 3.1.3. \square

The vector field associated with $(\mathcal{S}_{\text{epi}}^1)$ is represented in Figure 3.2.

The scaled epidemic process converges towards a solution of $(\mathcal{S}_{\text{epi}}^1)$ that reaches any ball centered on the equilibrium given by Proposition 3.1.5 in finite time. Results from Subsection 1.3.4.2 state that the time it takes to the scaled process to exit this ball grows exponentially with N . From the strong Markov property, we deduce that the scaled process observed from the moment it exits the ball converges again to a solution of $(\mathcal{S}_{\text{epi}}^1)$, that enters the ball again in finite time, then takes an exponential time to exit it and so on. We therefore have the following result, stating that over appropriate time scales the scaled process spends "most of its time" in a ball centered on the equilibrium.

PROPOSITION 3.1.6 (Time spent in a neighborhood of the equilibrium of $(\mathcal{S}_{\text{epi}}^1)$). — Assume that $I^N(0) = \lfloor NI(0) \rfloor$ for all $N \geq 1$. Then for every $\varepsilon > 0$ there exist $T > 0$ and $V > 0$ such that:

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(\int_0^{T+e^{VN}} \mathbf{1}_{\frac{(S^N(t), I^N(t), R^N(t))}{N} \in \mathcal{B}_2((s^*, i^*, r^*), \varepsilon)} dt > e^{VN} \right) = 1,$$

where (s^*, i^*, r^*) is the equilibrium given by Proposition 3.1.5.

This proposition is proved in the general multitype case in the next section. It suggests that the value of i (and in the general case, of $\|i\|_1$) at the equilibrium of $(\mathcal{S}_{\text{epi}}^1)$ is a relevant quantity to evaluate the outcome of an epidemic whenever immigration of infectives is allowed by the model.

3.1.2 The unitype logistic-driven SIR model

Results on the unitype logistic-driven SIR model are parallel to these on the unitype branching-driven SIR model we just presented. What opposes these two models are their demographic dynamics, that do not affect the form of the limiting branching process when the population process is started from the equilibrium.

We consider for every $N \geq 1$ a \mathbb{Z}_+^3 -valued pure Markovian jump process $(S^N(t), I^N(t), R^N(t))_{t \geq 0}$ defined on (Ω, \mathcal{A}) and described by the following transition rates at state (s, i, r) , where p, q, d, β and γ are nonnegative real numbers such that $p + q \leq 1$, $B > 0$ and $K > 0$, and where $x = s + i + r$:

Transition	Rate	
$(s, i, r) \rightarrow (s + 1, i, r)$	$\left(pB + \frac{b}{N}x\right)(NK - x)_+$	
$(s, i, r) \rightarrow (s, i + 1, r)$	$qB(NK - x)_+$	
$(s, i, r) \rightarrow (s, i, r + 1)$	$(1 - p - q)B(NK - x)_+$	
$(s, i, r) \rightarrow (s - 1, i, r)$	ds	(3.5)
$(s, i, r) \rightarrow (s, i - 1, r)$	di	
$(s, i, r) \rightarrow (s, i, r - 1)$	dr	
$(s, i, r) \rightarrow (s - 1, i + 1, r)$	$\beta \frac{is}{x}$	
$(s, i, r) \rightarrow (s, i - 1, r + 1)$	γi	

Table 3.2: Logistic-driven SIR process rates chart.

It is again easy to see that for any $N \geq 1$, $X^N := S^N + I^N + R^N$ is a unitype logistic population jump process as defined in Section 2.3.

3.1.2.1 The case $p = 1$

As in Subsection 3.1.1.1, we assume that $p = 1$ (so $q = 0$), and that $(S^N(0), I^N(0), R^N(0)) = (X^N(0) - I(0), I(0), 0)$ for some $I(0) \in \mathbb{Z}_+^*$ and for all $N \geq 1$ such that $X^N(0) = \lfloor Nz(0) \rfloor \geq I(0)$. Simple calculations show that the equilibrium value z^* of the logistic dynamical system $\dot{z} = (B + bz)(K - z)_+ - dz$ is

$$z^* = \frac{bK - d - B + \sqrt{(bK - d - B)^2 + 4KbB}}{2b}.$$

We get the following:

THEOREM 3.1.7 (Branching approximation, unitype logistic case). — *Theorems 3.1.1 and 3.1.2 are true, with the additional requirement that $z(0) = z^*$.*

Defining the dynamical system

$$\left. \begin{aligned} \dot{s} &= (B + b(s + i + r))(K - (s + i + r))_+ - ds - \beta i \frac{s}{s+i+r} \\ \dot{i} &= \beta i \frac{s}{s+i+r} - di - \gamma i \\ \dot{r} &= \gamma i - dr \end{aligned} \right\} \quad (\mathcal{S}_{\text{epi}}^{/1,0})$$

on \mathbb{R}_+^3 , we can show the existence, uniqueness and stability of an endemic equilibrium for $(\mathcal{S}_{\text{epi}}^{/1,0})$:

PROPOSITION 3.1.8 (Equilibrium for $(\mathcal{S}_{\text{epi}}^{/1,0})$). — *Assume $\beta > d + \gamma$. Then any solution (s, i, r) of $(\mathcal{S}_{\text{epi}}^{/1,0})$ such that $i(0) > 0$ converges to the endemic steady state*

$$(s^*, i^*, r^*) = \left(\frac{d+\gamma}{\beta} z^*, \frac{(B+bz^*)(K-z^*)}{d+\gamma} - \frac{dz^*}{\beta}, \frac{\gamma(B+bz^*)(K-z^*)}{d(d+\gamma)} - \frac{\gamma z^*}{\beta} \right)$$

The proof for this result is the same as that of Proposition 3.1.5 once noticed that $s + i + r$ necessarily converges to z^* as in the original logistic population model associated with the dynamical system $\dot{z} = (B + bz)(K - z)_+ - dz$ [Ver38].

The vector field associated with $(\mathcal{S}_{\text{epi}}^{/1,0})$ is represented in Figure 3.3.

The same reasoning as in the branching case yields the following:

THEOREM 3.1.9 (Outcome of a unitype logistic-driven epidemic). — *Assume that $\beta > d + \gamma$. Then there exists $V' > 0$ such that:*

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(\tau^N > e^{V'N} \mid Z' = +\infty \right) = 1 \quad (3.6)$$

and

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(Z^N > e^{V'N} \mid Z' = +\infty \right) = 1. \quad (3.7)$$

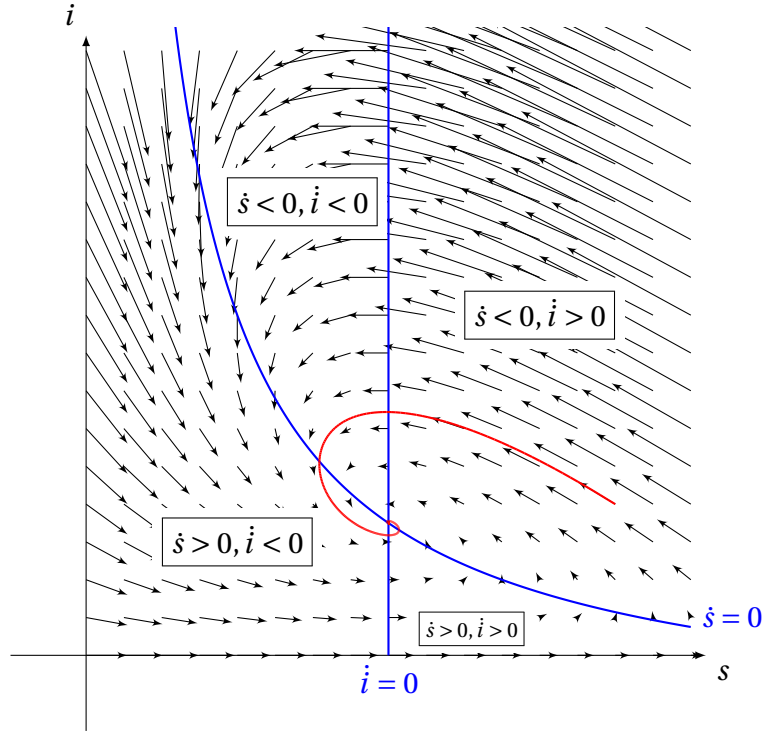


Figure 3.3: Projection on the (s, i) plane of the vector field associated with $(\mathcal{S}_{\text{epi}}^{1,0})$ with constant population $z^* = 10$, $K = 11$, $B = 5$, $d = 1$, $b = .5$, $\beta = 1$ and $\gamma = 3$. Blue curves are nullclines for s^* and i^* . The red curve is the solution of $(\mathcal{S}_{\text{epi}}^{1,0})$ starting from point $(7, 2)$.

3.1.2.2 The case $q > 0$

Assume that $q > 0$. Defining the dynamical system

$$\left. \begin{aligned} \dot{s} &= (pB + b(s+i+r))(K - (s+i+r))_+ - ds - \beta i \frac{s}{s+i+r} \\ \dot{i} &= qB(K - (s+i+r))_+ + \beta i \frac{s}{s+i+r} - di - \gamma i \\ \dot{r} &= (1-p-q)B(K - (s+i+r))_+ + \gamma i - dr \end{aligned} \right\} (\mathcal{S}_{\text{epi}}^{1,1})$$

we have the following convergence result.

PROPOSITION 3.1.10 (Equilibrium for $(\mathcal{S}_{\text{epi}}^{1,1})$). — $(\mathcal{S}_{\text{epi}}^{1,1})$ admits a unique equilibrium (s^*, i^*, r^*) , that is globally asymptotically stable and such that

$$i^* = \frac{2qBdz^*(K - z^*)}{\sqrt{\Delta} + (\gamma + d)dz^*(K - z^*) - \beta((p+q)B + bz^*)(K - z^*)},$$

where $\Delta := [(\gamma + d)dz^* - \beta((p+q)B + bz^*)(K - z^*)]^2 + 4\beta(\gamma + d)qBdz^*(K - z^*)$.

The vector field associated with $(\mathcal{S}_{\text{epi}}^1)$ is represented in Figure 3.4.

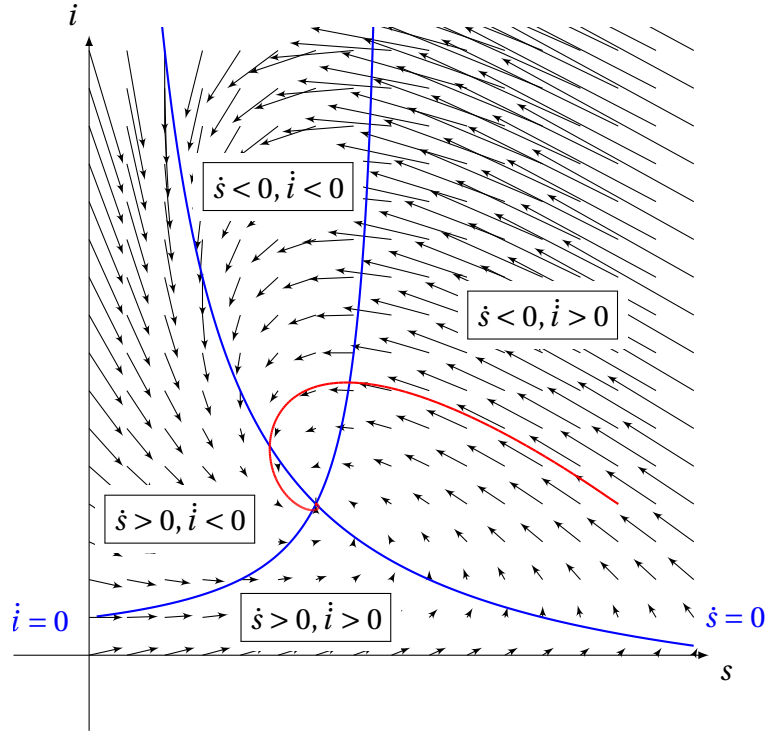


Figure 3.4: Projection on the (s, i) plane of the vector field associated with $(\mathcal{S}_{\text{epi}}^1)$ with constant population $z^* = 10$, $K = 11$, $p = .6$, $q = .4$, $B = 5$, $d = 1$, $b = .5$, $\beta = 1$ and $\gamma = 3$. Blue curves are nullclines for s^* and i^* . The red curve is the solution of $(\mathcal{S}_{\text{epi}}^{1,0})$ starting from point $(7, 2)$.

Finally, we can state a counterpart to Proposition 3.1.6:

PROPOSITION 3.1.11 (Time spent in a neighborhood of the equilibrium of $(\mathcal{S}_{\text{epi}}^1)$). — Assume that $I^N(0) = [NI(0)]$ for all $N \geq 1$. Then for every $\varepsilon > 0$ there exist $T > 0$ and $V' > 0$:

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(\int_0^{T+e^{V'N}} \mathbf{1}_{\frac{(S^N(t), I^N(t), R^N(t))}{N} \in \mathcal{B}_2((s^*, i^*, r^*), \varepsilon)} dt > e^{V'N} \right) = 1,$$

where (s^*, i^*, r^*) is the equilibrium given by Proposition 3.1.10.

3.2

The multitype case

Let us now turn to the general case, that is, to the definition and study of multitype epidemic processes coupled with the branching and logistic population models introduced in Chapter 2. Most results we presented for the unitype case still hold with an increased notational sophistication, but multitype models tend to prove less tractable and we must rely on numerical approximations for major outbreak probabilities and for the equilibria of the dynamical systems involved. Moreover, the uniqueness and global attractivity of such equilibria have not (yet) been established.

3.2.1 The branching-driven SIR model

Let us write the canonical basis of \mathbb{R}^{3n} as $(e_1^s, \dots, e_n^s, e_1^i, \dots, e_n^i, e_1^r, \dots, e_n^r)$. Let the B_i, b_i, d_i and $\theta_{i,j}$ be parameters abiding fulfilling the requirements of Section 2.2. Finally, for any $i \in \llbracket 1, n \rrbracket$, let $\beta_i, \gamma_i, p_i, q_i$ and r_i be nonnegative parameters such that $p_i + q_i + r_i = 1$.

We want to define a (S^N, I^N, R^N) process modeling a metapopulation on n patches divided each into three compartments S (for susceptibles), I (for infectives) and R (for removed) with respective populations $S_i^N(t), I_i^N(t)$ and $R_i^N(t)$ at time t . Each infected individual in node i makes a contact at rate β with an individual chosen independently and uniformly from the population of node i . Contacted individuals that are still susceptible get infected; otherwise their status does not change. No contact between individuals of different nodes occurs. When infected, an individual in node i recovers at rate γ_i . In addition, all individuals in node i die at rate d_i , give birth to new individuals in compartment S at rate b_i and migrate to node j at rate $\theta_{i,j}$. Immigration occurs in node i population at rate B_i , with a probability p_i for the new individual to arrive in compartment S, a probability q_i to arrive in compartment I, and a probability r_i to arrive in compartment R.

Definition of the epidemic process

Just as in the unitype case, when $p = \mathbb{1}$ we will be particularly interested in the probability for an epidemic started by a fixed number of initial infectives (typically one) to take off and cause a major epidemic outbreak, defined as the event of non-extinction of an approximating branching process. We therefore want to provide with a formal definition of the branching-driven SIR process that will make branching approximations of the epidemic dynamics straightforward. The strategy followed by [Cla96] in a closed framework with mobile populations is to first define a (limiting) branching process I' , then tweak its rates to obtain the various epidemic processes (S^N, I^N, R^N) . We will follow another approach and define all processes through a single set of Poisson point measures, which will both result in a lighter formalism and in easier computations.

We recall from the definition of the X^N processes from Subsection 2.2 that the N_i^B , N_i^b , N_i^d , N_i^β , N_i^Y and $N_{i,j}$ are independent Poisson random measures on $\mathbb{R}_+ \times \mathbb{R}_+$ with intensity $ds du$.

For any N , we define (S_i^N, I_i^N, R_i^N) as the solution of

$$\begin{aligned} S_i^N(t) = & \lfloor Nx_i(0) \rfloor - I_i^N(0) + \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{q_i \text{NB}_i < u \leq (p_i + q_i) \text{NB}_i} N_i^B(du, ds) \\ & + \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq b_i X_i^N(s^-)} N_i^b(du, ds) - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{d_i I_i^N(s^-) < u \leq d_i (S_i^N(s^-) + I_i^N(s^-))} N_i^d(du, ds) \\ & - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \beta_i I_i^N(s^-) \frac{S_i^N(s^-)}{X_i^N(s^-)}} N_i^\beta(du, ds) \\ & + \sum_{j \neq i} \left[\int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{\theta_{j,i} I_j^N(s^-) < u \leq \theta_{j,i} (S_j^N(s^-) + I_j^N(s^-))} N_{j,i}(du, ds) \right. \\ & \left. - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{\theta_{i,j} I_i^N(s^-) < u \leq \theta_{i,j} (S_i^N(s^-) + I_i^N(s^-))} N_{i,j}(du, ds) \right], \end{aligned}$$

$$\begin{aligned} I_i^N(t) = & I_i^N(0) + \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq q_i \text{NB}_i} N_i^B(du, ds) - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq d_i I_i^N(s^-)} N_i^d(du, ds) \\ & + \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \beta_i I_i^N(s^-) \frac{S_i^N(s^-)}{X_i^N(s^-)}} N_i^\beta(du, ds) - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \gamma_i I_i^N(s^-)} N_i^Y(du, ds) \\ & + \sum_{j \neq i} \left[\int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \theta_{j,i} I_j^N(s^-)} N_{j,i}(du, ds) - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \theta_{i,j} I_i^N(s^-)} N_{i,j}(du, ds) \right], \end{aligned}$$

and

$$\begin{aligned} R_i^N(t) = & \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{(p_i + q_i) \text{NB}_i < u \leq \text{NB}_i} N_i^B(du, ds) + \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \gamma_i I_i^N(s^-)} N_i^Y(du, ds) \\ & - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{d_i (S_i^N(s^-) + I_i^N(s^-)) < u \leq d_i X_i^N(s^-)} N_i^d(du, ds) \\ & + \sum_{j \neq i} \left[\int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{\theta_{j,i} (S_j^N(s^-) + I_j^N(s^-)) < u \leq \theta_{j,i} X_j^N(s^-)} N_{j,i}(du, ds) \right. \\ & \left. - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{\theta_{i,j} (S_i^N(s^-) + I_i^N(s^-)) < u \leq \theta_{i,j} X_i^N(s^-)} N_{i,j}(du, ds) \right] \end{aligned}$$

for all i and all t . Considering Equation 2.32, it is easy to see that $S^N + I^N + R^N = X^N$.

The (S^N, I^N, R^N) are jump processes on \mathbb{Z}_+^{3n} with transition rates given by the following chart, where $x_j = s_j + i_j + r_j$ for all $j \in \llbracket 1, n \rrbracket$:

Transition	Rate	
$(s, i, r) \rightarrow (s, i, r) + e_j^s$	$p_j \text{NB}_j + b_j x_j$	
$(s, i, r) \rightarrow (s, i, r) + e_j^i$	$q_j \text{NB}_j$	
$(s, i, r) \rightarrow (s, i, r) + e_j^r$	$r_j \text{NB}_j$	
$(s, i, r) \rightarrow (s, i, r) - e_j^s$	$d_j s_j$	
$(s, i, r) \rightarrow (s, i, r) - e_j^i$	$d_j i_j$	
$(s, i, r) \rightarrow (s, i, r) - e_j^r$	$d_j r_j$	(3.8)
$(s, i, r) \rightarrow (s, i, r) + e_k^s - e_j^s$	$\theta_{j,k} s_j$	
$(s, i, r) \rightarrow (s, i, r) + e_k^i - e_j^i$	$\theta_{j,k} i_j$	
$(s, i, r) \rightarrow (s, i, r) + e_k^r - e_j^r$	$\theta_{j,k} r_j$	
$(s, i, r) \rightarrow (s, i, r) + e_j^i - e_j^s$	$\beta_j \frac{i_j s_j}{x_j}$	
$(s, i, r) \rightarrow (s, i, r) + e_j^r - e_j^i$	$\gamma_j i_j$	

Table 3.3: Branching-driven SIR process rates chart ($p = \mathbb{1}$).

The properties of the epidemic process differs according to whether we assume or not that infectives can enter the system through immigration. We therefore devote the two next subsections to each of these two cases.

3.2.1.1 The case $p = \mathbb{1}$

Let us first consider the case where all p_i equal 1 (so $q_i = r_i = 0$ for all i), which corresponds to the assumption that all imported animals have the Susceptible health status. In all this section, we assume that the initial quantity of infectives is fixed, that is, that $I^N(0) = I(0) \in \mathbb{Z}_+^n$.

Branching approximation of the epidemic process

We define the multitype branching process I' as the solution of the integral equation

$$\begin{aligned}
 I'_i(t) = I_i(0) &- \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq d_i I'_i(s^-)} N_i^d(\mathbf{d}u, \mathbf{d}s) \\
 &+ \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \beta_i I'_i(s^-)} N_i^\beta(\mathbf{d}u, \mathbf{d}s) - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \gamma_i I'_i(s^-)} N_i^\gamma(\mathbf{d}u, \mathbf{d}s) \\
 &+ \sum_{j \neq i} \left[\int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \theta_{j,i} I'_j(s^-)} N_{j,i}(\mathbf{d}u, \mathbf{d}s) - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \theta_{i,j} I'_i(s^-)} N_{i,j}(\mathbf{d}u, \mathbf{d}s) \right],
 \end{aligned}$$

for all i and all t . I' is a \mathbb{Z}_+^n -valued multitype branching process with birth rates vector β , death rates vector $d + \gamma$ and transition rates matrix $\Theta = (\theta_{i,j})_{i,j \in \llbracket 1, n \rrbracket}$.

Our fundamental approximation result is the following Theorem. Heuristically, it relies on the fact that when N is large, so is the typical population in each node, with a proportion of susceptibles tending to one within the first infection events (remind that $I^N(0) = I(0)$ is independent from N and that $R^N(0) = 0$). Therefore, contacts made by infectives within their current node on a finite time interval have a high probability of actually being infectious (that is, to hit a susceptible individual). But the epidemic propagates like the branching process I' as long as no infective makes a contact with a non-susceptible individual, so I^N and I' coincide up to this time, that goes to infinity with N :

THEOREM 3.2.1 (Finite-time convergence to a branching process). — \mathbb{P} -almost surely:

$$\exists N_0 \in \mathbb{Z}_+^* : \forall N \geq N_0, \forall u \in [0, T], \quad I^N(u) = I'(u).$$

In particular, if τ^N (resp. Z^N) denotes the extinction time (resp. total size) of the epidemic and τ' (resp. Z') that of the branching process, then

$$\tau^N \xrightarrow{N \rightarrow +\infty} \tau' \quad \text{and} \quad Z^N \xrightarrow{N \rightarrow +\infty} Z' \quad (3.9)$$

\mathbb{P} -almost surely.

The quantity

$$\int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{\beta_i I'_i(s^-) \frac{S_i^N(s^-)}{X_i^N(s^-)} < u \leq \beta_i I'_i(s^-)} N_i^\beta(du, ds)$$

is the number of infections in node i occurred for the branching process I and not for the epidemic process I^N at time t . These infections, that correspond to contacts made by infectious individuals with non-susceptible ones, are called *ghost infections* [Mol77, Cla96]. The proof below relies on the idea that almost surely, the number of ghost infections before time t is zero for N large enough.

Proof of Theorem 3.2.1.— Processes I^N and I' coincide up to the smallest $t \geq 0$ such that

$$\int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{\beta_i I'_i(s^-) \frac{S_i^N(s^-)}{X_i^N(s^-)} < u \leq \beta_i I'_i(s^-)} N_i^\beta(du, ds) > 0$$

for some i . Now if $I_i^+(s)$ denotes the total number of births in node i for the branching process I' up to time s , is it straightforward that for any fixed t ,

$$\frac{S_i^N(s^-)}{X_i^N(s^-)} \geq \frac{X_i^N(s^-) - I_i(0) - I_i^+(s^-)}{X_i^N(s^-)} \xrightarrow{N \rightarrow +\infty} 1,$$

uniformly for $s \in [0, t]$. Therefore, for any fixed $T > 0$, almost surely one has:

$$\exists N_0 \geq 0 : \forall N \geq N_0, \forall t \leq T, \quad \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{\beta_i I'_i(s^-) \frac{S_i^N(s^-)}{X_i^N(s^-)} < u \leq \beta_i I'_i(s^-)} N_i^\beta(du, ds) = 0$$

by the dominated convergence theorem since $\int_0^T \int_{\mathbb{R}_+} 1_{u \leq \beta_i I_i(s^-)} N_i^\beta(du, ds)$ is almost surely finite and does not depend on N , which yields the first part of the Theorem.

To see that (3.9) holds, write that with probability 1,

$$\forall T \geq 0, \quad \exists N_0 \in \mathbb{N}^* : \forall N \geq N_0, \forall u \in [0, T], \quad I^N(u) = I'(u)$$

so

$$\exists N_0 \in \mathbb{N}^* : \forall N \geq N_0, \forall u \in [0, \tau'], \quad I^N(u) = I'(u) \quad (\text{so } \tau^N = \tau' \text{ and } Z^N = Z')$$

almost surely on the part of the sample space where $\tau' < +\infty$ and $Z' < +\infty$ (note that N_0 is random since it intrinsically depends on the value of τ'). On the other part of the sample space, $\tau' = +\infty$ so $Z' = +\infty$ (recall that Assumption G entails that deaths occur at a positive rate as long as the total population is not zero, so infinitely many new births for the branching process I' have to occur if we want τ' to be infinite) and almost surely,

$$\forall T \geq 0, \quad \exists N_0 \in \mathbb{N}^* : \forall N \geq N_0, \quad I^N(T) = I'(T) > 0 \quad (\text{so } \tau^N > T) \quad \text{and } Z_T^N = Z'_T$$

where Z_T^N and Z'_T are the number of upward jumps of $\|I\|_1$ and $\|I'\|_1$ before time T . This entails

$$\lim_{N \rightarrow +\infty} \tau^N = +\infty \quad \text{and} \quad \lim_{N \rightarrow +\infty} Z^N = Z' = +\infty$$

almost surely on this part of the sample space since both Z_T^N and Z'_T are increasing in T . \square

Just as in the unitype case, we will say that the epidemic undergoes a *minor outbreak* when the branching process I' goes extinct and a *major outbreak* if it does not. As Theorem 3.2.1 indicates, the extinction time and the total size of the epidemic are of the same order of those of the branching process in the minor outbreak case and tend to infinity with N in the major outbreak case.

Major outbreak probabilities

Our next results are devoted to computing the probability that a major outbreak occurs. Computing this probability for an epidemic started from a given node gives a first indicator of the criticality of this node in making the trade network vulnerable to an epidemic outbreak. Consequently, the major outbreak probability vector will be one of our main focuses when designing node-based control strategies in Chapter 4.

The following proposition is a direct consequence of Theorem 1.3.26:

PROPOSITION 3.2.2. — For any $i, j \in \llbracket 1, n \rrbracket$, let $W_{i,j}$ denote the number of offspring in node j of an individual born in node i for the branching process I' . Also set $\Sigma_i = \gamma_i + d_i + \sum_{j \neq i} \theta_{i,j}$ for any $i \in \llbracket 1, n \rrbracket$. Let Θ be the $n \times n$ matrix defined by $\Theta_{i,j} = \theta_{i,j}$ if $i \neq j$ and $\Theta_{i,i} = 0$. Then the matrix $C = (\mathbb{E}(W_{i,j}))_{1 \leq i, j \leq n}$ is given by

$$C = (\text{diag}(\Sigma_1, \dots, \Sigma_n) - \Theta)^{-1} \text{diag}(\beta_1, \dots, \beta_n). \quad (3.10)$$

Let R_0 denote the largest real eigenvalue of C . If $R_0 \leq 1$, then the major outbreak probability is 0. If $R_0 > 1$, then this probability is strictly positive and equals $1 - \prod_{k=1}^n \zeta_k^{1_k(0)}$, where ζ is the only fixed point in $[0, 1]^n$ of

$$G: \quad [0, 1]^n \quad \longrightarrow \quad [0, 1]^n \\ s = (s_1, \dots, s_n) \quad \longmapsto \quad \left(\mathbb{E} \left[\prod_{j=1}^n s_j^{W_{1,j}} \right], \dots, \mathbb{E} \left[\prod_{j=1}^n s_j^{W_{n,j}} \right] \right).$$

Moreover, the iterated sequence $(G^k(s))_{k \geq 0}$ converges to ζ for any $s \in [0, 1]^n$.

The basic reproduction number R_0 can be computed using a matrix describing changes in states for infected individuals $\text{diag}(\Sigma_1, \dots, \Sigma_n) - \Theta$ and a matrix describing the production of new infections $\text{diag}(\beta_1, \dots, \beta_n)$. It is interesting to relate this remark to the results of [DHR09] on next-generation matrices.

Proposition 1.3.25 now yields an explicit expression for G :

PROPOSITION 3.2.3. — *Let Θ be the matrix defined in Proposition 3.2.2. Then for any $s = (s_1, \dots, s_n)$ and any $i \in \llbracket 1, n \rrbracket$,*

$$G(s) = \left(\text{diag}(\lambda_1(s), \dots, \lambda_n(s)) - \Theta \right)^{-1} (d + \gamma) \quad (3.11)$$

where $\lambda_i(s) = (1 - s_i)\beta_i + \Sigma_i$.

The extinction time and final size of the epidemic

Just as in the unitype case, we are particularly interested in the behavior of the epidemic in the case of major outbreak, that causes the scaled epidemic process to enter the neighborhood of an attractive endemic equilibrium and remain within it for a large time scale before eventually going extinct. We will first exhibit a lower bound for the fraction of the population infected within a given time, then use it to derive an exponential lower bound for the epidemic extinction time and total size in the case where there exists a globally stable endemic equilibrium for some associated dynamical system. Contrary to the unitype setting, the existence of such an attractive equilibrium is still unclear.

The following proposition states that in the case of a major outbreak, the maximal number of infectives during the course of the epidemic is at least equal to a fraction of N with high probability as N goes to infinity, provided that the scaled population process starts at its equilibrium value $x^* := -A^{-1}B$. Its proof relies on the idea that until the number of infectives reaches the expected level, the proportion of susceptibles in the population is high enough for the epidemic process to dominate an epidemic branching process with tweaked rates, that itself reaches the said level in finite time.

PROPOSITION 3.2.4. — Assume that $x(0) = x^*$ and that $R_0 > 1$. Then

$$\limsup_{\varepsilon \rightarrow 0} \mathbb{P} \left(\max_{N \geq 1} \mathbb{P} \left(\max_{t \in \mathbb{R}_+} \|I^N(t)\|_1 \geq \varepsilon \|x^*\|_1 N \mid Z' = +\infty \right) = 1.$$

Proof of Proposition 3.2.4.— Let $\delta \in \left(0, \frac{\mathbb{P}(Z' = +\infty)}{2}\right)$. Let $\eta \in \left(0, \frac{R_0 - 1}{R_0 + 1}\right)$ and $\alpha \in \left(\eta, \frac{R_0 - 1 - \eta}{R_0}\right)$ be such that a branching process obtained from I' by replacing the birth rates β_i by $\beta_i \frac{1 - \alpha}{1 + \eta}$ survives with probability at least $\mathbb{P}(Z' = +\infty) - \delta$ (the existence of such a value of α is an easy consequence of Theorem 3.2.1 and Proposition 3.2.3). We will show that if η is small enough, then

$$\liminf_{N \rightarrow +\infty} \mathbb{P} \left(\max_{t \geq 0} \|I^N(t)\|_1 \geq \eta \|x^*\|_1 N \right) \geq \mathbb{P}(Z' = +\infty) - 2\delta, \quad (3.12)$$

which implies Proposition 3.2.4. Set

$$\sigma_\eta^N = \inf \{ t \geq 0 : \|I^N(t) + R^N(t)\|_1 \geq (\alpha - \eta) \|x^*\|_1 N \}.$$

Using the notation of Proposition 2.2.3 and setting $\eta' = \eta \|x^*\|_1 n^{-1/2}$, until time $\sigma_\eta^N \wedge \tau_{\eta'}^N$ every infective in node i makes contacts with other individuals in node j at rate at least $\beta_j \frac{1 - \alpha}{1 + \eta}$ since this node contains at least $(1 - \alpha) \|x^*\|_1 N$ susceptibles out of at most $(1 + \eta) \|x^*\|_1 N$ individuals. We can therefore define a \mathbb{R}_+^{2n} -valued multitype branching process $(I''(t), R''(t))_{t \geq 0}$ with rates given by

Transition	Rate at state (i, r)
$(i, r) \rightarrow (i, r) - e_j^i$	$d_j i_j$
$(i, r) \rightarrow (i, r) - e_j^r$	$d_j r_j$
$(i, r) \rightarrow (i, r) + e_k^i - e_j^i$	$\theta_{j,k} i_j$
$(i, r) \rightarrow (i, r) + e_k^r - e_j^r$	$\theta_{j,k} r_j$
$(i, r) \rightarrow (i, r) + e_j^i$	$\beta_j \frac{1 - \alpha}{1 + \eta}$
$(i, r) \rightarrow (i, r) + e_j^r - e_j^i$	$\gamma_j i_j$

and such that $\|I''(t \wedge \sigma_\eta^N \wedge \tau_{\eta'}^N)\|_1 \leq \|I^N(t \wedge \sigma_\eta^N \wedge \tau_{\eta'}^N)\|_1$ and $\|R''(t \wedge \sigma_\eta^N \wedge \tau_{\eta'}^N)\|_1 \leq \|R^N(t \wedge \sigma_\eta^N \wedge \tau_{\eta'}^N)\|_1$ for all $t \geq 0$ almost surely (so (I'', R'') may not go to infinity outside of the event $(Z' = +\infty)$). Therefore:

$$\mathbb{P} \left(\max_{t \geq 0} \|I(t)\|_1 \geq (\alpha - \eta) \|x^*\|_1 N \right) \geq \mathbb{P} \left(\exists t < \tau_{\eta'}^N \wedge \sigma_\eta^N : \|I''(t)\|_1 \geq (\alpha - \eta) \|x^*\|_1 N \right) \quad (3.13)$$

Set

$$\sigma_\eta^{\prime N} = \inf \{ t \geq 0 : \|I''(t) + R''(t)\|_1 \geq (\alpha - \eta) \|x^*\|_1 N \},$$

then

$$s_\eta^N = \inf \{ t \geq 0 : \|I(t)\|_1 \geq \eta \|x^*\|_1 N \}$$

and

$$s_\eta^{\prime N} = \inf \{ t \geq 0 : \|I''(t)\|_1 \geq \eta \|x^*\|_1 N \}.$$

The branching process (I'', R'') is non-explosive so $\sigma_\eta''^N$ goes to infinity almost surely with N . Moreover, Theorem 1.3.28 shows that there exists $\lambda \in (\mathbb{R}_+^*)^n$ such that:

$$\mathbb{P}\left(Z' = +\infty, \forall j \in \llbracket 1, n \rrbracket : \lim_{t \rightarrow +\infty} \frac{I_j''(t)}{R_j''(t)} = \lambda_j\right) \geq \mathbb{P}(Z' = +\infty) - \delta$$

and that for small enough values of η ,

$$\lambda_j > \frac{\eta}{\alpha - \eta} \tag{3.14}$$

for all $j \in \llbracket 1, n \rrbracket$. Hence

$$\mathbb{P}\left(Z' = +\infty, \forall j \in \llbracket 1, n \rrbracket : \lim_{N \rightarrow +\infty} \frac{I_j''(\sigma_\eta''^N)}{R_j''(\sigma_\eta''^N)} = \lambda_j\right) \geq \mathbb{P}(Z' = +\infty) - \delta$$

and (3.14) and Fatou's lemma yields

$$\liminf_{N \rightarrow +\infty} \mathbb{P}\left(Z' = +\infty, s_\eta''^N \leq \sigma_\eta''^N\right) \geq \mathbb{P}(Z' = +\infty) - \delta.$$

Therefore (3.13) implies

$$\begin{aligned} & \liminf_{N \rightarrow +\infty} \mathbb{P}\left(s_\eta^N < +\infty\right) \\ & \geq \liminf_{N \rightarrow +\infty} \mathbb{P}\left(Z' = +\infty, s_\eta^N < \tau_{\eta'}^N \wedge \sigma_\eta''^N\right) \\ & \geq \liminf_{N \rightarrow +\infty} \mathbb{P}\left(Z' = +\infty, s_\eta''^N < \tau_{\eta'}^N \wedge \sigma_\eta''^N\right) \\ & \geq \liminf_{N \rightarrow +\infty} \mathbb{P}\left(Z' = +\infty, s_\eta''^N < \tau_{\eta'}^N\right) - \delta. \end{aligned}$$

Proposition 2.2.3 now yields $u > 0$ such that

$$\lim_{N \rightarrow +\infty} \mathbb{P}\left(e^{uN} < \tau_{\eta'}^N\right) = 1,$$

from which we deduce

$$\begin{aligned} & \liminf_{N \rightarrow +\infty} \mathbb{P}\left(s_\eta^N < +\infty\right) \\ & \geq \liminf_{N \rightarrow +\infty} \mathbb{P}\left(Z' = +\infty, s_\eta''^N < e^{uN}\right) - \delta \\ & \geq \mathbb{P}\left(Z' = +\infty\right) \cap \liminf_{N \rightarrow +\infty} \left(s_\eta''^N < e^{uN}\right) - \delta \end{aligned} \tag{3.15}$$

where the second inequality proceeds from Fatou's lemma. But Theorem 1.3.28 implies that the supercritical branching process $(I''(t))_{t \geq 0}$ has a positive exponential growth almost surely on the event where it does not go extinct, so

$$\mathbb{P}\left(\liminf_{N \rightarrow +\infty} \left(s_\eta^N < e^{uN}\right)\right) = \mathbb{P}(\forall t \geq 0, I''(t) \neq 0). \tag{3.16}$$

This last probability is greater than $\mathbb{P}(Z' = +\infty) - \delta$ by definition of α , so using (3.16) then (3.15) yields (3.12), which ends the proof. \square

Let us now consider the dynamical system on $(\mathbb{R}_+^n)^3$ defined by:

$$\left. \begin{aligned} \dot{s}_j &= B_j + b_j(s_j + i_j + r_j) - d_j s_j + \sum_{k \neq j} \theta_{k,j} s_k - \sum_{k \neq j} \theta_{j,k} s_j - \beta_j i_j \frac{s_j}{s_j + i_j + r_j} \\ \dot{i}_j &= \beta_j i_j \frac{s_j}{s_j + i_j + r_j} - d_j i_j - \gamma_j i_j + \sum_{k \neq j} \theta_{k,j} i_k - \sum_{k \neq j} \theta_{j,k} i_j \\ \dot{r}_j &= \gamma_j i_j - d_j r_j + \sum_{k \neq j} \theta_{k,j} r_k - \sum_{k \neq j} \theta_{j,k} r_j \end{aligned} \right\} (\mathcal{S}_{\text{epi}}^0)$$

for all $k \in \llbracket 1, n \rrbracket$.

When $n \geq 2$, this system is much less tractable than its unitype version $(\mathcal{S}_{\text{epi}}^{1,0})$, and it is unclear whether a result similar to Proposition 3.1.3 holds whenever $R_0 > 1$. We can still show the following:

PROPOSITION 3.2.5 (Attractivity of the disease-free equilibrium for $(\mathcal{S}_{\text{epi}}^0)$). — *The disease-free equilibrium $(x^*, 0, 0)$ of $(\mathcal{S}_{\text{epi}}^0)$ is locally attractive if $R_0 < 1$ and is not if $R_0 > 1$. If an endemic equilibrium (s^*, i^*, r^*) for $(\mathcal{S}_{\text{epi}}^0)$ exists, then $i_j^* > 0$ for all $j \in \llbracket 1, n \rrbracket$.*

Proof of Proposition 3.2.5.— The Jacobian matrix associated to $(\mathcal{S}_{\text{epi}}^0)$ at the equilibrium $(z^*, 0, 0)$ writes

$$J = \begin{pmatrix} A & \text{diag}(-\beta_1, \dots, -\beta_n) & 0 \\ 0 & A' & 0 \\ 0 & \text{diag}(\gamma_1, \dots, \gamma_n) & A'' \end{pmatrix}$$

where A is defined by (1.4),

$$A' = \begin{pmatrix} \beta_1 - d_1 - \gamma_1 - \sum_{j \neq 1} \theta_{1,j} & \theta_{2,1} & \cdots & \theta_{n,1} \\ \theta_{1,2} & \beta_2 - d_2 - \gamma_2 - \sum_{j \neq 2} \theta_{2,j} & \ddots & \vdots \\ \vdots & \ddots & \ddots & \theta_{n,n-1} \\ \theta_{1,n} & \cdots & \theta_{n-1,1} & \beta_n - d_n - \gamma_n - \sum_{j \neq n} \theta_{n,j} \end{pmatrix}$$

and

$$A'' = \begin{pmatrix} -d_1 - \sum_{j \neq 1} \theta_{1,j} & \theta_{2,1} & \cdots & \theta_{n,1} \\ \theta_{1,2} & -d_2 - \sum_{j \neq 2} \theta_{2,j} & \ddots & \vdots \\ \vdots & \ddots & \ddots & \theta_{n,n-1} \\ \theta_{1,n} & \cdots & \theta_{n-1,1} & -d_n - \sum_{j \neq n} \theta_{n,j} \end{pmatrix}$$

The eigenvalues of J are those of A , those of A' and those of A'' . Now all the eigenvalues of A have negative real parts according to Assumption G. The same goes for A'' , since for all $\lambda \in \mathbb{C}$ with nonnegative real part $A'' - \lambda I_n$ is diagonally dominant and irreducible, and then nonsingular (see [Var62]). Proposition 1.3.27 shows that the same is true for the eigenvalues of A' if and only if $R_0 < 1$, which shows that the disease-free equilibrium is locally attractive in this case. If $R_0 > 1$, the dominant eigenvalue of A' has a positive real part according to Proposition 1.3.27, so the disease-free equilibrium is not locally attractive, which ends the proof. \square

Just as in the case of the limiting system $(\mathcal{S}'_{\text{pop}})$ for the logistic population process, numerical approximations suggest that there exists a globally asymptotically stable endemic equilibrium for $(\mathcal{S}^0_{\text{epi}})$ as soon as $R_0 > 1$. The following result gives an exponential lower bound for the extinction time and the total size of the epidemic in the major outbreak scenario when this stability property holds.

THEOREM 3.2.6. — *Assume that $x(0) = x^*$, that $R_0 > 1$ and that $(\mathcal{S}^0_{\text{epi}})$ restricted to $\mathbb{R}_+^n \times (\mathbb{R}_+^n \setminus \{0\}) \times \mathbb{R}_+^n$ admits a globally asymptotically stable endemic equilibrium (s^*, i^*, r^*) . Then there exists $V > 0$ such that:*

$$\lim_{N \rightarrow +\infty} \mathbb{P}(\tau^N > e^{VN} | Z' = +\infty) = 1. \quad (3.17)$$

and

$$\lim_{N \rightarrow +\infty} \mathbb{P}(Z^N > e^{VN} | Z' = +\infty) = 1. \quad (3.18)$$

Proof of Theorem 3.2.6.— Let $\delta = \min_j i_j^* > 0$ and let $\delta' > 0$. Let $\varepsilon > 0$ be such that setting

$$T_\varepsilon^N = \inf \{t \geq 0 : \|I^N(t)\|_1 \geq \varepsilon N\}$$

then

$$\liminf_{N \rightarrow +\infty} \mathbb{P}(T_\varepsilon^N < +\infty) > \mathbb{P}(Z' = +\infty) - \delta'. \quad (3.19)$$

Such a ε exists according to Proposition 3.2.4. Now set $E = \mathbb{R}_+^n \times (\mathbb{R}_+^n \setminus \{0\}) \times \mathbb{R}_+^n$ and define the flow $\Phi : E \times \mathbb{R}_+ \rightarrow E$ associated with the dynamical system $(\mathcal{S}_{\text{epi}})$. There exists $M > 1$ such that $\|x(t)\|_1$ only takes values below $M\|x^*\|_1$ for $t \geq 0$ whenever $x(0)$ is close enough from x^* . There also exists $T > 0$ such that:

$$\forall (s, i, r) \in E : \|i\|_1 \geq \varepsilon \text{ and } \|s + i + r\|_1 \leq M\|x^*\|_1, \quad \Phi((s, i, r), T) \in \mathcal{B}_\infty\left((s^*, i^*, r^*), \frac{\delta}{2}\right) \quad (3.20)$$

since $(s, i, r) \mapsto \inf \left\{t \geq 0 : \Phi((s, i, r), t) \in \mathcal{B}_\infty\left((s^*, i^*, r^*), \frac{\delta}{2}\right)\right\}$ is upper semi-continuous (and then upper bounded) on $\{(s, i, r) \in E : \|i\|_1 \geq \varepsilon, \|s + i + r\|_1 \leq M\|x^*\|_1\}$ that is a compact set. As a result:

$$\Phi\left(\frac{(S^N, I^N, R^N)}{N}(T_\varepsilon^N), T\right) \in \mathcal{B}_\infty\left((s^*, i^*, r^*), \frac{\delta}{2}\right) \quad (3.21)$$

almost surely conditionally on $(T_\varepsilon^N < +\infty, \|X^N(T_\varepsilon^N)\|_1 \leq M\|x^*\|_1 N)$. Mimicking the proof of Theorem 2.1 from Chapter 11 of [EK86], we get that

$$\sup_{t \in [0, T]} \left\| \frac{(S^N, I^N, R^N)}{N}(T_\varepsilon^N + t) - \Phi\left(\frac{(S^N, I^N, R^N)}{N}(T_\varepsilon^N), t\right) \right\|_\infty < \frac{\delta}{2}$$

and

$$\|X^N(T_\varepsilon^N)\|_1 \leq M\|x^*\|_1 N$$

with probability going to 1 conditionally on $(T_\varepsilon^N < +\infty)$ when $N \rightarrow +\infty$. This, (3.19), (3.21) and the definition of T show that

$$\begin{aligned} \liminf_{N \rightarrow +\infty} \mathbb{P}\left(T_\varepsilon^N < +\infty, \exists t \geq 0 : \frac{(S^N(t), I^N(t), R^N(t))}{N} \in \mathcal{B}_\infty((s^*, i^*, r^*), \delta)\right) \\ > \mathbb{P}(Z' = +\infty) - \delta', \end{aligned} \quad (3.22)$$

so $\frac{(S^N, I^N, R^N)}{N}$ hits $\mathcal{B}_\infty((s^*, i^*, r^*), \delta)$ with probability at least $\mathbb{P}(Z' = +\infty) - \delta'$ for N large enough. Using Theorem 1.3.37 just as in the proof of Proposition 2.2.3 along with the Markov property yields $V_1 > 0$ such that for all $\alpha > 0$,

$$\begin{aligned} \liminf_{N \rightarrow +\infty} \mathbb{P} \left(\exists T \geq 0, \forall t \in [T, T + e^{(V_1 - \alpha)N}], \forall j \in \llbracket 1, n \rrbracket, I_j^N(t) > (i_j^* - \delta)N \right) \\ > \mathbb{P}(Z' = +\infty) - \delta', \end{aligned} \quad (3.23)$$

and (3.17) follows, setting $\alpha > 0$ then defining $V := V_1 - \alpha$.

Now take $\alpha' \in (0, \alpha)$. Then, conditionally on the event

$$\left(\exists T \geq 0, \forall t \in [T, T + e^{(V_1 - \alpha')N}], \forall j \in \llbracket 1, n \rrbracket, I_j^N(t) > (i_j^* - \delta)N \right),$$

the total number of infected individuals recovering or dying during the course of the epidemic stochastically dominates the value at time $e^{(V_1 - \alpha')N}$ of a homogeneous Poisson counting process $(Q^N(t))_{t \geq 0}$ with intensity $\lambda_N := \min_j (\gamma_j + d_j)(i_j^* - \delta)N$. Yet the former number is also lower than Z^N with probability 1 since all infected individuals eventually have to die or recover, so we finally get:

$$\liminf_{N \rightarrow +\infty} \mathbb{P}(Z^N \geq e^{(V_1 - \alpha)N}) \geq \liminf_{N \rightarrow +\infty} \mathbb{P}\left(Q_{e^{(V_1 - \alpha)N}}^N \geq e^{(V_1 - \alpha')N}\right) (\mathbb{P}(Z' = +\infty) - \delta')$$

using (3.23), which yields

$$\liminf_{N \rightarrow +\infty} \mathbb{P}(Z^N \geq e^{(V_1 - \alpha)N}) \geq \mathbb{P}(Z' = +\infty) - \delta',$$

because the law of $Q^N(e^{(V_1 - \alpha')N})$ is Poisson with mean $\lambda_N e^{(V_1 - \alpha')N}$, hence (3.18), recalling that $V = V_1 - \alpha$. \square

The proof of Theorem 4.1 from [LS09] can be adapted to $(\mathcal{S}_{\text{epi}}^0)$, which shows that if $R_0 > 1$ and if there exists an endemic equilibrium $(s^*, i^*, r^*) \in \mathbb{R}_+^n \times (\mathbb{R}_+^n \setminus \{0\}) \times \mathbb{R}_+^n$ such that $s^* = \lambda i^*$ for some $\lambda > 0$, then this equilibrium is globally asymptotically stable and the conclusion of Theorem 3.2.6 is true.

Considering the proof of Proposition 3.2.4, we can see that the time needed for I^N to go above a given fraction of N is of order $\log(N)$ on the event $(Z' = +\infty)$. The proof of Theorem 3.2.6 shows that the subsequent convergence time of $(S^N, I^N, R^N)/N$ towards a given ball centered on the endemic equilibrium is upper bounded by some deterministic constant T with high probability. On the other hands, results from [PSK17] state that the time needed for the scaled process to leave the ball is of order $e^{V_1 N}$. This shows that for large N , the epidemic undergoing a major outbreak spends most of its time in its endemic phase where the scaled process lies close to the endemic equilibrium. This observation is reminiscent of metastability results stated in [VO05, Bov06].

We see in the proof of 3.2.6 that V_1 is the exit cost from a ball centered on (s^*, i^*, r^*) for a Poissonian perturbation of $(\mathcal{S}_{\text{epi}}^0)$ as defined in Section 1.3.4. Extrapolating from the results of [PSK17], we conjecture that under the assumptions of Theorem 3.2.6, for any $\alpha > 0$ the extinction time τ^N can be bounded below by $e^{(V^* - \alpha)N}$ and above by $e^{(V^* + \alpha)N}$ with probability tending to 1 as N tends to infinity, where V^* is the quasipotential of the set of disease-free states with respect to (s^*, i^*, r^*) for the Poissonian perturbation of the dynamical system $(\mathcal{S}_{\text{epi}}^0)$, that writes as in (1.13) with the first infimum being taken on $\{(s, i, r) \in \mathbb{R}_{3n} : i = 0\}$ and x being replaced by (s^*, i^*, r^*) .

3.2.1.2 The case $q \neq 0$

Let us now consider the case where at least one q_i is positive. As in the unitype setting, we focus on the behavior of an epidemic with an initial number of infectives proportional to N , and we therefore assume that $I^N(0) = \lfloor NI(0) \rfloor$ for some $I(0) \in \mathbb{R}_+^n$ such that $I_i(0) \leq x_i(0)$ for all $i \in \llbracket 1, n \rrbracket$.

Let us define the dynamical system $(\mathcal{S}_{\text{epi}})$ on $(\mathbb{R}_+^n)^3$ by

$$\left. \begin{aligned} \dot{s}_j &= p_j B_j + b_j(s_j + i_j + r_j) - d_j s_j + \sum_{k \neq j} \theta_{k,j} s_k - \sum_{k \neq j} \theta_{j,k} s_j - \beta_j i_j \frac{s_j}{s_j + i_j + r_j} \\ \dot{i}_j &= q_j B_j + \beta_j i_j \frac{s_j}{s_j + i_j + r_j} - d_j i_j - \gamma_j i_j + \sum_{k \neq j} \theta_{k,j} i_k - \sum_{k \neq j} \theta_{j,k} i_j \\ \dot{r}_j &= r_j B_j + \gamma_j i_j - d_j r_j + \sum_{k \neq j} \theta_{k,j} r_k - \sum_{k \neq j} \theta_{j,k} r_j \end{aligned} \right\} \quad (\mathcal{S}_{\text{epi}})$$

for all $k \in \llbracket 1, n \rrbracket$. There is no trivial disease-free equilibrium for this system. As for $(\mathcal{S}'_{\text{pop}})$, the existence of an equilibrium proceeds for $(\mathcal{S}_{\text{epi}})$ from Brouwer's fixed point theorem:

PROPOSITION 3.2.7 (Equilibrium for $(\mathcal{S}_{\text{epi}})$). — System $(\mathcal{S}_{\text{epi}})$ admits an equilibrium $(s^*, i^*, r^*) \in (\mathbb{R}_+^n)^3$, such that $s^* + i^* + r^* = x^*$ and $i_j^* > 0$ for all $j \in \llbracket 1, n \rrbracket$.

Proof of Proposition 3.2.7.— For any solution (s, i, r) of $(\mathcal{S}_{\text{epi}})$, $s + i + r$ is a solution of $x' = Ax + B$ so we necessarily have $s^* + i^* + r^* = x^*$ if (s^*, i^*, r^*) is an equilibrium of $(\mathcal{S}_{\text{epi}})$. It is therefore sufficient to show that the dynamical system on \mathbb{R}_+^{2n} defined by:

$$\left. \begin{aligned} \dot{s}_j &= p_j B_j + b_j x_j^* - d_j s_j + \sum_{k \neq j} \theta_{k,j} s_k - \sum_{k \neq j} \theta_{j,k} s_j - \beta_j i_j \frac{s_j}{x_j^*} \\ \dot{i}_j &= q_j B_j + \beta_j i_j \frac{s_j}{x_j^*} - d_j i_j - \gamma_j i_j + \sum_{k \neq j} \theta_{k,j} i_k - \sum_{k \neq j} \theta_{j,k} i_j \end{aligned} \right\} \quad (\tilde{\mathcal{S}}_{\text{epi}})$$

for all $j \in \llbracket 1, n \rrbracket$ admits a positive, finite number of equilibria.

Let $j \in \llbracket 1, n \rrbracket$ and assume that $i_1, \dots, i_{j-1}, i_{j+1}, \dots, i_n$ and $s_1, \dots, s_{j-1}, s_{j+1}, \dots, s_n$ are nonnegative numbers. Solving explicitly

$$\begin{cases} p_j B_j + b_j x_j^* - d_j s_j + \sum_{k \neq j} \theta_{k,j} s_k - \sum_{k \neq j} \theta_{j,k} s_j - \beta_j i_j \frac{s_j}{x_j^*} = 0 \\ q_j B_j + \beta_j i_j \frac{s_j}{x_j^*} - d_j i_j - \gamma_j i_j + \sum_{k \neq j} \theta_{k,j} i_k - \sum_{k \neq j} \theta_{j,k} i_j = 0 \end{cases} \quad (3.24)$$

defines s_j and i_j as continuous responses functions of the s_k and i_k with values in \mathbb{R}_+ . Now adding the lines of (3.24) yields

$$(p_j + q_j) B_j + b_j x_j^* - d_j (s_j + i_j) - \gamma_j i_j + \sum_{k \neq j} \theta_{k,j} (s_k + i_k) - \sum_{k \neq j} \theta_{j,k} (s_j + i_j) = 0 \quad (3.25)$$

so

$$-r_j B_j - d_j (s_j + i_j - x_j^*) - \gamma_j i_j + \sum_{k \neq j} \theta_{k,j} (s_k + i_k - x_k^*) - \sum_{k \neq j} \theta_{j,k} (s_j + i_j - x_j^*) = 0$$

since x^* is such that $Ax^* + B = 0$. If we assume that $s_k + i_k \leq x_k^*$ for every $k \neq j$, then (3.25) implies that $s_j + i_j \leq x_j^*$. The response (s_j, i_j) to any choice of (s_k, i_k) picked in convex compact

sets $\{(s_k, i_k) \in \mathbb{R}_+^2 : s_k + i_k \leq x_k^*\}$ is therefore a continuous function of the (s_k, i_k) with values in the convex compact set $\{(s_k, i_k) \in \mathbb{R}_+^2 : s_k + i_k \leq x_k^*\}$. Using Brouwer's fixed point theorem as in the proof of Proposition 2.3.3 therefore yields the existence of the expected equilibrium for $(\mathcal{S}_{\text{epi}})$. Finally, that $i_j^* > 0$ for all j proceeds from the fact that $q \neq 0$ and from the connectivity of the graph with vertices set $\llbracket 1, n \rrbracket$ and edges set $\{(j, k) : \theta_{j,k} > 0\}$. \square

Theorem 1.3.32 now implies the following:

PROPOSITION 3.2.8 (Scaling limit of a branching-driven SIR process). — Denoting (s, i, r) the solution of $(\mathcal{S}_{\text{epi}})$ with initial condition $(x(0) - I(0), I(0), r(0))$, we have:

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{t \in [0, T]} \left\| \frac{(S^N(t), I^N(t), R^N(t))}{N} - (s, i, r)(t) \right\|_{\infty} = 0 \right) = 1.$$

As a counterpart to Theorem 3.2.6 in this case allowing for immigration of infectives, we can describe the proportion of time spent by the scaled epidemic process in a neighborhood of (s^*, i^*, r^*) over a large time scale:

PROPOSITION 3.2.9 (Time spent in a neighborhood of the equilibrium of $(\mathcal{S}_{\text{epi}})$). — Assume that the equilibrium (s^*, i^*, r^*) given by Proposition 3.1.5 is globally asymptotically stable. Then for every $\varepsilon > 0$ there exist $T > 0$ and $V > 0$:

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(\int_0^{T+e^{VN}} \mathbf{1}_{\frac{(S^N(t), I^N(t), R^N(t))}{N} \in \mathcal{B}_2((s^*, i^*, r^*), \varepsilon)} dt > e^{VN} \right) = 1.$$

Proof of Proposition 3.2.9.— Let us denote $\mathcal{B}_2((s^*, i^*, r^*), \varepsilon)$ by \mathcal{B} . For any $N \geq 1$, let $\tilde{\tau}_\varepsilon^N$ be the first hitting time of \mathcal{B}^c by the scaled process $(S^N, I^N, R^N)/N$ after reaching \mathcal{B} . Let $V_2 := \bar{V}_\varepsilon(s^*, i^*, r^*)$ be the exit cost of \mathcal{B} for the Poisson perturbation of the dynamical system $(\mathcal{S}_{\text{epi}})$ as introduced in Section 1.3.4, and let $\alpha > 0$. As in the proof of Theorem 3.2.6, let $T > 0$ be such that the flow associated with $(\mathcal{S}_{\text{epi}})$ lies in $\mathcal{B}_2((s^*, i^*, r^*), \frac{\varepsilon}{2})$ at time T for any initial condition in $\{x \in \mathbb{R}_+^n : \|x\|_1 \leq M \|x^*\|_1\}$. Now write:

$$\begin{aligned} \mathbb{P} \left(\int_0^{T+e^{(V_2-\alpha)N}} \mathbf{1}_{\frac{(S^N, I^N, R^N)(t)}{N} \in \mathcal{B}} dt > e^{(V_2-\alpha)N} \right) &\geq \mathbb{P} \left(\frac{(S^N, I^N, R^N)(T)}{N} \in \mathcal{B}, T + e^{(V_2-\alpha)N} < \tilde{\tau}_\varepsilon^N \right) \\ &= \mathbb{P} \left(\frac{(S^N, I^N, R^N)(T)}{N} \in \mathcal{B} \right) \mathbb{P} \left(T + e^{(V_2-\alpha)N} < \tilde{\tau}_\varepsilon^N \mid \frac{(S^N, I^N, R^N)(T)}{N} \in \mathcal{B} \right) \end{aligned} \quad (3.26)$$

Reasoning as in the proof of Theorem 3.2.6, we see that the first term of this product goes to 1 as N tends to infinity. Using Theorem 1.3.37 with a smaller α , we get that the second term of the product also tends to 1 as N goes to infinity. Finally (3.26) yields the expected result, with $V := V_2 - \alpha$. \square

This proposition relies on the assumption that the equilibrium found in Proposition 3.1.5 is unique and globally asymptotically stable. It is still unsure under which conditions on the parameters this is the case. Once again, numerical approximations suggest that it holds for all the choices of parameters we experienced as long as $R_0 > 1$.

3.2.2 The logistic-driven SIR model

The study of the branching-driven SIR model may be adapted and used to provide valuable information about the logistic case. The main difference between both settings is twofold, and raises an additional difficulty when $p = \mathbb{1}$. First, individual jump rates in the logistic-driven SIR process depend on the current population state. Therefore, we cannot copy the formal definition of the branching process from the branching case since its rates must not depend on N . Second, we ignore whether the population equilibrium for the logistic population model is stable (see the remark following Proposition 2.3.3). As a result, we cannot consider that the scaled logistic population process remains approximately constant over non-fixed time scales, which was a key ingredient to proving Proposition 3.2.4 in the branching case. A workaround is to use Proposition 2.3.4 to localize the logistic population process over large time scales, which results once again in a N -exponential lower bound for the extinction time and final size of the epidemic in the major outbreak case under appropriate stability conditions.

We take up the parameters already introduced in Subsection 3.2.1 and we additionally define the carrying capacities K_i as in Subsection 2.3. **Throughout this section, we assume that $z(0) = z^*$ is an equilibrium of $(\mathcal{S}'_{\text{pop}})$.**

The definition of the epidemic process in this case is reminiscent of this given in Subsection 3.2.1.1. Yet, this time infective movements rates $\frac{\theta_{i,j}}{N} I_i^N (NK_j - X_j^N)_+$ involve current total populations X_j^N that cannot be used to define the limiting branching process. A solution is to consider that if the population process starts at its equilibrium value, these rates can be approximated on finite time scales by $\theta_{i,j} I_i^N (K_j - z_j^*)$ as N becomes large because of Proposition 2.3.2. We will therefore use these approximated rates to define I' , as is done in [Cla96].

We recall from the definition of the logistic population processes X^N in Subsection 2.3 that the N_i^B , N_i^b , N_i^d , N_i^β , N_i^Y and $N_{i,j}$ are independent Poisson random measures on $\mathbb{R}_+ \times \mathbb{R}_+$ with intensity $ds du$. For any N , we define (S_i^N, I_i^N, R_i^N) as the solution of

$$\begin{aligned} S_i^N(t) = & [Nz_i(0)] - I_i^N(0) + \int_0^t \int_{\mathbb{R}_+} \mathbb{1}_{q_i B_i(NK_i - X_i^N(s^-)) + u \leq (p_i + q_i) B_i(NK_i - X_i^N(s^-))_+} N_i^B(du, ds) \\ & + \int_0^t \int_{\mathbb{R}_+} \mathbb{1}_{u \leq \frac{b_i}{N} X_i^N(s^-) (NK_i - X_i^N(s^-))_+} N_i^b(du, ds) - \int_0^t \int_{\mathbb{R}_+} \mathbb{1}_{d_i I_i^N(s^-) < u \leq d_i (S_i^N(s^-) + I_i^N(s^-))} N_i^d(du, ds) \\ & - \int_0^t \int_{\mathbb{R}_+} \mathbb{1}_{u \leq \beta_i I_i^N(s^-) \frac{S_i^N(s^-)}{X_i^N(s^-)}} N_i^\beta(du, ds) \\ & + \sum_{j \neq i} \left[\int_0^t \int_{\mathbb{R}_+} \mathbb{1}_{\frac{\theta_{j,i}}{N} I_j^N(s^-) (NK_i - X_i^N(s^-))_+ < u \leq \frac{\theta_{j,i}}{N} (S_j^N(s^-) + I_j^N(s^-)) (NK_i - X_i^N(s^-))_+} N_{j,i}(du, ds) \right. \\ & \left. - \int_0^t \int_{\mathbb{R}_+} \mathbb{1}_{\frac{\theta_{i,j}}{N} I_i^N(s^-) (NK_j - X_j^N(s^-))_+ < u \leq \frac{\theta_{i,j}}{N} (S_i^N(s^-) + I_i^N(s^-)) (NK_j - X_j^N(s^-))_+} N_{i,j}(du, ds) \right], \end{aligned}$$

$$\begin{aligned}
 I_i^N(t) = & I_i^N(0) + \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq q_i B_i(NK_i - X_i^N(s^-))_+} N_i^B(du, ds) + \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \beta_i I_i^N(s^-) \frac{S_i^N(s^-)}{X_i^N(s^-)}} N_i^\beta(du, ds) \\
 & - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq d_i I_i^N(s^-)} N_i^d(du, ds) - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \gamma_i I_i^N(s^-)} N_i^\gamma(du, ds) \\
 & + \sum_{j \neq i} \left[\int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \frac{\theta_{j,i}}{N} I_i^N(s^-) (NK_i - X_i^N(s^-))_+} N_{j,i}(du, ds) - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \frac{\theta_{i,j}}{N} I_i^N(s^-) (NK_j - X_j^N(s^-))_+} N_{i,j}(du, ds) \right],
 \end{aligned}$$

and

$$\begin{aligned}
 R_i^N(t) = & \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{(p_i + q_i) B_i(NK_i - X_i^N(s^-))_+ < u \leq B_i(NK_i - X_i^N(s^-))_+} N_i^B(du, ds) \\
 & + \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \gamma_i I_i^N(s^-)} N_i^\gamma(du, ds) - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{d_i (S_i^N(s^-) + I_i^N(s^-)) < u \leq d_i X_i^N(s^-)} N_i^d(du, ds) \\
 & + \sum_{j \neq i} \left[\int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{\frac{\theta_{j,i}}{N} (S_j^N(s^-) + I_j^N(s^-)) (NK_i - X_i^N(s^-))_+ < u \leq \frac{\theta_{i,j}}{N} X_j^N(s^-) (NK_i - X_i^N(s^-))_+} N_{j,i}(du, ds) \right. \\
 & \left. - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{\frac{\theta_{i,j}}{N} (S_i^N(s^-) + I_i^N(s^-)) (NK_j - X_j^N(s^-))_+ < u \leq \frac{\theta_{j,i}}{N} X_i^N(s^-) (NK_j - X_j^N(s^-))_+} N_{i,j}(du, ds) \right]
 \end{aligned}$$

for all i and all t . Here again, it is easy to see using Equation 2.39 that $S^N + I^N + R^N = X^N$.

The (S^N, I^N, R^N) are jump processes on \mathbb{Z}_+^{3n} with transition rates given by the following rates chart, where $x_j = s_j + i_j + r_j$ for all $j \in \llbracket 1, n \rrbracket$:

Transition	Rate	
$(s, i, r) \rightarrow (s, i, r) + e_j^s$	$\left(p_j B_j + \frac{b_j}{N} x_j\right) (K_j - x_j)_+$	(3.27)
$(s, i, r) \rightarrow (s, i, r) + e_j^i$	$q_j B_j (K_j - x_j)_+$	
$(s, i, r) \rightarrow (s, i, r) + e_j^r$	$r_j B_j (K_j - x_j)_+$	
$(s, i, r) \rightarrow (s, i, r) - e_j^s$	$d_j s_j$	
$(s, i, r) \rightarrow (s, i, r) - e_j^i$	$d_j i_j$	
$(s, i, r) \rightarrow (s, i, r) - e_j^r$	$d_j r_j$	
$(s, i, r) \rightarrow (s, i, r) + e_k^s - e_j^s$	$\frac{\theta_{j,k}}{N} s_j (K_k - x_k)_+$	
$(s, i, r) \rightarrow (s, i, r) + e_k^i - e_j^i$	$\frac{\theta_{j,k}}{N} i_j (K_k - x_k)_+$	
$(s, i, r) \rightarrow (s, i, r) + e_k^r - e_j^r$	$\frac{\theta_{j,k}}{N} r_j (K_k - x_k)_+$	
$(s, i, r) \rightarrow (s, i, r) + e_j^i - e_j^s$	$\beta_j \frac{i_j s_j}{x_j}$	
$(s, i, r) \rightarrow (s, i, r) + e_j^r - e_j^i$	$\gamma_j i_j$	

Table 3.4: Logistic-driven SIR process rates chart ($p = 1$)

3.2.2.1 The case $p = 1$

We first consider the case where $p = 1$. We assume that $I^N(0) = I(0) \in \mathbb{Z}_+^n$ for all $N \geq 1$.

Branching approximation of the epidemic process

Define the multitype branching process I' as the solution of the integral equation

$$\begin{aligned} I'_i(t) = & I_i(0) + \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \beta_i I'_i(s^-)} N_i^\beta(du, ds) \\ & - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq d_i I'_i(s^-)} N_i^d(du, ds) - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \gamma_i I'_i(s^-)} N_i^\gamma(du, ds) \\ & + \sum_{j \neq i} \left[\int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \theta_{j,i} I'_j(s^-)(K_i - z_i^*)} N_{j,i}(du, ds) - \int_0^t \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \theta_{j,i} I'_i(s^-)(K_j - z_j^*)} N_{i,j}(du, ds) \right], \end{aligned}$$

for all i and all t . I' is a \mathbb{Z}_+^n -valued multitype branching process with birth rates vector β , death rates vector $d + \gamma$ and transition rates $\theta_{i,j}(K_j - z_j^*)$.

Ghost infections for I' may occur as in the branching-driven SIR case (see the comments before Theorem 3.2.1). Here the rates of movements between nodes for the epidemic process I' are not exactly these of the I^N either. Mimicking the terminology of [Mol77, Cla96], this approximation results to what could be called *ghost movements*, that is, movements of I' that are not movements of the I^N , and to *shadow movements*, that is, movements of the I^N that are not movements for I' . We will prove a result analogous to Theorem 3.2.1:

THEOREM 3.2.10 (Convergence of the logistic-driven SIR to a branching process). — \mathbb{P} -almost surely:

$$\exists N_0 \in \mathbb{Z}_+^* : \forall N \geq N_0, \forall u \in [0, T], \quad I^N(u) = I'(u).$$

In particular, if τ^N (resp. Z^N) denotes the extinction time (resp. total size) of the epidemic and τ' (resp. Z') that of the branching process, then

$$\tau^N \xrightarrow{N \rightarrow +\infty} \tau' \quad \text{and} \quad Z^N \xrightarrow{N \rightarrow +\infty} Z' \tag{3.28}$$

\mathbb{P} -almost surely.

Proof of Theorem 3.2.10.— The proof of this theorem is based on the same reasoning as that of Theorem 3.2.1, which is to show that for any $T \geq 0$, with probability going to 1 as N tends to infinity no ghost infection, no ghost movement nor shadow movement occurs before time T .

We have

$$\lim_{N \rightarrow +\infty} \sup_{u \in [0, T]} \left\| \frac{1}{N} (NK_i - X_i^N(u))_+ - z^* \right\|_\infty = 0$$

according to Proposition 2.3.2, so the dominated convergence theorem applies to show that for any $T \geq 0$, almost surely there exists $N_0 \geq 0$ such that for any $N \geq N_0$,

$$\int_0^T \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \beta_i I'_i(s^-) \frac{S_i^N(s^-)}{X_i^N(s^-)}} N_i^\beta(du, ds) = \int_0^T \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \beta_i I'_i(s^-)} N_i^\beta(du, ds),$$

and

$$\begin{aligned} & \sum_{j \neq i} \left[\int_0^T \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \frac{\theta_{j,i}}{N} \Gamma'_j(s^-) (\mathbf{N}K_i - X_i^N(s^-))_+} \mathbf{N}_{j,i}(d\mathbf{u}, d\mathbf{s}) - \int_0^T \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \frac{\theta_{i,j}}{N} \Gamma'_i(s^-) (\mathbf{N}K_j - X_j^N(s^-))_+} \mathbf{N}_{i,j}(d\mathbf{u}, d\mathbf{s}) \right] \\ &= \sum_{j \neq i} \left[\int_0^T \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \theta_{j,i} \Gamma'_j(s^-) (\mathbf{K}_i - z_i^*)} \mathbf{N}_{j,i}(d\mathbf{u}, d\mathbf{s}) - \int_0^T \int_{\mathbb{R}_+} \mathbf{1}_{u \leq \frac{\theta_{i,j}}{N} \Gamma'_i(s^-) (\mathbf{K}_j - z_j^*)} \mathbf{N}_{i,j}(d\mathbf{u}, d\mathbf{s}) \right]. \end{aligned}$$

This implies that almost surely, for N large enough there are no ghost infections, no ghost transfers and no shadow transfers before time T , which yields the first part of the theorem.

The rest of the proof proceeds as in the proof of Theorem 3.2.1. \square

Major outbreak probabilities

The following results are similar to those derived in the branching case and their proof raises no additional technical difficulty. We therefore state them without further comment.

PROPOSITION 3.2.11. — For any $i, j \in \llbracket 1, n \rrbracket$, let $W_{i,j}$ denote the number of offspring in node j of an individual born in node i for the branching process Γ' . Also set $\Sigma'_i = \gamma_i + d_i + \sum_{j \neq i} \theta_{i,j} (\mathbf{K}_j - z_j^*)$ for any $i \in \llbracket 1, n \rrbracket$. Let Θ' be the $n \times n$ matrix defined by $\Theta'_{i,j} = \theta_{i,j} (\mathbf{K}_j - z_j^*)$ if $i \neq j$ and $\Theta'_{i,i} = 0$. Then the matrix $C = (\mathbb{E}(W_{i,j}))_{1 \leq i, j \leq n}$ is given by

$$C = (\text{diag}(\Sigma'_1, \dots, \Sigma'_n) - \Theta')^{-1} \text{diag}(\beta_1, \dots, \beta_n). \quad (3.29)$$

Let R_0 denote the largest real eigenvalue of C . If $R_0 \leq 1$, then the major outbreak probability is 0. If $R_0 > 1$, then this probability is strictly positive and equals $1 - \prod_{k=1}^n \zeta_k^{1k(0)}$, where ζ is the only fixed point in $[0, 1]^n$ of

$$\begin{aligned} G: \quad [0, 1]^n & \longrightarrow [0, 1]^n \\ s = (s_1, \dots, s_n) & \longmapsto \left(\mathbb{E} \left[\prod_{j=1}^n s_j^{W_{1,j}} \right], \dots, \mathbb{E} \left[\prod_{j=1}^n s_j^{W_{n,j}} \right] \right). \end{aligned}$$

Moreover, the iterated sequence $(G^k(s))_{k \geq 0}$ converges to ζ for any $s \in [0, 1]^n$.

PROPOSITION 3.2.12. — Let Θ' be the matrix defined in Proposition 3.2.11. Then for any $s = (s_1, \dots, s_n)$ and any $i \in \llbracket 1, n \rrbracket$,

$$G(s) = (\text{diag}(\lambda'_1(s), \dots, \lambda'_n(s)) - \Theta')^{-1} (d + \gamma) \quad (3.30)$$

where $\lambda'_i(s) = (1 - s_i)\beta_i + \Sigma'_i$.

The extinction time and final size of the epidemic

The next Proposition is reminiscent of Proposition 3.2.4. Its proof relies on Proposition 2.3.4 rather than on the (hypothetical) attractivity of z^* for $(\mathcal{S}'_{\text{pop}})$.

PROPOSITION 3.2.13. — *Assume that $R_0 > 1$. Then*

$$\limsup_{\varepsilon \rightarrow 0} \sup_{N \geq 1} \mathbb{P} \left(\max_{t \in \mathbb{R}_+} \|I^N(t)\|_1 \geq \varepsilon \|z^*\|_1 N \mid Z' = +\infty \right) = 1.$$

Proof of Proposition 3.2.13.— Reproduce the proof of Proposition 3.2.4 using that $\varepsilon \leq X_i^N/N \leq \lceil NK_i \rceil/N$ for all $i \in \llbracket 1, n \rrbracket$ (and not $X_i^N/N \in \mathcal{B}_2(x^*, \eta')$ anymore) over an exponential time scale, where ε is given by Proposition 2.3.4. \square

Let us now consider the dynamical system on $(\mathbb{R}_+^n)^3$ defined by:

$$\left. \begin{aligned} \dot{s}_j &= (B_j + b_j z_j^*)(K_j - z_j^*) - d_j s_j + \sum_{k \neq j} \theta_{k,j} s_k (K_j - z_j^*) - \sum_{k \neq j} \theta_{j,k} s_j (K_k - z_k^*) - \beta_j i_j \frac{s_j}{z_j^*} \\ \dot{i}_j &= \beta_j i_j \frac{s_j}{z_j^*} - (d_j + \gamma_j) i_j + \sum_{k \neq j} \theta_{k,j} i_k (K_j - z_j^*) - \sum_{k \neq j} \theta_{j,k} i_j (K_k - z_k^*) \\ \dot{r}_j &= \gamma_j i_j - d_j r_j + \sum_{k \neq j} \theta_{k,j} r_k (K_j - z_j^*) - \sum_{k \neq j} \theta_{j,k} r_j (K_k - z_k^*) \end{aligned} \right\} (\mathcal{S}_{\text{epi}}^0)$$

for all $j \in \llbracket 1, n \rrbracket$.

On $\{(s, i, r) \in (\mathbb{R}_+^n)^3 : s + i + r = z^*\}$, this system coincides with a version of $(\mathcal{S}_{\text{epi}}^0)$ with the B_j , the b_j and the $\theta_{k,j}$ multiplied by $(K_j - z_j^*)$. Easy calculations show that the R_0 for the branching-driven model with these parameters, given by Proposition 3.2.2, is the R_0 given by Proposition 3.2.11. Showing that z^* is unique as an equilibrium of $(\mathcal{S}'_{\text{pop}})$ and that $(\mathcal{S}_{\text{epi}}^0)$ admits a unique endemic equilibrium in the $R_0 > 1$ case would therefore imply that the same holds for $(\mathcal{S}_{\text{epi}}^0)$.

The proof of Proposition 3.2.5 adapts *mutatis mutandis* to yield the following result:

PROPOSITION 3.2.14 (Attractivity of the disease-free equilibrium for $(\mathcal{S}_{\text{epi}}^0)$). — *The disease-free equilibrium $(z^*, 0, 0)$ of $(\mathcal{S}_{\text{epi}}^0)$ is not locally attractive if $R_0 > 1$. If an endemic equilibrium (s^*, i^*, r^*) for $(\mathcal{S}_{\text{epi}}^0)$ exists, then $i_j^* > 0$ for all $j \in \llbracket 1, n \rrbracket$.*

Finally, the same arguments as in the proof for Theorem 3.2.6 yield an exponential lower bound for τ^N and Z^N in the case of a major epidemic outbreak leading towards an attractive endemic equilibrium.

THEOREM 3.2.15. — Assume that $R_0 > 1$ and that (\mathcal{S}'_{epi}) restricted to $\mathbb{R}_+^n \times (\mathbb{R}_+^n \setminus \{0\}) \times \mathbb{R}_+^n$ admits a globally asymptotically stable endemic equilibrium (s^*, i^*, r^*) . Then there exists $V' > 0$ such that:

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(\tau^N > e^{V'N} \mid Z' = +\infty \right) = 1. \quad (3.31)$$

and

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(Z^N > e^{V'N} \mid Z' = +\infty \right) = 1. \quad (3.32)$$

The remarks following Theorem 3.2.6 still apply. In particular, we conjecture that under the assumptions of Theorem 3.2.15, for any $\alpha > 0$ the extinction time τ^N can be bounded below by $e^{(V^* - \alpha)N}$ and above by $e^{(V^* + \alpha)N}$ with probability tending to 1 as N tends to infinity, where V^* is the quasipotential of the set of disease-free states with respect to (s^*, i^*, r^*) for the Poissonian perturbation of the dynamical system (\mathcal{S}'_{epi}) .

3.2.2.2 The case $q \neq 0$

Let us now consider the case where at least one q_i is positive. We assume that $I^N(0) = \lfloor NI(0) \rfloor$ for all $N \geq 1$, with $I(0) \in \mathbb{R}_+^n$.

Let us define the dynamical system on $(\mathbb{R}_+^n)^3$ by the following set of equations, for all $k \in \llbracket 1, n \rrbracket$:

$$\left. \begin{aligned} \dot{s}_j &= (p_j B_j + b_j z_j^*) (K_j - z_j^*) - d_j s_j + \sum_{k \neq j} \theta_{k,j} s_k (K_j - z_j^*) - \sum_{k \neq j} \theta_{j,k} s_j (K_k - z_k^*) - \beta_j i_j \frac{s_j}{z_j^*} \\ \dot{i}_j &= q_j B_j (K_j - z_j^*) + \beta_j i_j \frac{s_j}{z_j^*} - (d_j + \gamma_j) i_j + \sum_{k \neq j} \theta_{k,j} i_k (K_j - z_j^*) - \sum_{k \neq j} \theta_{j,k} i_j (K_k - z_k^*) \\ \dot{r}_j &= r_j B_j (K_j - z_j^*) + \gamma_j i_j - d_j r_j + \sum_{k \neq j} \theta_{k,j} r_k (K_j - z_j^*) - \sum_{k \neq j} \theta_{j,k} r_j (K_k - z_k^*) \end{aligned} \right\} (\mathcal{S}'_{epi})$$

PROPOSITION 3.2.16 (Equilibrium for (\mathcal{S}'_{epi})). — (\mathcal{S}'_{epi}) admits an equilibrium $(s^*, i^*, r^*) \in \prod_{j=1}^n \{(s, i, r) \in \mathbb{R}_+^3 : s + i + r \leq z_j^* \leq\}$, such that $i_j^* > 0$ for all $j \in \llbracket 1, n \rrbracket$.

Proof of Proposition 3.2.13. — Reasoning as in the proof of Proposition 3.2.7 shows that there exists an equilibrium in $(s^*, i^*, r^*) \in \prod_{j=1}^n \{(s, i, r) \in \mathbb{R}_+^3 : s + i + r \leq z_j^*\}$, and the fact that all i_j^* are positive stems from the irreducibility of Θ and the assumption that $B \neq 0$. \square

Theorem 1.3.32 now implies the following:

PROPOSITION 3.2.17 (Scaling limit of a logistic-driven SIR process). — Denoting (s, i, r) the solution of (\mathcal{S}_{epi}) with initial condition $(z^* - I(0), I(0), r(0))$, we have:

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{t \in [0, T]} \left\| \frac{(S^N(t), I^N(t), R^N(t))}{N} - (s, i, r)(t) \right\|_{\infty} = 0 \right) = 1.$$

from which we deduce, as in the branching-driven case, a result describing the proportion of time spent by the scaled epidemic process in a neighborhood of (s^*, i^*, r^*) over a large time scale:

PROPOSITION 3.2.18 (Time spent in a neighborhood of the equilibrium of $(\mathcal{S}_{\text{epi}}^1)$). — Assume that the equilibrium (s^*, i^*, r^*) given by Proposition 3.1.5 is globally asymptotically stable. Then for every $\varepsilon > 0$ there exist $T' > 0$ and $V' > 0$ such that:

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(\int_0^{T' + e^{V'N}} \mathbf{1}_{\left(\frac{S^N(t), I^N(t), R^N(t)}{N} \in \mathcal{B}_2((s^*, i^*, r^*), \varepsilon) \right)} dt > e^{V'N} \right) = 1.$$

4

Network vulnerability assessment and numerical applications

We wish to apply the results of the models studied in Chapter 3 to the identification of nodes making a trade network vulnerable to the spread of an infectious disease, and to the design and evaluation of control policies. We will provide numerical applications of this theoretical discussion to a subset of the French cattle trade network.

In all this chapter, we assume that we observe realizations of a logistic-driven SIR model as introduced in Subsection 3.2.2, with no infective immigration, that is, with $p = 1$. This assumption allows to focus on the behavior of an epidemic started by a small number of infectives introduced accidentally into the system rather than entering it structurally through immigration. It also makes the notions of extinction time and final size of the epidemic relevant. Section 4.1 gives a description of the dataset used in the application and the demographic parameters calibrated using these data. In Section 4.2, we put forward a set of theoretical indicators of the trade network vulnerability induced by a given node. They are used in Section 4.3 to devise and evaluate strategies targeting critical nodes or links and aiming at making the network more resistant to the propagation of an epidemic.

4.1

Dataset description and parameter calibration

In our numerical application, demographic parameters will be calibrated using a subset of the FNCD database corresponding to the 2015 trade network of Finistère, a densely populated livestock farming region in western France. We first describe the corresponding subnetwork (Subsection 4.1.1), before examining the distribution of the resulting estimates for the demographic parameters (Subsection 4.1.2).

4.1.1 Dataset description

Trade networks built using the FNCD data described in Subsection 1.1.1.2 present temporal stability, both in their topological and macroscopic properties ([DEV14] and Figure 4.1), and in the volume of trade flows. In order to keep computation time moderate, we extracted information from the FNCD corresponding to the Finistère department for year 2015, which are

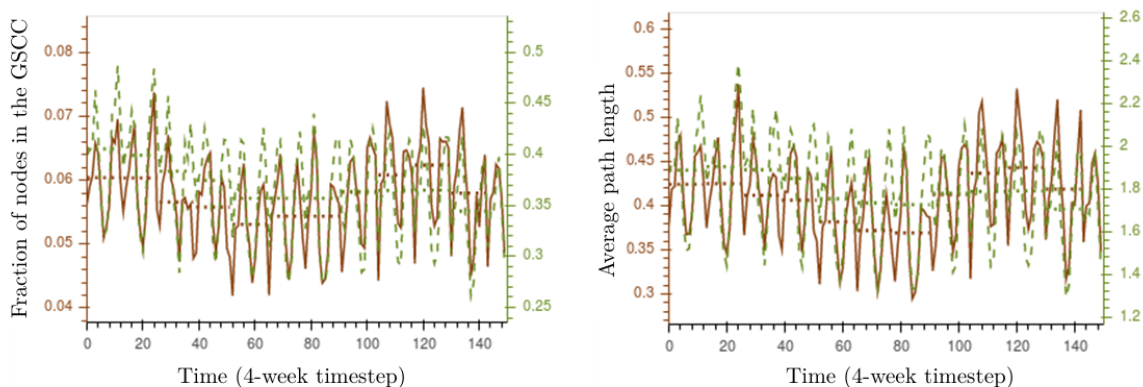


Figure 4.1: Stability over time of the average connectivity properties of the empirical French cattle trade network. On the left, fraction of nodes belonging to the greatest strongly connected component (GSCC) of the dynamical trade network observed over 4-week timesteps. On the right, average path length between two nodes belonging to the same connected component, on the same observations. Red plain lines correspond to holding-specific data, green dashed lines to data aggregated by commune. On both panels, Time 0 corresponds to January 1, 2005, and the observations range up to December 31, 2015. Graphics stem from the 2017 internship of Ambre Giguelay at the French National Institute for Agricultural Research (INRA), MaIAGE, Jouy-en-Josas (France), in the framework of the ANR project Cadence.

the most recent observations in the FNCD and target a region densely populated with dairy cattle. The subnetwork we obtained (see Figure 4.2) exhibits connectivity and degree distribution properties (power-law distributions inducing the *scale-free* property) that are comparable to those of the French network as a whole, especially for unweighted out-degrees (see Figure 4.3). It contains 4,183 vertices and 10,036 edges. It consists of 4,163 farms (with internal population dynamics) and 20 commercial operators (without internal population dynamics) among which 3 markets (with an average staying times of animals of approximately one day) and 17 assembly centers (with sojourn times between 1 and 7 days). These holdings exchange a total of 117,910 animals, receive 55,325 from the outside of the subnetwork and send 243,449 to the outside of Finistère or to slaughterhouses, these movements being considered as deaths (87,121 from operators and 156,328 from farms). Exchanges amount to 11,728 animals between operators, 18,734 animals from operators to farms, 71,532 from farms to operators and 15,916 between farms. The average total population on the network over the year is of 424,105 animals.

4.1.2 Calibration of the demographic parameters

We use a simple approach to calibrate the parameters of the logistic population model associated to the observed network, that relies on the assumption that the population size in each holding is roughly stable over the year. Much finer calibration procedures can be thought of, that we will not deal with in the present work. Note that more sophisticated mathematical methods to estimate the growth rates in the case of an observed branching process (that is, under the assumption that the underlying population process is that described in Section 1.2.2.1) can be found in [AK78] (also see [WW90] in the unitype case).

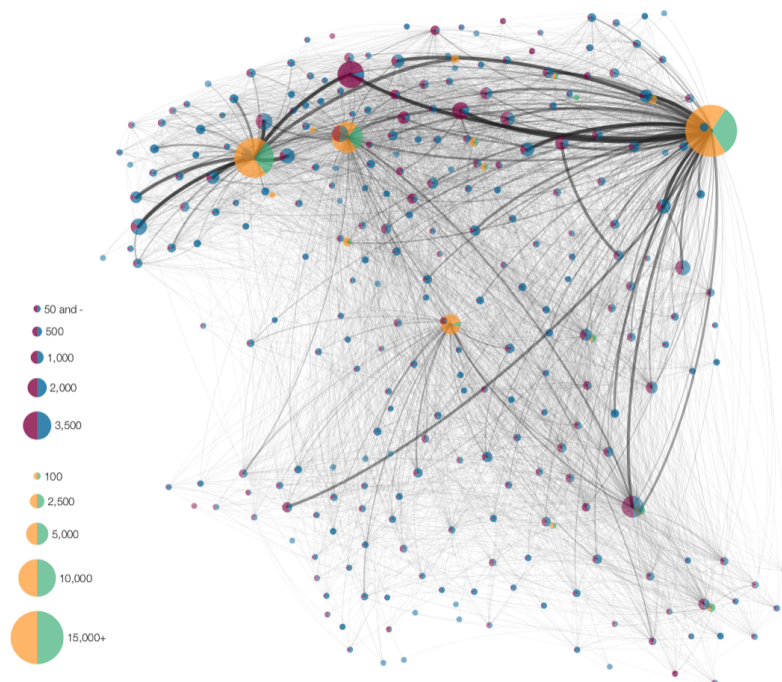


Figure 4.2: Geographical location of exchanging cattle holdings of Finistère in 2015, aggregated at the commune level. The size of a node represents its mean population over the year. Colours on the nodes represent the share of buying (orange for operators and red for farms) and selling (green for operators and blue for farms). The edges represent the existence of a movement between two holdings in the dataset, with their width indicative of the observed trading volume along this edge. The picture is courtesy of Gaël Beaunée.

We recall the logistic population process rates chart. Since the parameters we will calibrate are in fact the NK_i , $\frac{b_i}{N}$, d_i , $B_i(NK_i - x_i)_+$ and $\theta_{i,j}(NK_j - x_j)_+$, and since N will not vary, we drop the scaling parameter, that is, we take it equal to 1:

Transition	Rate at state x	
$x \rightarrow x + e_i$	$(B_i + b_i x_i) (K_i - x_i)_+$	(1.5)
$x \rightarrow x - e_i$	$d_i x_i$	
$x \rightarrow x - e_i + e_j$	$\theta_{i,j} x_i (K_j - x_j)_+$	

Table 4.1: Logistic population process jump rates chart.

with $x \rightarrow x + e_i$ transitions decomposed between imports (occurring at rate $B_i(K_i - x_i)_+$) and births (occurring at rate $b_i x_i (K_i - x_i)_+$). Assuming that the total population x is stationary over a unit period of time, the expected number of imports to node i is $B_i(K_i - x_i)_+$, the expected number of births in node i is $b_i x_i (K_i - x_i)_+$, the expected number of deaths in (or exports from) node i is $d_i x_i$ and the expected number of transfers from node i to node j is $\theta_{i,j} x_i (K_j - x_j)_+$.

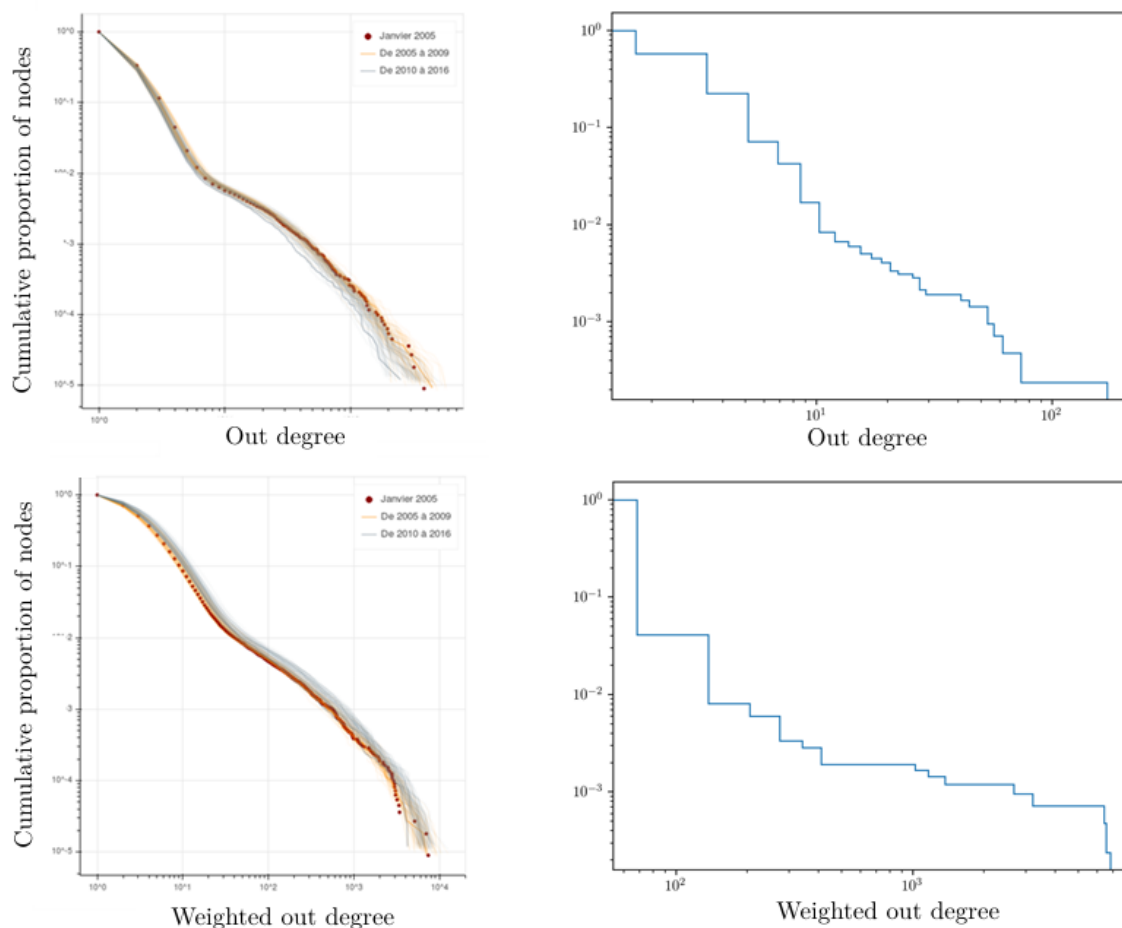


Figure 4.3: Monthly out-degree distributions for observed cattle trade networks in France between 2005 and 2015, and in Finistère in January 2015. On the left, reverse cumulative distribution of unweighted out-degrees (number of nodes of the network to which a given node sends animals) and weighted out-degrees (number of animals sent from a node to other nodes of the network) for the French trade network for every month of years 2005 to 2015. On the right, reverse cumulative distribution of unweighted and weighted out-degrees for the January 2015 Finistère subnetwork. Graphics from the left panel stem from the 2017 internship of Ambre Giguélay at the French National Institute for Agricultural Research (INRA), MaIAGE, Jouy-en-Josas (France), in the framework of the ANR project Cadence.

We denote by \bar{x} the vector of average observed populations over the year, A the vector of total observed number of imported animals, C the vector of births, D the number of deaths and E the matrix of population transfers ($E_{i,j}$ being the number of animals sent from i to j over the year), then set:

$$\begin{aligned} K_i &= 1.2\bar{x}_i, \\ B_i &= \frac{A_i}{(K_i - \bar{x}_i)} = 5\frac{A_i}{\bar{x}_i}, \\ b_i &= \frac{C_i}{\bar{x}_i(K_i - \bar{x}_i)} = 5\frac{C_i}{\bar{x}_i^2}, \\ d_i &= \frac{D_i}{\bar{x}_i} \end{aligned}$$

and

$$\theta_{i,j} = \frac{E_{i,j}}{(K_j - \bar{x}_j)} = 5\frac{E_{i,j}}{\bar{x}_j}$$

for every i and j in $\llbracket 1, n \rrbracket$. Setting K to 120% of the vector of average populations is an arbitrary choice, that could be improved using more specific information on the holdings involved that would help estimate their actual carrying capacity.

Once computed the values of the K_i , B_i , b_i , d_i and $\theta_{i,j}$, we run a numerical approximation of System ($\mathcal{S}'_{\text{pop}}$) with initial condition $z(0) = \bar{x}$ until it converges to a value that we take to be z^* . Further simulations will be ran assuming that the population process is at this state (which was already an assumption made throughout Subsection 3.2.2).

The distribution of computed values of K_i , $B_i(K_i - z_i^*)$, $b_i(K_i - z_i^*)$, d_i and $\theta_{i,j}(K_j - z_j^*)$ are displayed in Figure 4.4. Carrying capacities K_i have mean 124.52 individuals and standard deviation 106.32 individuals. Due to the definition of K_i as 120% of the average yearly population in node i over the year, some values of K_i are below 1. Recall that in our model, this does not mean that the population of node i has to be null but that it is bounded by $\lceil K_i \rceil = 1$. The approximated equilibrium populations z_i^* have mean 92.20 individuals and standard deviation 84.67 individuals. The mean of the immigration rates $B_i(K_i - z_i^*)$ is 7.79 individuals.year⁻¹ and their standard deviation 247.50 individuals.year⁻¹ (these quantities falling at respectively 0.25 and 4.09 when excluding operators). The mean of the individual birth rates $b_i(K_i - z_i^*)$ is 0.59 year⁻¹ and their standard deviation 1.41 year⁻¹. The individual death rates d_i have mean 15.42 year⁻¹ and standard deviation 407.79 year⁻¹ (these quantities being respectively 0.65 and 5.71 when excluding operators). Finally, the total transfer outflows $\sum_{j=1}^n \theta_{i,j}(K_j - z_j^*)$ have mean 4.3 individuals.year⁻¹ and standard deviation 108.05 individuals.year⁻¹ (respectively 0.74 and 4.22 when excluding operators). 980 nodes are such that $\sum_{j=1}^n \theta_{i,j}(K_j - z_j^*) = 0$, which means that the corresponding holdings did not send any animal to other holdings of Finistère during 2015.

The FNCD does not contain information about the sanitary status of registered animals, so we cannot calibrate the epidemic parameters β_i and γ_i using our dataset. Numerical explorations on epidemic scenarii will be conducted using parameters calibrated to match foot-and-mouth disease (FMD) epidemics, that have traditionally been modeled using stochastic SIR

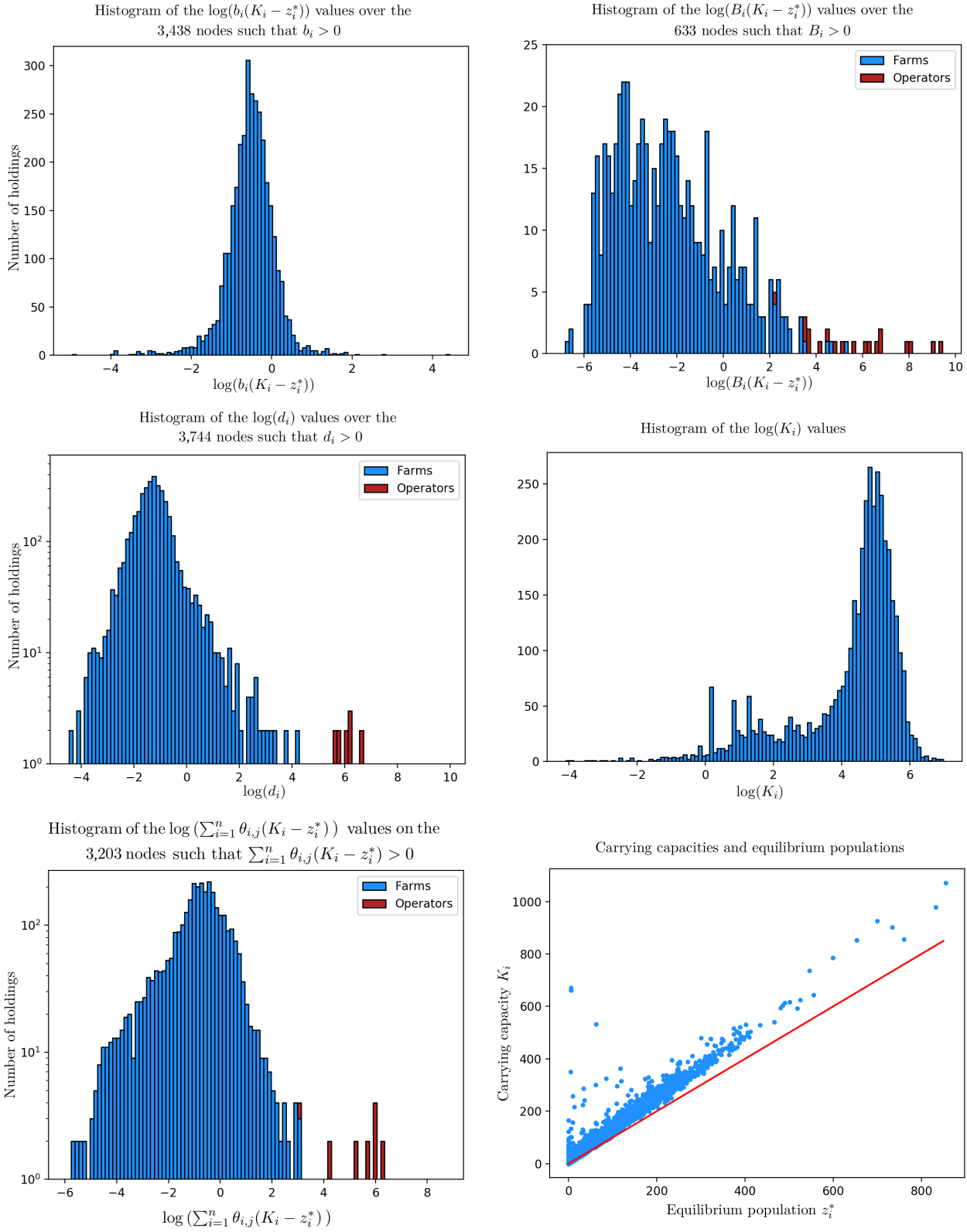


Figure 4.4: Rates, flows and population sizes computed from the parameters K_i , B_i , b_i , d_i and $\theta_{i,j}$ computed for the 2015 Finistère cattle trade network. Values corresponding to farms and operators are distinguished when they significantly differ between these two types of holdings.

specifications [Mil76, HK96, HWK97, DM00, HD00]. FMD is a viral multi-species disease affecting livestock, highly infectious and easy to spread through close contacts and aerosol propagation, which leads to fast dynamics. Estimations of epidemic parameters for the FMD are given in [BdRa15] as $\beta_i = \beta \approx 0.67 \text{ days}^{-1}$ and $\gamma_i = \gamma \approx \frac{1}{5.5} \text{ days}^{-1}$. As Keeling notices in his review of models for FMD epidemics [Kee05], single-node models with homogeneous mixing ignore a key feature of FMD that is its spatial clustering [WSKM03]. Spatial models of epidemics on networks as the one we are considering therefore appear to be a relevant framework to study FMD epidemics. Yet we will see in the next section that the dynamics of FMD are relatively fast as compared to the population dynamics involved, which makes FMD a lesser instructive case for our analysis of graph-based control strategies and will motivate the introduction of an epidemic slowing parameter. Moreover, cases of FMD usually entail trade bans, the immediate culling of all animals in detected infected herds and ring culling, so FMD shall mostly be thought of as a merely illustrative example in the present framework.

4.2

Indicators of node criticality

The theoretical results of Subsection 3.2.2 can be used to derive several types of indicators that quantify the criticality of a given node in making the network vulnerable to the spread of an epidemic. These indicators can be used both to identify critical nodes on which control strategies should act in priority, and to assess the overall network vulnerability consecutively to control measures. The latter task can also be carried out through simulations or numerical approximations of dynamical systems, as we shall see in Section 4.3.

In the case considered here, no infectives structurally enter the system through immigration, and a natural idea is to consider the major outbreak probability for an epidemic started by one single infective accidentally introduced in a given node (Subsection 4.2.1). However, this quantity fails to account for the potential of an epidemic to spread *across* the graph. Moreover, it is less relevant when the population of the node considered is small, since it is the probability of explosion of a branching process that approximates the epidemic process for large typical populations. This leads to considering the propensity of an infective introduced in one node to carry the pathogen and make infectious contacts in *other* nodes during its lifetime, which we do in Subsection 4.2.2. We then propose composite indicators that jointly take into account several aspects of the node criticality, including major outbreak probabilities, probability for the infection to begin in a given node and spatial spread potential (Subsection 4.2.3). Finally, we suggest a Monte-Carlo method (Subsection 4.2.4) that is computationally costly but helps evaluate the relevance of the analysis of major outbreak probabilities.

4.2.1 Major outbreak probabilities

Recall that $p = \mathbb{1}$ (and therefore $q = r = 0$). Propositions 3.2.11 and 3.2.12 then imply that the probability of a major outbreak for an epidemic started by one single initial infective in node i in an otherwise fully susceptible population is

$$\pi_i := 1 - \zeta_i = 1 - \left(\lim_{k \rightarrow +\infty} G^k(s) \right)_i$$

for any $s \in [0, 1]^n$, where G^k is the k -th iteration of function

$$G : s \mapsto \left(\text{diag}(\lambda_1(s), \dots, \lambda_n(s)) - \tilde{\Theta} \right)^{-1} (d + \gamma)$$

where $\lambda_i(s) = (1 - s_i)\beta_i + d_i + \gamma_i + \sum_{j=1}^n \theta_{i,j}(K_j - z_j^*)$ and $\tilde{\Theta} = (\tilde{\theta}_{i,j})_{i,j} := \left(\theta_{i,j}(K_j - z_j^*) \right)_{i,j}$. Throughout this chapter and with no risk of confusing with the limiting probability of the population processes considered, we will write $\pi := \mathbb{1} - \zeta$ to denote the vector of major outbreak probabilities.

Iterating G on an arbitrary point in $[0, 1]^n$, here $0.5 \times \mathbb{1}$, yields an approximation for π having mean 0.7218, standard deviation 0.0413 and ranging from 0 to 0.7286 over the set of nodes. Most of the π_i probabilities are close to the maximal value 0.7286, that corresponds to the major outbreak probability

$$1 - \frac{\gamma + d_i}{\beta} \approx 1 - \frac{\gamma}{\beta}$$

derived in the case where the node is isolated and d_i is small compared to β and γ (see Theorem 3.1.7 and the case $k = 1$ in Figures 4.5 and 4.6). This observation can be explained by the fact that demographic dynamics (and in particular deaths and exchanges) are slow as compared to the FMD epidemic dynamics, so with high probability local epidemics develop and get extinct before the first transfer or death of an infective occurs and most nodes can therefore be considered isolated. This type of mostly local events are of lesser interest in our study that focuses on epidemic spread over the network. We therefore introduce a parameter $k \geq 1$ and virtually slow down the course of the epidemic by dividing both β and γ by k , which decreases the transmission rate and increases the infection period proportionally with k . Increasing the value of k increases the role of inter-nodal transfers and deaths in the determination of major outbreak probabilities. As a consequence, it yields a lower mean value and a higher variance for the $\mathbb{1} - \zeta$ vector, for which the isolation approximation by the vector of the $\left(1 - \frac{\gamma + d_i}{\beta} \right)_+$ does not hold anymore, as we illustrate in Figures 4.5 and 4.6.

For high values of k (e.g. $k = 100$), the distribution of π is fairly spread out but still exhibits two peaks, slightly above 0 and below 0.7286. Further observation suggests that the nodes with the lower probabilities of major outbreak are associated with high removal rates $d_i + \gamma$ (which is typically the case for operators), realize strong transfers to nodes with high removal rates, or are more generally at the origin of heavily weighted paths to exit the system. Nodes with a high probability of major outbreak, at the contrary, are generally almost isolated and with low death rates, or in general at the origin of only low weighted paths to exit the system.

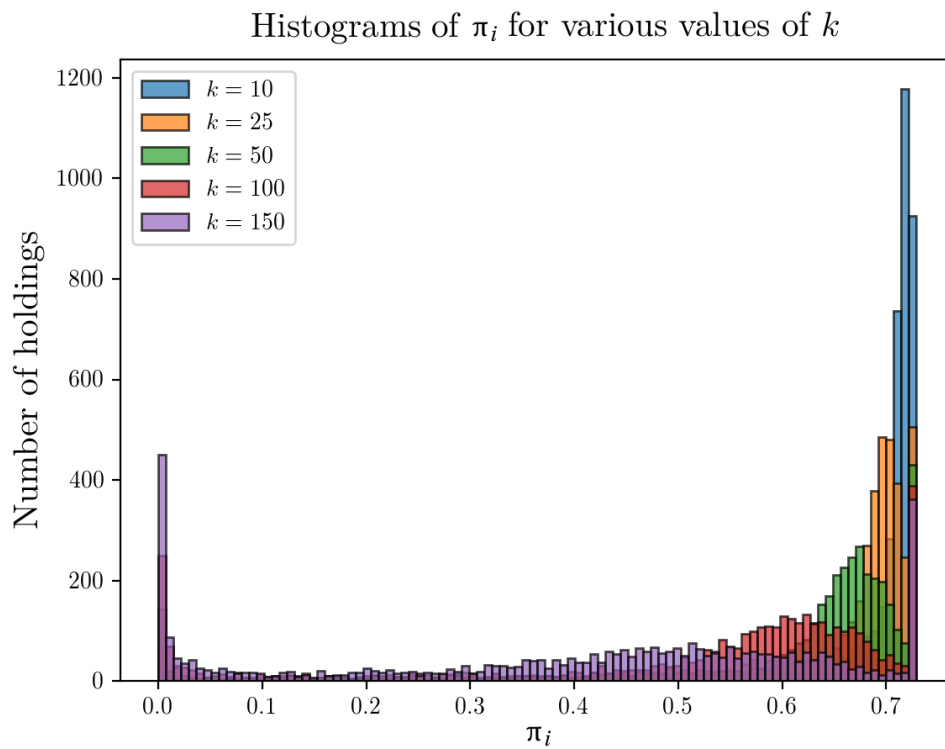
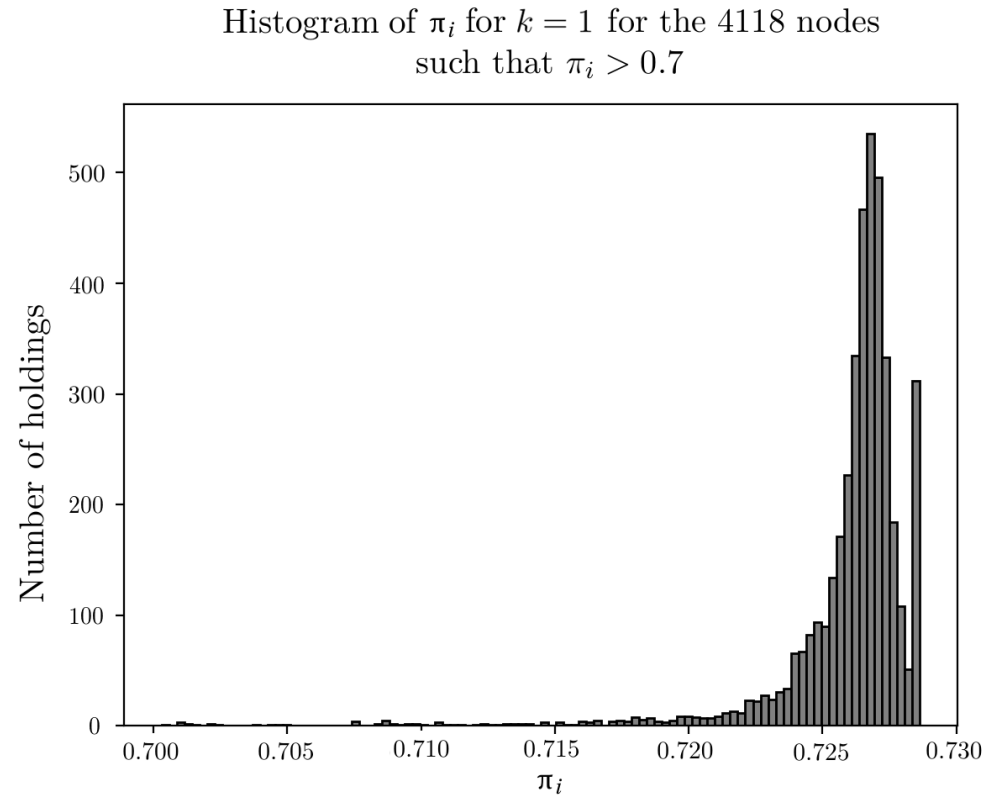


Figure 4.5: Histograms of π_i probabilities for various values of the epidemic slowing parameter k . For $k \neq 1$, histograms are plotted over all 4,183 computed values of π_i . Note the difference in range between both figures.

Due to local saturation effects, the branching approximation given by Theorem 3.2.1 may fail to hold within relatively few propagation steps in practice, which makes the probability of major outbreak irrelevant to qualify the criticality of the smallest nodes. Moreover, as just mentioned, holdings sending few animals towards other nodes of the network and with low death rates are associated with high probabilities of major outbreak. While this observation is quite conform to the intuition one can have on the behavior of the branching approximation for an epidemic process initiated in such nodes, it does not seem reasonable to identify these nodes as critical regarding the vulnerability of the network as a whole. Indeed, major epidemic outbreak in such nodes have a high probability to be only local epidemic events, with a high proportion of the population of the node being infected but a low geographical spread. We must therefore look for vulnerability indicators taking into account the spatial dimension of the pathogen spread, which will be done in the next subsection.

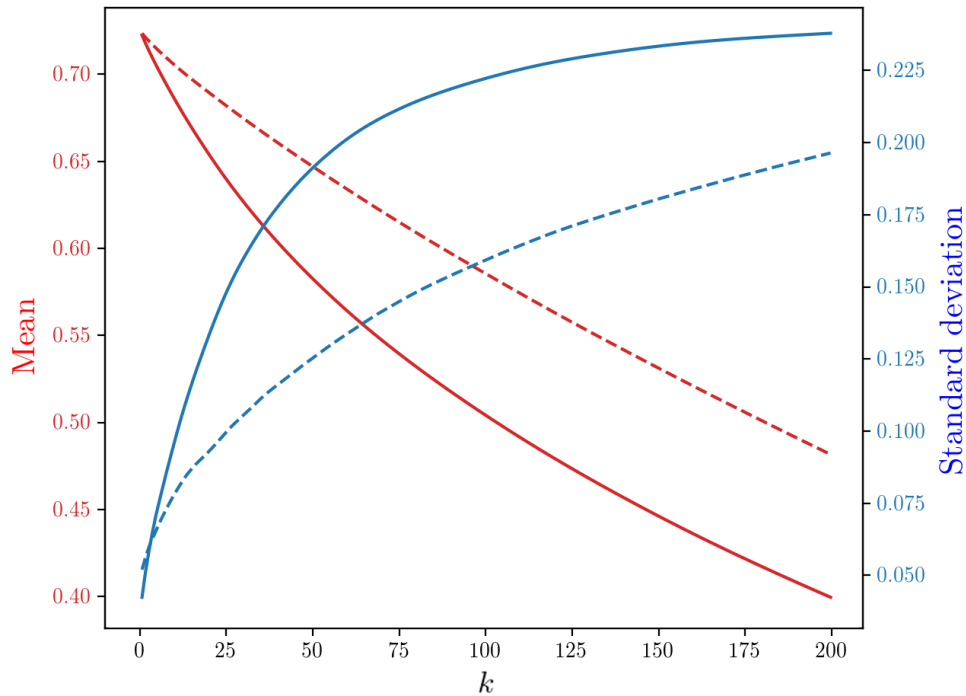


Figure 4.6: In plain lines: mean (red plot) and standard deviation (blue plot) of the vector of probabilities of major outbreak π_i for k ranging from 1 to 200. In dashed lines: mean (red plot) and standard deviation (blue plot) of the vector of probabilities of major outbreak for isolated nodes, that is, the vector of $\left(1 - \frac{\gamma/k + d_i}{\beta/k}\right)_+$ values.

4.2.2 Mean number of contaminated nodes

A simple indicator for the criticality of a node i in terms of spatial propagation of an epidemic is the mean number of nodes reached and infected by an epidemic started by one initial infective initially in node i . However, we are not able to provide an analytical expression for this quantity in the framework of our model. As a first approximation of this indicator and with the

notations of Subsection 3.2.2, we therefore consider the quantity defined by

$$m_i := \mathbb{E} \left(\sum_{j \neq i} \mathbb{1}_{W_{i,j} > 0} \right) = \sum_{j \neq i} (1 - \mathbb{P}(W_{i,j} = 0)) = \sum_{j \neq i} (\mathbb{1} - G(\mathbb{1} - e_j))_i, \quad (4.1)$$

that is, the average number of nodes other than i where the initial infective itself makes infectious contacts during its infectious period.

This indicator is reminiscent of the *household reproduction number* [PBT11, BPT16] defined in the framework of household-structured networks with two levels of mixing. In this latter case, local small-sized populations are homogeneously mixing, and the epidemic processes obtained by considering these dynamics are superimposed to a homogeneous mixing of the global population at a smaller rate. Because of the difference between local and global rates and the limited size of the households, it is reasonable to assume that local epidemics follows their course and hit a proportion of individuals within their original subpopulation before they spread to other households. In this context, the household reproduction number gives the number of households hit by the epidemic consecutively to infectious contacts by members of an initially infected household. This quantity therefore appears like a basic reproduction number for a model in which households, and not individuals anymore, would make infectious contact with each other and contribute to the spread of the pathogen following dynamics that can be approximated by a branching process as the number of households becomes large. Although the situation is not the same in our framework, where no homogeneous mixing with the global population is considered, the definition of the m_i relies on the same idea of characterizing the mean number of nodes infected during the first step of an epidemic.

The distribution of m_i for $k = 1$, $k = 10$ and $k = 100$ is given in Figure 4.7. For $k = 1$, their values range from 0 for 0.707 nodes reached by the infection, with mean 0.0049 and standard deviation 0.0224. For $k = 10$, they range from 0 to 0.4194, have mean 0.0222 and standard deviation 0.0379. Finally, for $k = 100$, their values range from 0 to 0.7021, with mean 0.0480 and standard deviation 0.0694. The m_i values are therefore non monotonic with k : as k grows higher, the generation of new infectives is slowed down, which hampers epidemic propagation, but so is the remission process, which makes infectives (and in particular, the initial infective considered in the calculation of m_i) able to cause infections for a longer time and therefore fosters epidemic spread.

The graph-based indicator m seems relevant even in the case of small local populations, since it focuses on the trajectory of one single infective and the number of nodes in which it makes infectious contacts. However, it may underestimate the spread potential from a node within which the infection develops quickly and from which many second-generation infectives leave to carry the infection forward. More generally, it only takes into account the spatial propagation of the epidemic, and presents the opposite drawback from the major outbreak probabilities vector, which is to miss information on the number of infected individuals in the visited nodes. In the next subsection, we will therefore be looking for indicators combining considerations on the volume of the epidemic in terms of numbers of individuals affected and on its geographical spread.

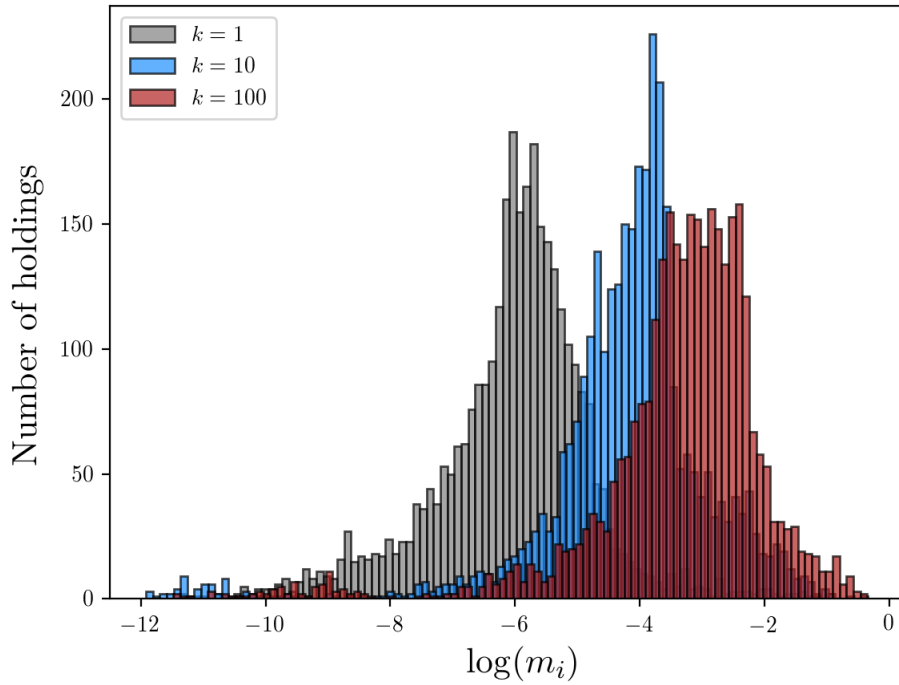


Figure 4.7: Histogram of $\log(m_i)$ values different values of the epidemic slowing parameter k , on the holdings such that $m_i > e^{-12}$ (3202 for $k = 1$, 3185 for $k = 10$ and 3199 for $k = 100$).

4.2.3 Composite indicators

More sophisticated composite indicators for the criticality of a given node in making the network vulnerable can be built using the π and m vectors.

Since $p = \mathbb{1}$, the proportion of infectives entering the system through immigration is zero, so we consider that the epidemic starts from one infective introduced in a given node in an exogeneous fashion. Considering that this rare event is in practice realized through importations (which in reality is not necessarily the case for an FMD infection that can be airborne), it is reasonable to think that the probability for an infective to enter the system through node i is proportional to the immigration flow in node i , that is, to $B_i(K_i - z_i^*)$. This suggests the use of the composite indicator

$$\pi'_i = B_i(K_i - z_i^*)\pi_i. \tag{4.2}$$

This number, that will be referred to as *weighted major outbreak probability* (but that is not a probability itself!), takes into account the risk of an epidemic to be started from node i . Yet it fails to identify as critical some nodes with no immigration but with a central position in the trade network that makes them likely to receive and dispatch infective individuals. Moreover, π'_i may take a high value for a node i with few or no population outflow, associated with a high risk of a major but strictly local epidemic outbreak, just as π_i . The distribution of the π'_i is represented in Figure 4.8 for various values of the slowing parameter k . Its tail corresponds mostly to operators nodes, while this is not the case for the major outbreak probability indicator. This observation is to be related to the distribution of the $B_i(K_i - z_i^*)$ given in Subsection 4.1.2.

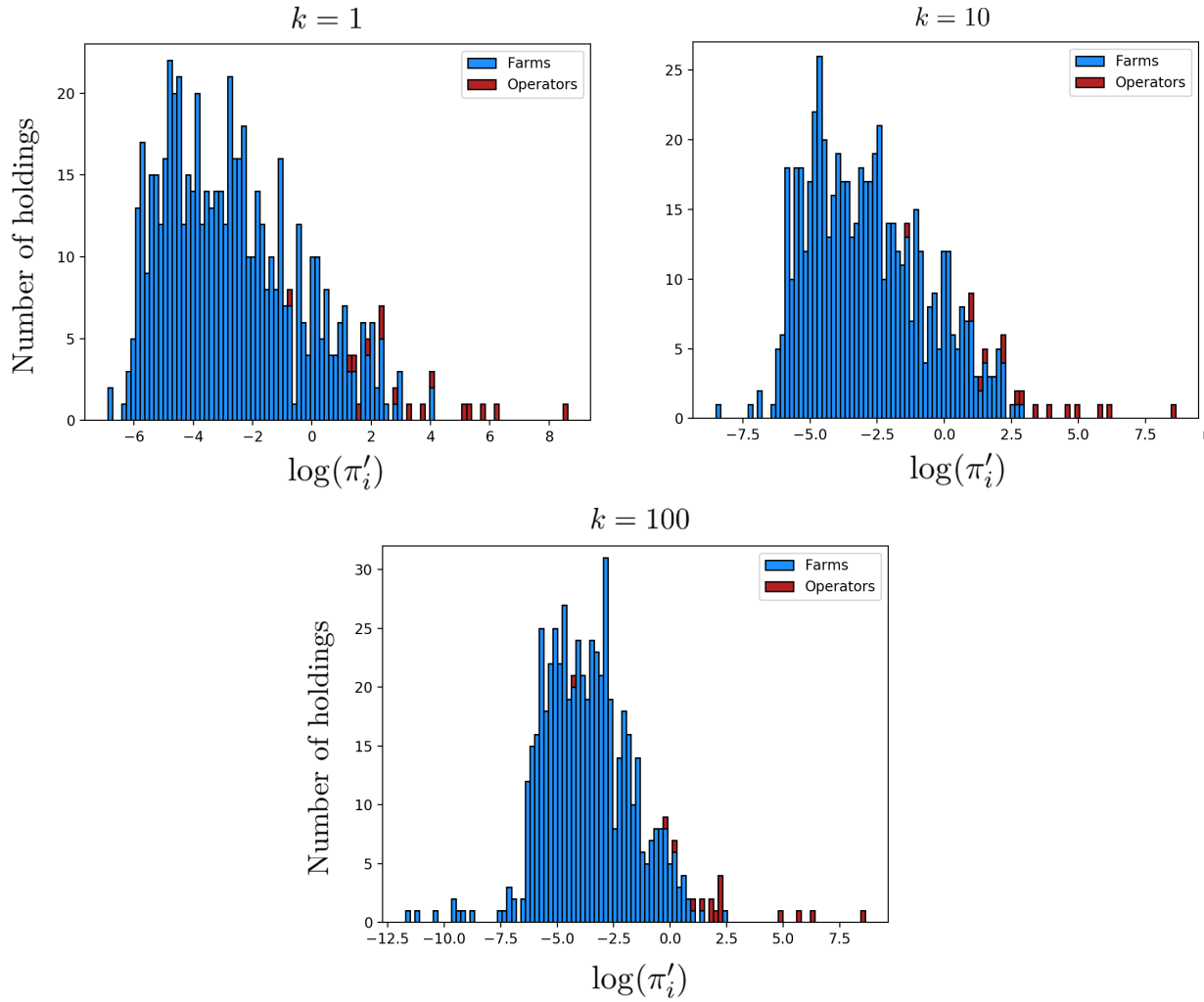


Figure 4.8: Histograms of $\log(\pi'_i)$ indicators for various values of the epidemic slowing parameter k .

Combining volume and spatial considerations may yield to the following "second-step" indicator:

$$v_i = \mathbb{E} \left(\sum_{j=1}^n (1 - (1 - \pi_j)^{W_{i,j}}) \right) = \mathbb{E} \left(\sum_{j=1}^n (1 - \zeta_j^{W_{i,j}}) \right) = N - \sum_{j=1}^n G_i (\mathbb{1} + (\zeta_j - 1) e_j) \quad (4.3)$$

that involves the number $W_{i,j}$ of infections directly caused in node j by an initial infective introduced in node i , $1 - (1 - \pi_i)^{W_{i,j}}$ being the probability that these second-generation infectives introduced in the otherwise fully susceptible population of node j (if $j \neq i$, and with only one infective if $j = i$) cause a major outbreak under the branching process approximation for an epidemic process started at node j .

Indicators v_i attribute a low weight to infectious contacts realized in nodes j such that ζ_j is close to 0, that is, in nodes that act as sinks for the epidemic process. At the contrary, they strongly take into account infectious contacts made in nodes with high probabilities of starting major epidemic events. Yet the contribution of a node j to v_i is bounded by 1, which minimizes the role of strong inter-nodal transfers in the epidemic spread. Using the approximation

$$(1 - (1 - \pi_j)^{W_{i,j}}) \approx -W_{i,j} \log(1 - \pi_j) = -W_{i,j} \log(\zeta_j)$$

that holds when $W_{i,j}$ is small, we come up with the following variant of v_i :

$$v'_i = \mathbb{E} \left(- \sum_{j=1}^n W_{i,j} \log(\zeta_j) \right) = - \sum_{j=1}^n \mathbb{E}(W_{i,j}) \log(\zeta_j). \tag{4.4}$$

Using Proposition 3.2.11, we get the following formula for v' :

$$v' = -C^t (\log(\zeta_1), \dots, \log(\zeta_n)) = -(\text{diag}(\Sigma'_1, \dots, \Sigma'_n) - \Theta')^{-1} (\beta_1 \log(\zeta_1), \dots, \beta_n \log(\zeta_n)). \tag{4.5}$$

where we recall that $\gamma_i + d_i + \sum_{j \neq i} \theta_{i,j} (K_j - z_j^*)$, that $\Theta'_{i,i} = 0$ and that $\Theta'_{i,j} = \theta_{i,j} (K_j - z_j^*)$ for all i and all $j \neq i$.

Histograms of v'_i for various values of k

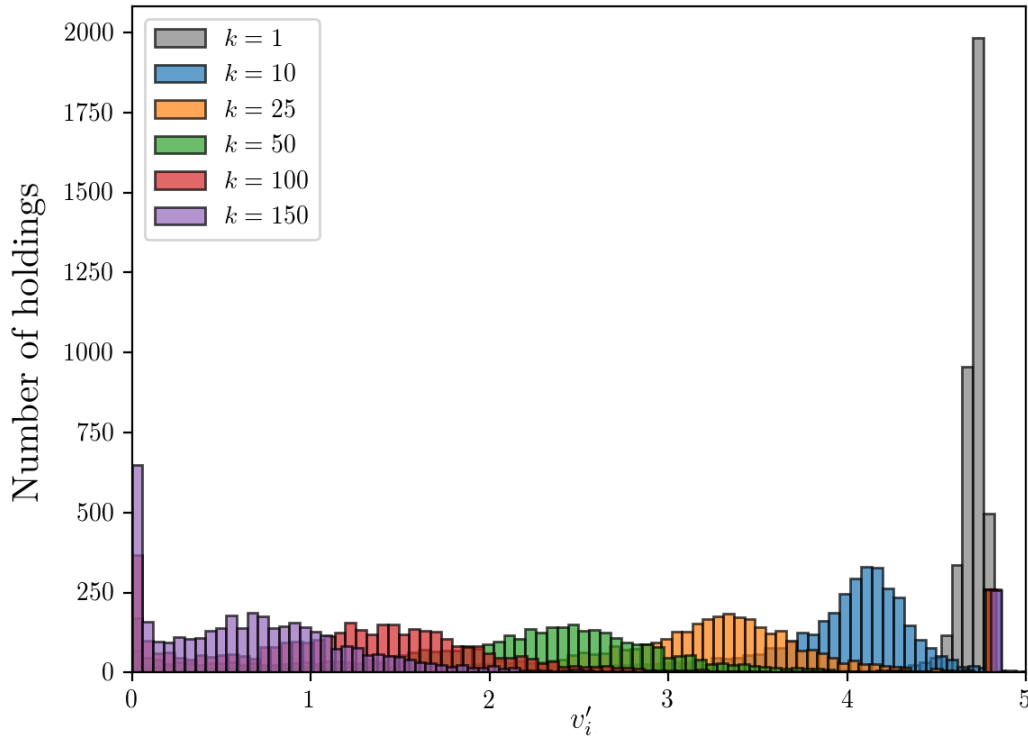


Figure 4.9: Histograms of v'_i indicators for various values of the epidemic slowing parameter k .

We note that the contribution of node j to v'_i cannot be infinite since all the ζ_j are positive — indeed, the empirical bound $\zeta_j \leq 1 - \beta/\gamma \approx 0.7286$ may be proved by remarking that $\|I'\|_1$ (where

I' is the branching process given by Theorem 3.2.10) can be bounded above by a unitype branching process with birth rate β and death rate γ , that survives with probability $1 - \beta/\gamma$. Comparing Equations (4.3) and (4.5) shows that the computation time for v' is much lower than that of v since it does not require evaluating the moment generating function G at the n vectors $\mathbb{1} - (\zeta_j - 1)e_j$. The distributions of the v'_i for various values of the epidemic slowing parameter k can be found in Figure 4.9. For all values of k , the distribution of v' is more spread out than the distribution of π . Consistently with the decrease of the π_i with k and the fact that the $\mathbb{E}(W_{i,j})$ are bounded by β/γ , the mean of vector v'_i decreases as k gets larger (see Figure 4.10), but the v'_i stay high (above 4.5) for a number of nodes that seems to stabilize around 260. Further investigations show that these are the 261 nodes of the graph with no mortality and no outgoing flows, that is, the nodes for which $d_i = 0$ and $\sum_{j=1}^n \theta_{i,j}(K_j - z_j^*) = 0$; the v'_i value for such nodes is therefore equal to the corresponding unitype value with $d = 0$, that is, $\log(\zeta)\mathbb{E}(W) = \log(\gamma/\beta)\beta/\gamma \approx 4.806$ (see Theorems 3.1.7 and 3.1.2). It can be seen on Figure 4.11 that restricting the analysis to a subsample of *sender* nodes with high enough outflow rates makes this density peak disappear from the distribution of v'_i for $k = 100$, and to a lesser extent from that of the π_i .

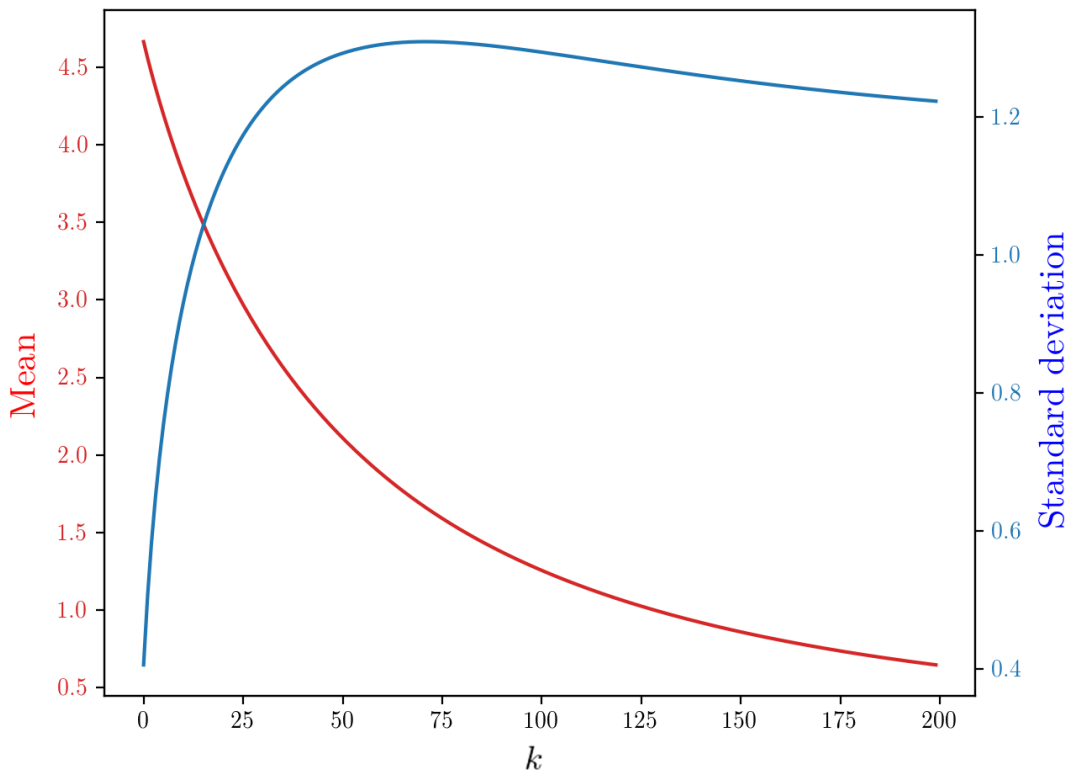


Figure 4.10: Mean and standard deviation of the vector v' for k ranging from 1 to 200.

In Section 4.3, we will examine node-based control strategies designed using the major outbreak probabilities π_i , the mean number of contaminated nodes m_i defined by (4.1), the weighted major outbreak probabilities π'_i defined by (4.2) and the second-step indicators v'_i defined by (4.4).

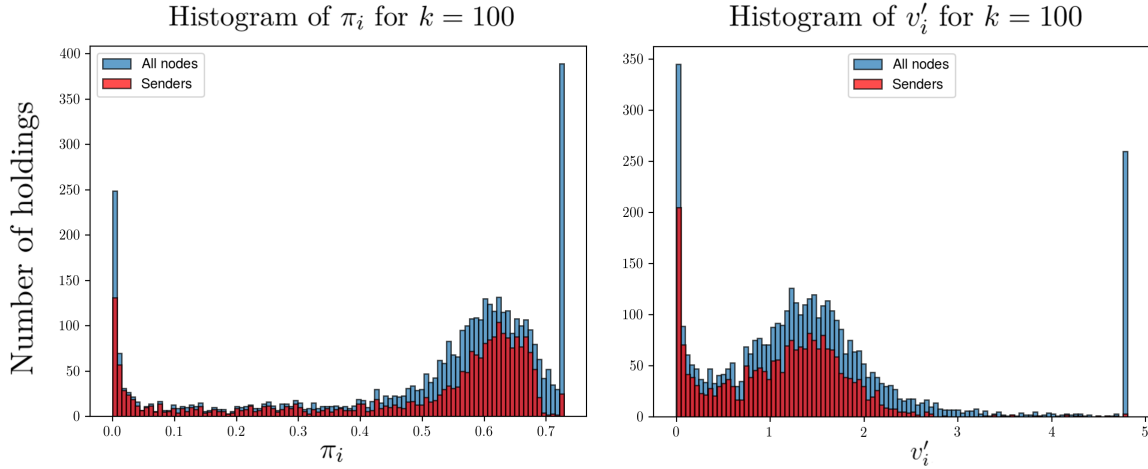


Figure 4.11: Histograms of π_i (on the left) and v'_i (on the right) indicators for $k = 100$, for the 4,183 nodes (in blue) and for the subset of the 2278 sender nodes defined by $d_i \geq 0.1$ and $\sum_{j=1}^n \theta_{i,j}(\mathbb{K}_j - z_j^*) \geq 0.1$.

4.2.4 Simulation-based indicators

A last set of indicators can be derived from a Monte-Carlo method consisting in simulating trajectories of the epidemic process started by one infective introduced in one node, and recording interest quantities such as the epidemic total size, the number of nodes it reached and infected or its extinction time. Observing the epidemic until it goes extinct makes it possible to estimate a great variety of parameters, among which the empirical counterparts of those introduced in the previous subsections. For instance, theory (namely Theorem 3.2.10) predicts that with high probability and when the epidemic is started from nodes with a high enough population, trajectories will either reach the disease-free states in a relatively short time (corresponding to a low epidemic total size) or reach an endemic level and gravitate around it before going extinct, yielding a much longer extinction time and a much higher epidemic total size. Computing the proportion of simulated trajectories that correspond to the second case provides a direct estimation for the probability of major outbreak of the epidemic — defined this time as the probability of an *actual* major epidemic event for the epidemic process, and not of the survival of the approximating branching process I' .

Conversely, we may use the Monte-Carlo method discussed here to illustrate the relevance of the (quickly computable) π_i indicators in the case of nodes with moderate to high populations. Figure 4.12 shows the final size of 100 simulated epidemics started in an example node (a farm with $z_i^* \approx 144$), for different values of the slowing parameter k , the corresponding π_i values and the empirical proportion of major outbreaks. A typical trajectory corresponding to a major epidemic outbreak is represented in Figure 4.13.

Besides allowing to check the validity of theoretical indicators, Monte-Carlo based investigations allow to estimate quantities that cannot be derived analytically due to the complexity of the epidemic process. Its most obvious drawback is its computational cost, since estimating for

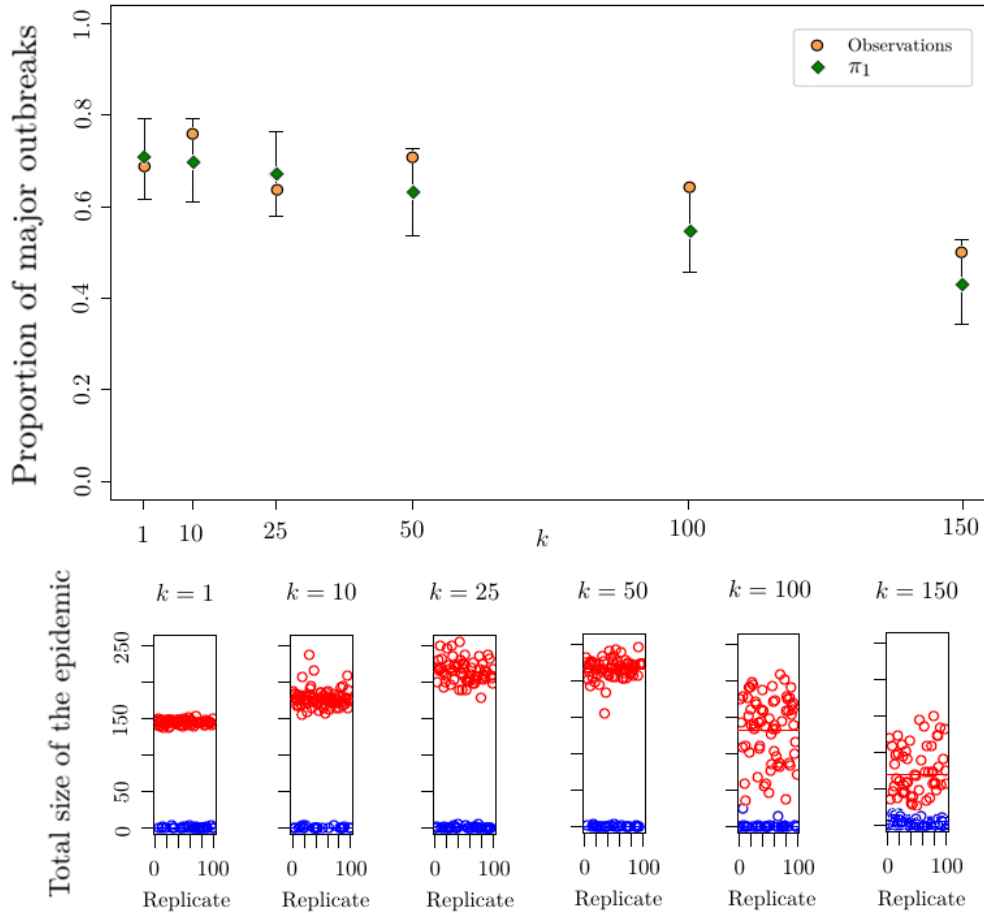


Figure 4.12: Empirical and theoretical proportions of major epidemic outbreaks for an epidemic started by one initial infective in a node associated to demographic parameters $b_1 = 0.01$, $B_1 = 0$, $K_1 = 194.34$, $z_1^* = 144.21$ and such that $\sum_{j \neq i} \theta_{i,j} (K_j - z_j^*) = 0.36$. For each value of the slowing parameter k , 100 epidemic processes have been simulated until extinction or until a three-year limit. The corresponding epidemic total sizes have been represented in the lower panel, with observations at 25 individuals or above (in red) being interpreted as results of major epidemic outbreaks and observations strictly below 25 (in blue) being seen as corresponding to minor epidemic outbreaks — setting a threshold at 25 individuals in an arbitrary choice. The proportions of major outbreaks observed have been reported in the upper panel (dots), along with the corresponding theoretical values of major outbreak probabilities π_1 (diamonds) with the associated 95% percentile theoretical intervals. Simulations and their representation have been realized by François Deslandes.

instance the probabilities of major outbreak for epidemics started by one initial case in a given node requires $n \times m$ runs of the simulation algorithm, where m is the number of simulated trajectories for each initial condition $I(0) = e_i$. Using the tau-leaping simulation algorithm 1.4.3 presented in Section 1.4 is likely to make individual simulations faster than using the standard SSA algorithm. However, SSA simulations might already prove fairly efficient for the specification we are considering, since only a limited number of jump rates needs to be updated after

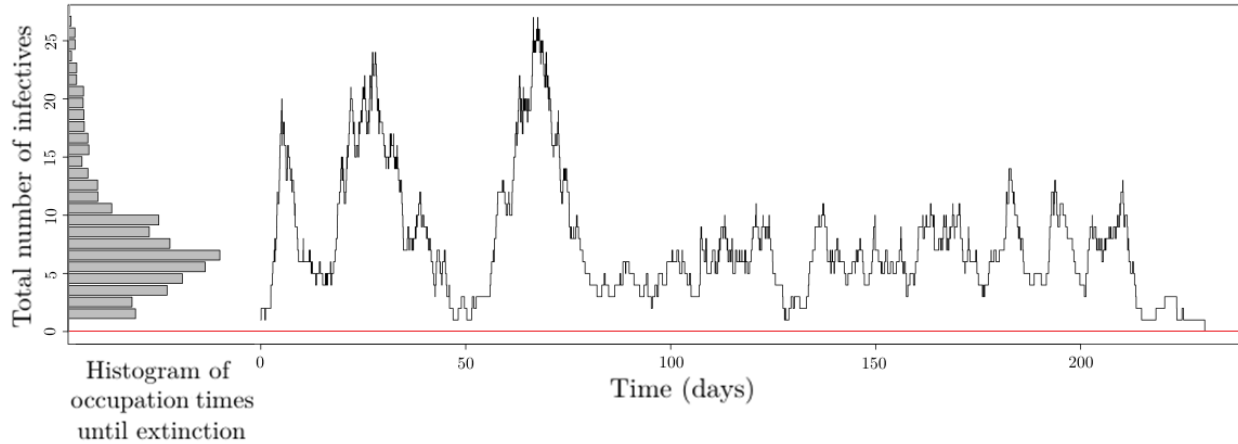


Figure 4.13: Simulated trajectory of $\|I^N\|_1$ for an epidemic started at a node i with $K_i = 286.78$, $z_i^* = 34.09$, $d_i = 2.61$, $b_i(K_i - z_i^*) = 0$, $B_i(K_i - z_i^*) = 13.54$ and $\sum_{j \neq i} \theta_{i,j}(K_j - z_j^*) = 0$, with the slowing parameter k set to 100. The epidemic goes extinct in 230 days, after undergoing a major outbreak then stabilizing around a moderate level. The histogram of occupation times before extinction is plotted on the left side of the panel. The simulation and its representation have been realized by François Deslandes.

each jump of the epidemic process. At the time of writing this manuscript, the tau-leaping algorithm still is to be implemented and only some SSA simulations have been performed. In our application, about one node out of five (among 4,183) has an empirical population lower than 10 individuals, so we cannot take $n_c = 10$ in the modified tau-leaping Algorithm 1.4.3 as recommended in [CGP06] without ignoring most of the population dynamics in these nodes with low population. We will therefore take $n_c = 5$ instead, which hopefully should already prove efficient in limiting the number of loops to Step 5 from Step 10.

4.3

Elaboration, choice and evaluation of targeted control strategies

Having defined criticality indicators that qualify how a given node makes the graph vulnerable to the spread of an epidemic, we may design control strategies on the nodes identified as critical. In order to evaluate different types of measures, we first need to be able to estimate the epidemic severity for a given setting of the model parameters (Subsection 4.3.1). It is then possible to design (Subsection 4.3.2) node-based control strategies under cost constraints and assess their effect on the final outcome of the epidemic (Subsection 4.3.3).

4.3.1 Assessing the severity of an epidemic event

Defining quantities related to the severity of an epidemic event is necessary to guide and evaluate epidemic control strategies. The best option would certainly be to derive theoretically a computable threshold parameter that would help predict the behavior of the epidemic and its final size. Another, more costly method, is to rely on another Monte-Carlo approach based on simulations of trajectories of the epidemic process.

4.3.1.1 The quest for a threshold parameter

Results on the final size and extinction time of the epidemic in the case of a major outbreak scenario, such as Theorem 3.2.15, do not provide with numerical estimates precise enough to evaluate the influence of model parameters on these quantities. We are left looking for a synthetic and easily computable indicator of the severity of an epidemic event. A natural candidate for this purpose is the basic reproduction number R_0 defined in Proposition 3.2.11, which is an epidemiological key parameter:

"The basic reproduction number R_0 is arguably the most important quantity in infectious disease epidemiology. It is among the quantities most urgently estimated for emerging infectious diseases in outbreak situations, and its value provides insight when designing control interventions for established infections." [DHB12]

In the standard monotype SIR model without demography (corresponding to any of the SIR models introduced in Section 3.2 with $n = 1$ and $B = b = d = 0$), the basic reproduction number $R_0 = \frac{\beta}{\gamma}$ is a relevant quantity to evaluate the severity of an epidemic. Indeed, the total size of the epidemic in case of a major outbreak is approximately a fraction τ of the population, where τ is the only positive solution of the equation $1 - e^{-R_0\tau} = \tau$ (see Chapter 4 of [AB00a]). Moreover, the major outbreak probability may also be expressed as a function of R_0 (it is $(1 - 1/R_0)_+$) if $I(0) = 1$.

We can see by Proposition 3.2.11 that the general, multitype-case basic reproduction number still exhibits a threshold property concerning the occurrence of a major outbreak. Yet, as the dominant eigenvalue of the mean offspring matrix C , it only contains partial information about it if $n \geq 2$, and does not yield a clear insight anymore on the final outcome of an epidemic in the case of a major outbreak. An instructive case to consider is when there exists i such that $d_i = 0$ and such that $\sum_{j=1}^n \theta_{i,j}(K_j - z_j^*) = 0$ (that is, nodes with no outflows); then R_0 is close to β/γ regardless of the setting of the rest of the network. In particular, slowing down the epidemic by dividing β and γ by k does not affect much this value. Such is the case in the network we consider, and computations indicate that for all values of k , the R_0 estimate is less than 10^{-12} distant from the the basic reproduction number $\beta/\gamma = 3.685$ of a unitype, closed and homogeneously mixing SIR model.

In our logistic-driven SIR framework, the reason why R_0 determines whether the major outbreak probability is positive for an epidemic initiated in *any* node is straightforward. Every node i for which the local basic reproduction number

$$R_0^i := \frac{\beta}{d_i + \gamma_i + \sum_{j=1}^n \theta_{i,j}(K_j - z_j^*)}$$

is close to β/γ is reachable from any other node in the network thanks to the connectivity assumption we made on Θ (and therefore on $\tilde{\Theta}$), and any infective introduced in i among an otherwise fully susceptible population starts a major epidemic outbreak with positive probability. This observation holds regardless of the probability for an infective initially individual situated in a given node to reach node i . That R_0 is a threshold parameter for our model in the sense of Proposition 3.2.11 is therefore of lesser interest. Yet the question of defining a proper threshold parameter for graph-based models such as the one under study is still open, and one of the challenges left to spatial epidemic modeling in general [REI⁺15]. Alternative definitions of R_0 as the eigenvalue of a very general "next generation matrix" linear operator have been put forward [DHM90, DHR09], and various threshold parameters, among which the *household reproduction number* discussed in Subsection 4.2.2, proved to give good results in specific modeling contexts [BST09, PBT11, BBH⁺15, BPT16]. However, absence of global homogeneous mixing, clumping effects inherent to spatial models (as in the case of nearest neighbor lattice contact structures [MK85]) and possible fast depletion of susceptibles in low populated nodes make our model unfit for being described by these parameters. The very idea of the existence of a unique parameter assessing the severity of an epidemic in our framework is therefore debatable.

4.3.1.2 Monte-Carlo estimation of the epidemic final outcome

An alternative idea to evaluate the severity of the epidemic is again to use Monte-Carlo-inspired explorations, where the mean epidemic final size and the mean epidemic extinction time are estimated based on simulated trajectories of the epidemic process. In the present framework, we consider epidemics started from the accidental introduction of an infectious individual in an otherwise fully susceptible population through immigration. As stated when building the criticality indicators m_i in Subsection 4.2.2, we may therefore assume that the probability for this first infective to be introduced in node i is proportional to the immigration flux $B_i(K_i - z_i^*)$ in this node. A baseline for the evaluation procedures described in Subsection 4.3.3 will therefore be to simulate trajectories of an epidemic process started at state $(\tilde{z}^*, e_i, 0) \in (\mathbb{Z}_+^n)^3$ (where \tilde{z}_j^* is the closest integer to z_j^*) for a node i chosen at random among $\llbracket 1, n \rrbracket$ with probability proportional to $B_i(K_i - z_i^*)$. We will then record these trajectories to obtain a control sample to be compared with trajectories obtained under new rules that correspond to the policy under study.

Once again, tau-leaping algorithms for the simulation of the epidemic process have not yet been implemented at the time of writing this manuscript. Their effect on the computation time of the numerous trajectories necessary for the precise assessment of control measures remains unknown, although results from [KPSK15] on unitype SIS epidemic simulations are a cause for optimism.

4.3.2 Design of control strategies

Control and containment of human [HBG04, CPJEJG06, CBBV06, FCF⁺06] and animal diseases [Mye88, WS18] is an active field of theoretical research, and of course a major issue of sanitary legislation [FAO99]. Concerning cattle diseases, epidemic containment measures range from avoiding contacts between infected and susceptible animals, performing random screening to detect and remove infected animals from the herds, vaccinating susceptible animals or

reducing access of pathogen vectors to susceptible animals, to geographic zoning, slaughter and ring culling [TBKW09]. In the context of the present work, we shall not review the abundant literature on disease control, but will instead focus on graph-based control strategies that consist in actions on parameters and initial populations related to critical nodes.

4.3.2.1 Identification of critical nodes

The first step of designing graph-based control strategies consists in identifying the nodes that will be referred to as *critical* regarding the graph vulnerability they induce.

We saw in the previous section that unweighted and weighted major outbreak probabilities π_i and π'_i take high values even on nodes with a low inter-nodal outflow $\sum_{j=1}^n \theta_{i,j}(K_j - z_j^*)$, that yet cannot be considered as making the network vulnerable. We therefore define as *critical with respect to π* (resp. to π') every node i such that $\sum_{j=1}^n \theta_{i,j}(K_j - z_j^*) \geq 0.1$ and $\pi_i \geq \alpha$ (resp. $\pi'_i \geq \alpha$), where $\alpha > 0$ is a quantity to be determined according to the possible scale of the control strategy. Note that α may depend on the empirical distribution of the π_i , for instance when the chosen rule is to act on a given number of holdings with the higher π_i such that $\sum_{j=1}^n \theta_{i,j}(K_j - z_j^*) \geq 0.1$, or when it is stated in terms of number of individuals affected by an action on critical nodes. The condition $\sum_{j=1}^n \theta_{i,j}(K_j - z_j^*) \geq 0.1$ is entirely arbitrary but seemed like a good option to rule out the case of holdings without significant population outflows while not excluding too many nodes from the analysis (see again the distribution of $\sum_{j=1}^n \theta_{i,j}(K_j - z_j^*)$ in Figure 4.4).

Similarly, the rule for defining a node i as *critical with respect to m* is of the form $m_i \geq \alpha$ (resp. $\pi'_i \geq \alpha$), and that for defining it as *critical with respect to v'* is of the form $v'_i \geq \alpha$.

Having these rules in mind, a legitimate interrogation is whether the nodes identified as critical for one indicator are also critical for others. In order to quantify the correlation between critical nodes sets, we use a rank similarity measure that puts an emphasis on overlaps of the top ranks, the Rank-Biased Overlap (RBO) measure [WMZ10]. Roughly speaking, the RBO measure computes the expected value of the average overlap between partial lists browsed by an observer until a random rank $D \wedge n$, where D has a geometric distribution of parameter $p \in (0, 1)$. An interpretation for parameter p is simply the probability for the observer who read the list until a given rank to keep reading until the next rank instead of getting tired, not going to the next rank and computing the average overlap of all the partial lists read so far. We take p to be 0.95, so 20 indexes out of 4,183 are scanned by the observer on average. With this value of p , we observed that the RBO of two independent random permutations of $\llbracket 1, 4183 \rrbracket$ ranges between $9,54 \times 10^{-6}$ to 0.0349, with mean 0.0041 and standard deviation 0.0068 on 100 trials. For $k = 100$, we get the following RBO measures:

	π	π'	m	v'
π	1	0.261	0.107	0.769
π'	0.261	1	1.15×10^{-5}	0.229
m	0.107	1.15×10^{-5}	1	0.117
v'	0.769	0.229	0.117	1

Table 4.2: RBO measures for couples of indicators $A, B \in \{\pi, \pi', m, v'\}$.

It appears from such measures that top-rank indexes for π and ν' are highly correlated (which is confirmed by the Spearman correlation coefficient for π and ν' being 0.9866, while other correlations are close to or below 0). We thus expect a strong overlap between critical nodes sets for π and ν' .

4.3.2.2 Actions on critical nodes

We hereby focus on three types of possible strategies on nodes identified as critical. The protocols we put forward are purportedly simplistic so they can be adapted to fit given cost constraints. A review on strategies to control the spread of an epidemic on a complex network may be found in [PCVV15].

Preventive measures to block infectives importation: the screening strategy

In our framework, epidemic events start from the accidental immigration of an infective individual. Controlling the sanitary status of imported animals in nodes identified as critical and preventing the immigration of infectives in these nodes is therefore likely to reduce the probability that an epidemic starts in a node where its probability to undergo a major outbreak or to reach a high number of nodes is important. This strategy, that we will refer to as *screening at importation*, naturally applies to nodes that are critical with respect to π , π' or ν' . We may assume that the cost of such a strategy is roughly proportional to the number of screened animals, which commands to choose the threshold α such that the total number of screened animals $\sum_{i \text{ critical}} B_i(K_i - z_i^*)$ is below a given level.

Spread containment: the isolation strategy

Another approach is to delete edges of the graph through which the epidemic is likely to spread, that is, to set $\theta_{i,j}$ to zero for critical nodes i and for a selection or for all their neighbours j . This isolation strategy is reminiscent of the preventive rewiring [BJS16] or preventive dropping of edges [BBLS18] involved in models for SIR epidemics on random networks, in which susceptible individuals (modeled as nodes) can take preventive measures by deleting edges (that is, possibilities of contact) to their infectious neighbours. Once again, we may consider as a first approximation that the cost of an edge deletion is proportional to the mean number of animals involved, that is, to $\theta_{i,j}(K_j - z_j^*)$, which results in taking α such that $\sum_{(i,j) \text{ deleted}} \theta_{i,j}(K_j - z_j^*)$ is below a given level. A clever selection of edges to be deleted for each critical node requires a deep graph connectivity analysis, examples of which can be found in [DEV14, MGM⁺16, PCVV15]. Note that deleting all edges coming out of a holding (that is, preventing it from sending individuals anywhere else in the graph) turns it into an epidemiological sink. From the point of view of graph vulnerability analysis, this amounts to its deletion. A simple control strategy, that we will refer to as *isolation*, could therefore be to set to 0 all $\theta_{i,j}$ for nodes i that are identified as critical. This policy is expected to apply best to nodes that are critical with respect to m' .

Local control: the vaccination strategy

A third strategy is *vaccination*, that mathematically consists in turning the sanitary status of a proportion of individuals from S to R in targeted nodes. A great amount of literature has been endeavouring to design optimal vaccination policies for given vaccination costs and epidemic dynamics [MW74, HW73, DH00]. A straightforward result for closed SIR models is that

vaccinating a proportion $(1 - 1/R_0)_+$ of susceptible animals leads to a new basic reproduction number below 1, and therefore prevents major epidemic outbreaks from occurring. However, as discussed in Subsection 4.3.1.1, this costly method (here $1 - 1/R_0 \approx 0.73!$) focuses on reducing a parameter that, even when above 1, is poorly indicative of the severity and the expected outcome of the epidemic in a structured metapopulation. Local vaccination strategies have been considered in the framework of structured populations [BPT16] and household models [BS18], comparing individual-based and household-based vaccination schemes. In this context, vaccination policies targeting households with a strong network centrality have been proved to yield good results. Inspired by this observation, we define our vaccination strategy as the fact of turning a fraction $(1 - 1/R_0)_+$ of Susceptibles into Removed individuals for critical nodes. We expect criticality with respect to m' or v' to be the most relevant in this case. We assume the costs of vaccination to increase linearly with the number of treated animals, so the threshold α will be chosen such that $\sum_{i \text{ critical}} (1 - 1/R_0)_+ z_i^*$ is below a given level.

4.3.3 Control strategies assessment

At the time of writing this manuscript, the assessment of the control strategies presented above by the final outcome of simulated epidemics is still in progress. We detail the procedure that will be used to evaluate the outcome of all three types of control strategies put forward in the previous subsection.

We henceforth set the slowing parameter value to $k = 100$. All control strategies will be carried out with the constraint of involving at most 5,000 animals, and our procedure will make sure that this constraint is saturated. Setting a limit to 5,000 animals regardless of the type of policy considered is of course an arbitrary choice that has to be discussed using a sensitivity analysis. Moreover, finer efficiency comparisons need to be based on a preliminary cost analysis, so the threshold is not expressed in terms of animals any longer but rather in terms of monetary costs.

4.3.3.1 Screening at importation

First consider the "screening at importation" control strategy described in Subsection 4.3.2.2. Critical nodes with respect to π , π' , m and v have been identified under the condition that only 5,000 of the 32593 yearly imported animals can be screened, that is, $\sum_{i \text{ critical}} B_i(K_i - z_i^*) \leq 5,000$. To each set of critical nodes, we added one last holding referred to as *borderline*, that would have been the first to be selected if the 5,000 animals threshold had been risen. This holding will only be partially acted on so the total number of screened animals is *exactly* 5,000. We obtain corresponding "critical or borderline" index sets \mathcal{C}_π , $\mathcal{C}_{\pi'}$, \mathcal{C}_m and $\mathcal{C}_{v'}$, the cardinals of which are given below.

	\mathcal{C}_π	$\mathcal{C}_{\pi'}$	\mathcal{C}_m	$\mathcal{C}_{v'}$
\mathcal{C}_π	2,792	3	233	2,772
$\mathcal{C}_{\pi'}$	3	3	3	3
\mathcal{C}_m	233	3	233	233
$\mathcal{C}_{v'}$	2,772	3	233	4,035

Table 4.3: Chart of $\mathcal{C}_A \cap \mathcal{C}_B$ cardinals, with $A, B \in \{\pi, \pi', m, v'\}$, for the "screening at importation" policy.

These index sets appear to overlap considerably. All three indices in $\mathcal{C}_{\pi'}$ — that is, the three indices with the higher value of π'_i — correspond to assembly centers. They also belong to sets \mathcal{C}_{π} , \mathcal{C}_m and $\mathcal{C}_{v'}$. The borderline holding is the same for all these sets. It is most acted on by the screening policy focused on π' -critical nodes, for which 3,588 of the 12,544 animals imported yearly in the node are screened (against 2,257 when the indicator considered is π , 3,048 when it is m and 1,602 when it is v'). Screening is applied to a vast majority of nodes of the system when the policy is conducted on the nodes with high values of v'_i .

Reference simulations will be ran for the epidemic process until its extinction, for an epidemic started by one infective individual located in a node i drawn among $\llbracket 1, n \rrbracket$ with probability

$$\frac{B_i(K_i - z_i^*)}{\sum_{j=1}^n B_j(K_j - z_j^*)}$$

Three quantities of interest will be recorded for any of these trajectories: the total size of the epidemic, its extinction time and the number of nodes reached by the infection.

We will then apply the same procedure for simulations realized as follows. For $A = \pi, \pi', m$ or v , we will start the epidemic in a non-critical node i with the same probability as before, in the borderline node with probability

$$\frac{\sum_{j \in \mathcal{C}_A} B_j(K_j - z_j^*) - 5,000}{\sum_{j=1}^n B_j(K_j - z_j^*)},$$

and otherwise set the epidemic total size, extinction time and number of nodes reached to zero, which therefore happens with probability

$$\frac{5,000}{\sum_{j=1}^n B_j(K_j - z_j^*)}$$

We will then evaluate the effect of the screening strategy on the average of the quantities of interest.

4.3.3.2 Isolation

Similarly, we will apply the isolation strategy to critical nodes under the constraint of preventing at most 5,000 of the 230,055 average yearly individual animal movements, that is, under the condition $\sum_{i \text{ critical}} z_i^* \sum_{j \neq i} \theta_{i,j} (K_j - z_j^*) \leq 5,000$. Defining \mathcal{C}_{π} , $\mathcal{C}_{\pi'}$, \mathcal{C}_m and $\mathcal{C}_{v'}$ as before regarding to this constraint, we get the following cardinals chart.

	\mathcal{C}_{π}	$\mathcal{C}_{\pi'}$	\mathcal{C}_m	$\mathcal{C}_{v'}$
\mathcal{C}_{π}	236	2	26	186
$\mathcal{C}_{\pi'}$	2	4	149	0
\mathcal{C}_m	26	149	116	19
$\mathcal{C}_{v'}$	186	0	19	765

Table 4.4: Chart of $\mathcal{C}_A \cap \mathcal{C}_B$ cardinals, with $A, B \in \{\pi, \pi', m, v'\}$, for the isolation policy.

For every indicator $A = \pi, \pi', m$ or v' , we will run simulations of the epidemic process started by one initial infective in a node selected as in the reference simulation procedure, replacing this time $\theta_{i,j}$ by $\theta'_{i,j} = 0$ for all $j \in \llbracket 1, n \rrbracket$ whenever i is critical and by

$$\theta'_{i,j} = \left(1 - \frac{5,000 - \sum_{k \text{ critical}} z_k^* \sum_{j \neq k} \theta_{k,j} (K_j - z_j^*)}{z_i^* \sum_{j \neq i} \theta_{i,j} (K_j - z_j^*)} \right) \theta_{i,j}$$

for all j when i is the borderline node.

The isolation policy consists in changing the value of some parameters of the model, so it is possible to observe its effect on indicators themselves. New calculations using the values of $\theta_{i,j}$ corresponding to the isolation of critical nodes yield results reported in the table below:

	No policy	Isolation of nodes critical for			
		π	π'	m	v'
Mean of π	0.4285	0.4326	0.4250	0.4302	0.4330
Mean of π'	0.1063	0.1067	0.0241	0.0487	0.1067
Mean of m	0.0480	0.0423	0.0329	0.0366	0.0428
Mean of v'	1.4286	1.5167	1.4235	1.5267	1.5254

Table 4.5: Effects of the isolation of A-critical nodes on the mean of B for all indicators $A, B \in \{\pi, \pi', m, v'\}$. The value of the indicator is given in bold fonts when it is made smaller by the isolation policy.

That the major outbreak probability itself is relatively unaffected on average by the isolation measure has to be related to the analysis of the π_i sketched in Subsection 4.2.1, where we state that nodes with low major outbreak probabilities are in general nodes that are the origin of strongly weighted paths through which the system empties. Deleting edges until 5,000 exchanges are prevented directly decreases the weight of such paths, but only by a relatively small total amount. The indicators mostly affected by the isolation policy are π' and m when the measure is targeted either on nodes with high π'_i or on nodes with high m_i . The high effect of the policy on the π' mostly indicates that nodes that are acted on are nodes with high importation levels, which is intuitive for π' -critical nodes but less for m -critical ones. The reduction of m suggests that the isolation policy does prevent the spread of the epidemic from nodes with high spreading potential, which is conform to intuition.

4.3.3.3 Vaccination

Finally, we will assess the vaccination strategy detailed in Subsection 4.3.2.2, under the constraint of treating no more than 5,000 animals of the $\sum_{i=1}^n z_i^* = 385,653$ total population, that is, $\sum_{i \text{ critical}} z_i^* \leq \frac{5,000 R_0}{R_0 - 1}$. We build the \mathcal{C}_A sets as before and get:

	\mathcal{C}_π	$\mathcal{C}_{\pi'}$	\mathcal{C}_m	$\mathcal{C}_{\nu'}$
\mathcal{C}_π	608	77	186	295
$\mathcal{C}_{\pi'}$	77	579	149	95
\mathcal{C}_m	186	149	993	40
$\mathcal{C}_{\nu'}$	295	95	40	927

Table 4.6: Chart of $\mathcal{C}_A \cap \mathcal{C}_B$ cardinals, with $A, B \in \{\pi, \pi', m, \nu'\}$, for the vaccination policy.

Simulations will again be run for every indicator $A = \pi, \pi', m$ or ν' . In critical nodes, we will turn a fraction $(1 - 1/R_0)$ of susceptible individuals to immune (that is, transfer $(1 - 1/R_0)z_i^*$ individuals from compartment S to compartment R inside node i , rounded to the closest integer). In the borderline node for A , we will only transfer $5,000 - \left(1 - \frac{1}{R_0}\right) \sum_{i \text{ critical}} z_i^*$ animals. We will then start the epidemic in a node selected as in the reference simulation procedure, and record the epidemic final size, its extinction time and the total number of nodes it reached to be compared with the corresponding values for the focus trajectories sample.

5

Conclusion and perspectives

Let us quickly review the results of the previous chapters and draw some perspectives for further research.

Summary of the previous chapters

In Chapter 2, we designed and studied network-structured metapopulation models accounting for immigration, births, deaths and migrations between nodes. We first discussed recurrence and ergodicity properties for multi-dimensional population processes with deterministic dynamics between jumps, that we called *metapopulation PDMP* (Section 2.1). Two instances of interest (the so-called *multiplicative* and *unitary* models) were thoroughly investigated, using mathematical ingredients likely to transpose in a greater variety of cases. Turning to more a tractable pure jump specification, we stated scaling limits and long-term stability results for an ergodic multitype *branching population process* (Section 2.2). In particular, we showed that the scaled process took its values in an arbitrary small ball around an equilibrium value over times scales that are exponential in the scaling parameter N . The cattle trade application we had in mind then commanded that we consider a more realistic finite-state variation on this model, referred to as the *logistic population process* (Section 2.3). In this framework, the limiting dynamical system for the scaled population processes proved highly non-trivial, only allowing to retrieve a positive lower bound for scaled populations over N -exponential time scales.

We then studied SIR epidemic processes on metapopulation networks, driven either by branching or by logistic population dynamics (Chapter 3). Strong finite-time approximation and long-time asymptotic results were derived in the one-population case (Section 3.1), that transposed to the multitype case under stability assumptions (Section 3.2). The very construction of the epidemic processes varies according to whether infectives are or not allowed to enter the system through immigration. In the case where only susceptible individuals immigrate and the epidemic is started by the introduction of a finite quantity of infectives in the system, we approximated the epidemic process by a multitype branching process on finite time intervals. This led to a distinction between two types of epidemic events (*minor* and *major* epidemic outbreaks), the probabilities of which could be evaluated using an iterative method. We showed that in the case of a major epidemic outbreak, endemicity occurs with high probability and entails, under appropriate stability conditions for the limiting dynamical system, N -exponential lower bounds for the extinction time and the total size of the epidemic. If a proportion of infectives is allowed to enter the system through immigration, the epidemic process is best approximated using a

dynamical system. In this case, we showed that provided the endemic equilibrium is stable, the scaled epidemic process spends a fraction of its time tending to 1 in a neighborhood of this equilibrium as N goes to infinity.

In Chapter 4, we performed a numerical application of the theoretical results on the logistic-driven epidemic process to design and evaluation of disease control strategies. This application is based on population parameters evaluated using the 2015 Finistère cattle trade network and epidemic parameters corresponding to a slowed version of foot-and-mouth disease dynamics (Section 4.1). We came up with four different indicators of the graph vulnerability to an epidemic started in a given node by one single infective, that relate alternatively to the local severity or to the spatial spreading potential of the epidemic (Section 4.2). The present focus of our ongoing research is to evaluate *screening*, *isolation* and *vaccination* control strategies applied to the nodes identified as critical for the various indicators (Section 4.3), so as to maximize the efficiency of a holding-based intervention under fixed cost constraints.

Perspectives

Some mathematical questions on the population and epidemic models under study remain open.

First, we conjecture the uniqueness and global asymptotic stability of the equilibrium of system $(\mathcal{S}'_{\text{pop}})$, and of the equilibria of systems $(\mathcal{S}'_{\text{epi}})$ and $(\mathcal{S}'_{\text{epi}'})$ when the corresponding R_0 are strictly greater than 1. Proving these results would make the conclusions of Theorems 3.2.6 and 3.2.15 automatically true when $R_0 > 1$.

Second, an important mathematical object left aside in our study is the *quasi-stationary distribution* (QSD) for the epidemic process, quickly evoked in our Introduction. The QSD is the (potential) limit for the distribution $\mathbb{P}(X^N(t) \in \cdot \mid I^N(t) \neq 0)$ of $X^N(t)$ conditionally on the fact that the epidemic has not gone extinct at time t . It also appears like the limiting distribution of the empirical occupancy times over the trajectory considered before extinction (see Figure 4.13, and Figure 1 of [VDP13]). While simple matrix theory shows that such a distribution exists for the finite-state logistic-driven SIR model [FKMP95], it is less clear that the result holds in the case of the branching-driven SIR model. Classical mathematical techniques to show such existence results involve Foster-Lyapunov criteria [CV14, CV15, CV16, CV17] or spectral theory [RCCM14] that do not adapt easily to multidimensional jump processes that do not come down from infinity, or fixed point approaches [FKMP95]. A review on existence criteria for QSD can be found in [VDP13], with an emphasis on birth and death processes for which 0 is an absorbing state. In this case, it has been shown that the speed of convergence in total variation of the process distribution conditioned to non-absorption towards a QSD is exponential [VD91]. This result has been generalized to multi-dimensional birth and death processes absorbed whenever one of the coordinates reaches 0 [CV15]. It trivially holds for the finite-state logistic-driven SIR model (see again [VDP13]), and the similarities between the latter and the branching-driven SIR model let us hope that they should still be true in the branching case.

We are currently investigating the possible identity between the limit as N tends to infinity of the QSD of a density-dependent population process X^N and the stationary distribution of

the diffusive processes approximating the scaled process X^N/N over finite time intervals, given in Chapter 11 of [EK86]. It could be verified using results from [RCCM14] that these two distributions coincide in the case of the unitype logistic population process. This comparison is used in [AB00b, Nå99], that study the properties and the recurrence equations determining the QSD assuming its existence in an open unitype or decomposable SIR model. In particular, they show that the extinction time of the epidemic follows an exponential distribution, and derive an approximation for the the mean of this distribution using the second-order diffusive approximation for the scaled epidemic process.

Perspectives for improving the accuracy of the numerical analysis carried out in the present work include a finer evaluation of demographic parameters by maximum likelihood estimation [BS05] and a calibration of the carrying capacities K_i using the objective capacities of the observed holdings. Data related to the latter may be found both in the FNCD records and by direct observation. Moreover, the values chosen for epidemic parameters correspond to a virtually slowed version of FMD and would of course need to be redefined if an application to an actual disease were to be conducted. Progress is still to be made on the definition of synthetic vulnerability indicators and quantities allowing to assess the severity of an epidemic without having to run a full simulation of the epidemic process.

On a modeling point of view, considering variations on the epidemic transmission mode, for instance by taking into account the action of wind in the case of airborne pathogens, or of animal contacts at pasture, could result in spatial models with various levels of mixing, in the spirit of household models [BN08, BHL⁺15, BBH⁺15, NT19]. It is also necessary to wonder about the suitability of SIR compartmental models to describe the spread of a given disease, as compared to other compartmental specifications allowing for instance for eventual loss of immunity (SIRS) or incubation periods (SEIR) [Bra08]. Another direction to explore is explaining the trade fluxes between nodes, using for instance gravitational microeconomic models [MGM⁺16]. As a general fact, questioning the biological and economic relevance of the models used to represent the spread of a disease is a matter of paramount importance. Choosing simplistic specifications for practical purposes may indeed result in misleading recommendations, as shown for instance in [VBE10] on the choice of exponential infection durations. This is the meaning of a quote from [Bra08] about the 1665 plague in Eyam (England):

In the village of Eyam the rector persuaded the entire community to quarantine itself to prevent the spread of disease to other communities. This policy actually increased the infection rate in the village by keeping fleas, rats, and people in close contact with one another, and the mortality rate from bubonic plague was much higher in Eyam than in London. Further, the quarantine could do nothing to prevent the travel of rats and thus did little to prevent the spread of disease to other communities. One message this suggests to mathematical modelers is that control strategies based on false models may be harmful, and it is essential to distinguish between assumptions that simplify but do not alter the predicted effects substantially, and wrong assumptions which make an important difference.

6

Appendices

Appendix A: On the invariant probability of a metapopulation PDMP

Let us consider a piecewise deterministic metapopulation process as defined in Section 2.1. It is clear by the proof of Proposition 2.1.7 that if Assumption F holds and if X admits an invariant probability π , then π dominates the Lebesgue measure on some open subset of an affine subspace of \mathbb{R}^n . Its support may yet not be limited to this subspace, as can be seen in Figure 6.1 below. Determining conditions for the absolute continuity of π restricted to given areas of \mathbb{R}_+^n is a non-trivial matter that still has to be discussed. Interested readers are referred to [Löc18] for a discussion about the absolute continuity of π in a *house of cards* model.

If X is positive Harris recurrent with invariant probability π and $\int \|x\|_1 d\pi(x) < +\infty$, we see by (2.3) that for any \mathcal{C}^1 function $f : \mathbb{R}_+^n \rightarrow \mathbb{R}$ with bounded differential the classical relation hereafter holds:

$$\int \left(\sum_{i=1}^n \frac{\partial f}{\partial x_i}(x) \phi_i(x) + \sum_{(i,j) \in \mathcal{I}} \theta_{i,j}(x) \int (f(x + \xi(e_j - e_i)) - f(x)) \mu_{i,j}(x, d\xi_i) \right) d\pi(x) = 0. \quad (6.1)$$

It is worth noting that the second term of the integrand in the left hand side above is zero whenever $f(x)$ only depends on $x_1 + \dots + x_n$. Equation (6.1) then takes a simple form that may provide valuable information on π .

In particular, applying (6.1) to the projection functions $\langle \cdot, e_i \rangle$ yields:

$$\forall t \geq 0, \forall i \in \llbracket 1, n \rrbracket, \quad \mathbb{E}_\pi(\phi_i(X(t))) + \sum_{j \neq i} \mathbb{E}_\pi(d_{j,i}(X(t)) - d_{i,j}(X(t))) = 0 \quad (6.2)$$

where we recall that $d_{i,j} : \mathbb{R}_+^n \rightarrow \mathbb{R}$ is the *mean debit from i to j* defined by

$$d_{i,j}(x) = \theta_{i,j}(x) \int \xi \mu_{i,j}(x, d\xi). \quad (6.3)$$

EXAMPLE 5. Let us assume that the following conditions hold:

$$\begin{cases} \phi_i(x) = a_i - x_i \\ \theta_{i,j}(x) = 1 \\ \int \xi \mu_{i,j}(x, d\xi) = m_i x_i \end{cases}$$

where the a_i and m_i are non-negative real numbers, and that X is positive Harris recurrent and integrable under its invariant probability. Then (6.2) becomes:

$$\forall t \geq 0, \forall i \in \llbracket 1, n \rrbracket, \quad (1 + m_i(n-1)) \mathbb{E}_\pi(X_i(t)) - \sum_{j \neq i} m_j \mathbb{E}_\pi(X_j(t)) = a_i$$

and can be written as a dominant diagonal linear system, which makes it possible to determine the $\mathbb{E}_\pi(X_i(t))$ explicitly.

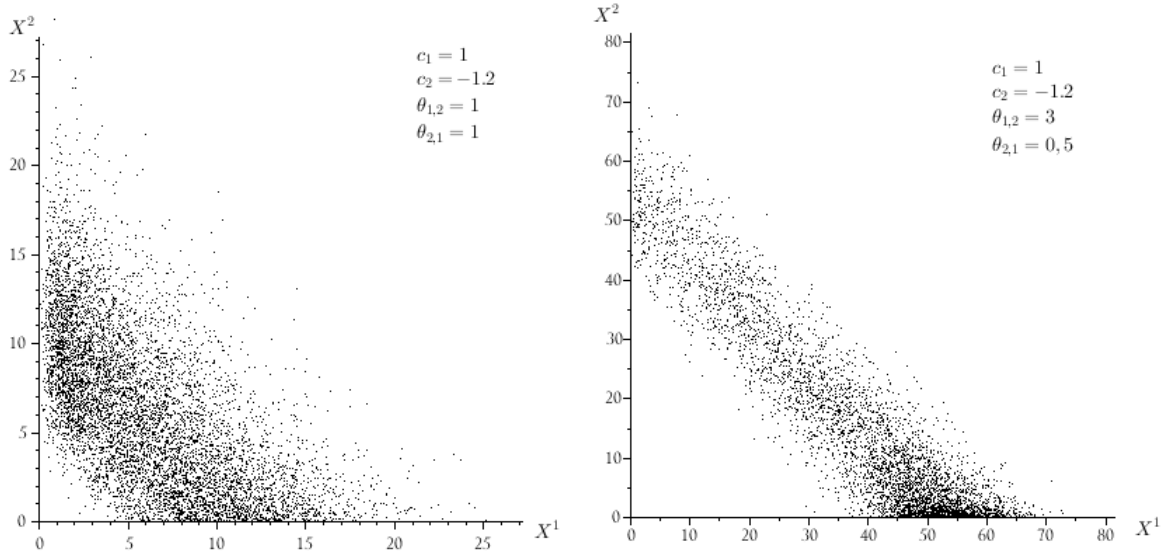


Figure 6.1: Plotting of 10000 simulated instances of $X(100)$ in the two-patch uniform model with constant growth for specified parameters, with initial value $(5, 5)$. In accordance with equation (6.4) of example 6, about 17.67% of points in both figures lie on the x axis.

EXAMPLE 6. Let us consider the one-exit constant growth framework, that is, a constant growth model with $c_i \geq 0$ for all $i \in \llbracket 1, n-1 \rrbracket$ and $c_n < 0$, and assume that X is positive Harris recurrent with invariant probability π and $\int \|x\|_1 d\pi(x) < +\infty$. It is an easy exercise to prove that

$$\mathbb{P}_\pi(X_n(t) > 0) = \frac{\sum_{j=1}^{n-1} c_j}{|c_n|} \quad (6.4)$$

and that the event $(X_n(t) > 0)$ is independent from the variable $\sum_{i=1}^n X_i(t)$ for all $t \geq 0$ under \mathbb{P}_π .

Appendix B: Additional results on the invariant measure of the branching population process

Recall that the almost sure value of $X^N(0)$ is $\lfloor Nx(0) \rfloor \in \mathbb{Z}_+^n$. For notational convenience and since N does not vary, we drop the N superscripts in the rest of this Appendix. Immigration in each node occurs at fixed rate, so our population process is a superimposition of independent multitype branching processes without immigration initiated at the jump times of a Poisson process. More precisely, let $(Y^{i,k})_{i \in \llbracket 1, n \rrbracket, k \in \mathbb{Z}} = ((Y^{i,k}(t))_{t \geq 0})_{i \in \llbracket 1, n \rrbracket, k \in \mathbb{Z}}$ be a sequence of iid Markovian jump processes on \mathbb{Z}_+^n with transition rates given by

Transition	Rate at state x
$x \rightarrow x + e_i$	$b_i x^i$
$x \rightarrow x - e_i$	$d_i x^i$
$x \rightarrow x - e_i + e_j$	$\theta_{i,j} x^i$

and such that

$$Y^{i,k}(0) = e_i$$

for any $i \in \llbracket 1, n \rrbracket$ and any $k \in \mathbb{Z}$. Then $Y^{i,k}$ is a branching process that has the same distribution as the population process without immigration started from just one individual in node i at time 0. Now immigration in node i can be modeled by a Poisson process with intensity B_i , so we can write:

$$\forall t \geq 0, \quad X(t) \stackrel{d}{=} \sum_{i=1}^n \left(\sum_{k=-\lfloor Nx(0) \rfloor_i + 1}^0 Y^{i,k}(t) + \sum_{k=1}^{Q^i(t)} Y^{i,k}(t - T_k^i) \right) \quad (6.5)$$

where the Q^i are independent Poisson processes with intensities B_i and jump times sequences $(T_k^i)_{k \geq 0}$, independent from each other and from the $Y^{i,k}$, $\stackrel{d}{=}$ denoting the equality in distribution under \mathbb{P} .

Using this representation, it is possible to derive much more information about the limiting probability π of X than we did in Theorem 2.2.1.

PROPOSITION 6.0.1. — [*Characteristic function and Laplace transform of the invariant distribution*] The characteristic function χ of π^N (resp. its Laplace transform ϕ) is given by

$$\chi : \xi \mapsto \exp \left(\sum_{i=1}^n B_i \int_0^{+\infty} (\chi_u^i(\xi) - 1) du \right)$$

resp.

$$\phi : \xi \mapsto \exp \left(\sum_{i=1}^n B_i \int_0^{+\infty} (\phi_u^i(\xi) - 1) du \right)$$

where χ_u^i (resp. ϕ_u^i) is the characteristic function (resp. the Laplace transform) of $Y^{i,0}(t)$.

Proof of Proposition 6.0.1.— We will only prove the proposition for characteristic functions since deriving Laplace transforms is based on similar arguments. The $Y^{i,k}$ are non-explosive pure jump processes with unitary jumps, so the $t \mapsto \chi_t^i(\xi)$ are continuous for fixed i and ξ . Using (6.5) and the independence of the $Y^{i,k}$ yields:

$$\begin{aligned}
\chi_t(\xi) &= \mathbb{E} \left(e^{i \langle \xi, X(t) \rangle} \right) \\
&= \mathbb{E} \left[\exp \left(i \left\langle \xi, \sum_{j=1}^n \left(\sum_{k=-x(0)^{j+1}}^0 Y^{j,k}(t) + \sum_{k=1}^{Q^j(t)} Y^{j,k}(t - T_k^j) \right) \right\rangle \right) \right] \\
&= \mathbb{E} \left[\exp \left(i \left\langle \xi, \sum_{j=1}^n \sum_{k=-x(0)^{j+1}}^0 Y^{j,k}(t) \right\rangle \right) \right] \mathbb{E} \left[\exp \left(i \left\langle \xi, \sum_{j=1}^n \sum_{k=1}^{Q^j(t)} Y^{j,k}(t - T_k^j) \right\rangle \right) \right] \\
&= \left(\prod_{j=1}^n \left(\chi_t^j(\xi) \right)^{x_j(0)} \right) \mathbb{E} \left[\exp \left(i \left\langle \xi, \sum_{j=1}^n \sum_{k=1}^{Q^j(t)} Y^{j,k}(t - T_k^j) \right\rangle \right) \right]. \tag{6.6}
\end{aligned}$$

Now

$$\begin{aligned}
&\mathbb{E} \left[\exp \left(i \left\langle \xi, \sum_{j=1}^n \sum_{k=1}^{Q^j(t)} Y^{j,k}(t - T_k^j) \right\rangle \right) \right] \\
&= \mathbb{E} \left[\mathbb{E} \left(\exp \left(i \left\langle \xi, \sum_{j=1}^n \sum_{k=1}^{Q^j(t)} Y^{j,k}(t - T_k^j) \right\rangle \right) \middle| Q^j(u), u \in [0, t], j \in \llbracket 1, n \rrbracket \right) \right] \\
&= \mathbb{E} \left[\mathbb{E} \left(\prod_{j=1}^n \prod_{k=1}^{N^j(t)} \exp \left(i \left\langle \xi, Y^{j,k}(t - T_k^j) \right\rangle \right) \middle| Q^j(u), u \in [0, t], j \in \llbracket 1, n \rrbracket \right) \right]. \tag{6.7}
\end{aligned}$$

Conditionally on $Q^j(t)$, the jump times T_k^j of Q^j up to time t have the same distribution than a $Q^j(t)$ -sample of uniform distribution $\mathcal{U}([0, t])$ sorted in ascending order, so the $t - T_k^j$ up to time t have the same distribution than a $Q^j(t)$ -sample of uniform distribution $\mathcal{U}([0, t])$ sorted in descending order. From this and the independence of the Q^j we deduce:

$$\begin{aligned}
&\mathbb{E} \left[\mathbb{E} \left(\prod_{j=1}^n \prod_{k=1}^{Q^j(t)} \exp \left(i \left\langle \xi, Y^{j,k}(t - T_k^j) \right\rangle \right) \middle| Q^j(u), u \in [0, t], j \in \llbracket 1, n \rrbracket \right) \right] \\
&= \mathbb{E} \left[\prod_{j=1}^n \prod_{k=1}^{Q^j(t)} \int_0^t \frac{1}{t} \mathbb{E} \left(\exp \left(i \left\langle \xi, Y_u(j, k) \right\rangle \right) \right) du \right] \\
&= \mathbb{E} \left[\prod_{j=1}^n \prod_{k=1}^{Q^j(t)} \int_0^t \frac{1}{t} \chi_u^j(\xi) du \right] \\
&= \prod_{j=1}^n \mathbb{E} \left[\left(\int_0^t \frac{1}{t} \chi_u^j(\xi) du \right)^{Q_t^j} \right]. \tag{6.8}
\end{aligned}$$

Finally, $Q^j(t)$ has Poisson distribution with mean $B_j t$ for all j , so

$$\begin{aligned} \mathbb{E} \left[\left(\int_0^t \frac{1}{t} \chi_u^j(\xi) du \right)^{Q^j(t)} \right] &= \exp \left(B_j t \left(\int_0^t \frac{1}{t} \chi_u^j(\xi) du - 1 \right) \right) \\ &= \exp \left(B_j \int_0^t (\chi_u^j(\xi) - 1) du \right). \end{aligned}$$

Combining (6.6), (6.7) and (6.8) then entails

$$\chi_t(\xi) = \left(\prod_{j=1}^n (\chi_t^j(\xi))^{[N x_j(0)]} \right) \exp \left(\sum_{j=1}^n B_j \int_0^t (\chi_u^j(\xi) - 1) du \right). \quad (6.9)$$

Recall that the $Y^{k,i}$ go extinct almost surely, so the $(\chi_t^j(\xi))_{t \geq 0}$ processes tend to 1 as $t \rightarrow +\infty$, hence

$$\prod_{j=1}^n (\chi_t^j(\xi))^{[N x_j(0)]} \xrightarrow[t \rightarrow +\infty]{} 1$$

Using the fact that $t \mapsto \mathbb{E}(Y^{j,0}(t))$ is a solution of $x' = Ax$ and a generalized eigendecomposition of A then grants

$$\begin{aligned} \left| \chi_u^j(\xi) - 1 \right| &\leq \mathbb{E} \left(\left| e^{i \langle \xi, Y^{j,0}(u) \rangle} - 1 \right| \right) \\ &= 2 \mathbb{E} \left(\left| \sin \left(\frac{\langle \xi, Y^{j,0}(u) \rangle}{2} \right) \right| \right) \\ &\leq \mathbb{E} \left(\left| \langle \xi, Y^{j,0}(u) \rangle \right| \right) \\ &\leq \|\xi\|_\infty \mathbb{E}(\|Y^{j,0}(u)\|_1) \\ &= \|\xi\|_\infty o(e^{\alpha' u}) \end{aligned} \quad (6.10)$$

as $u \rightarrow +\infty$, so we may take $t \rightarrow +\infty$ in (6.9) and get:

$$\forall \xi \in \mathbb{R}, \quad \lim_{t \rightarrow +\infty} \chi_t(\xi) = \exp \left(\sum_{j=1}^n B_j \int_0^{+\infty} (\chi_u^j(\xi) - 1) du \right).$$

Now the right hand side term is a continuous function of ξ by the dominated convergence theorem since the $o(e^{\alpha' u})$ term in (6.10) does not depend on ξ . Lévy's theorem then implies that $(X(t))_{t \geq 0}$ converges in distribution to a \mathbb{Z}_+^n -valued random variable with characteristic function

$$\chi : \xi \mapsto \exp \left(\sum_{j=1}^n B_j \int_0^{+\infty} (\chi_u^j(\xi) - 1) du \right),$$

hence the result. \square

Using a coupling argument, we are also able to obtain a value for the rate of convergence towards the equilibrium distribution:

PROPOSITION 6.0.2. — [Convergence rate towards equilibrium] Let $K > 0$ and $g : \mathbb{R}_+^n \rightarrow \mathbb{C}$ be a K -Lipschitz continuous function. If ν is a distribution on \mathbb{Z}_+^n with finite first moment $\nu(\text{Id}) \in \mathbb{R}_+^n$ and if $\|\cdot\|$ denotes the matrix norm associated with $\|\cdot\|_1$, then:

$$|\mathbb{E}_\pi(g(X(t))) - \mathbb{E}_\nu(g(X(t)))| \leq K \|e^{tA}\| \cdot (\| -A^{-1}B \|_1 + \|\nu(\text{Id})\|_1) \underset{t \rightarrow +\infty}{=} o(e^{\alpha' t})$$

for any α' strictly greater than the highest real part of A 's eigenvalues.

Proof of Proposition 6.0.2.— Let Z^π and Z^ν be \mathbb{Z}_+^n -valued random variables on (Ω, \mathcal{A}) , independent from the $Y^{i,k}$, such that Z^π has law π and Z^ν has law ν under \mathbb{P} . Now define X' and X'' as:

$$\forall t \geq 0, \quad X'(t) = \sum_{i=1}^n \left(\sum_{k=-Z_i^\pi+1}^0 Y^{i,k}(t) + \sum_{k=1}^{N^i(t)} Y^{i,k}(t - T_k^i) \right)$$

and

$$\forall t \geq 0, \quad X''(t) = \sum_{i=1}^n \left(\sum_{k=-Z_i^\nu+1}^0 Y^{i,k}(t) + \sum_{k=1}^{N^i(t)} Y^{i,k}(t - T_k^i) \right)$$

X' and X'' are versions of the population process started with respective initial laws π and ν under \mathbb{P} and only differing from each other by their initial lineages. In particular, the law of X' under \mathbb{P} is that of X under \mathbb{P}_π (that is, π) and the law of X'' under \mathbb{P} is that of X under \mathbb{P}_ν . For any $t \geq 0$, we get:

$$\begin{aligned} |\mathbb{E}_\pi(g(X(t))) - \mathbb{E}_\nu(g(X(t)))| &\leq K \mathbb{E}(\|X'(t) - X''(t)\|_1) \\ &= K \mathbb{E} \left(\left\| \sum_{i=1}^n \left(\sum_{k=-Z_i^\pi+1}^0 Y^{i,k}(t) - \sum_{k=-Z_i^\nu+1}^0 Y^{i,k}(t) \right) \right\|_1 \right) \\ &\leq K \sum_{i=1}^n \mathbb{E}(|Z_i^\pi - Z_i^\nu|) \mathbb{E}(\|Y^{i,0}(t)\|_1) \\ &\leq K \mathbb{E}(\|Z^\pi - Z^\nu\|_1) \|e^{tA}\| \\ &= K (\| -A^{-1}B \|_1 + \|\nu(\text{Id})\|_1) \|e^{tA}\| \end{aligned}$$

Now we saw before that a generalized eigendecomposition of A yields

$$\|e^{tA}\| \underset{t \rightarrow +\infty}{=} o(e^{\alpha' t}),$$

which ends the proof. □

7

Contexte et résultats de la thèse

Ce chapitre est construit à partir du contenu de l'Introduction générale. Il en reprend les premières sections 1.1 et 1.2, ainsi que les résultats de la thèse exposés dans la section 1.3.

Le présent manuscrit est dédié à l'analyse mathématique de modèles de métapopulations stochastiques à temps continu, couplés avec des processus épidémiques aléatoires sur un graphe. On s'intéresse tout d'abord à la modélisation de dynamiques de populations sur un réseau d'échanges de bovins (chapitre 2), en considérant que les échanges marchands se produisent à des temps aléatoires et en examinant alternativement des régimes déterministes ou stochastiques pour expliquer l'évolution locale des populations. Restreignant notre analyse à des processus markoviens de sauts, on construit ensuite des modèles épidémiques liés aux processus de population considérés et permettant de décrire l'évolution d'une épidémie sur le réseau (chapitre 3). Les résultats théoriques obtenus à partir de ces modèles permettent d'évaluer la vulnérabilité d'un réseau d'échanges réel et de construire et évaluer des stratégies de contrôle (chapitre 4).

Ce chapitre est structuré comme suit. On expose dans la section 7.1 le contexte scientifique et la problématique pratique à l'origine du présent travail. Dans la section 7.2, on esquisse ensuite la définition des modèles de populations et des modèles épidémiques à l'étude et les questions à l'origine des résultats des chapitres 2 et 3. On présente enfin dans la section 7.3 un panorama de ces résultats.

7.1

Contexte scientifique et problématique pratique

Les échanges marchands d'animaux sont un facteur majeur de la propagation d'épidémies entre des exploitations bovines sur des échelles spatiales importantes [KDGK06]. La motivation pratique du présent travail provient d'un projet de recherche nommé Cadence et financé par l'ANR, centré sur l'étude statistique et la modélisation mathématique des maladies infectieuses bovines se propageant sur le réseau d'échanges français au gré des mouvements d'animaux. L'étude de vulnérabilité et l'évaluation de stratégies de contrôle font partie intégrante des problématiques du projet.

Il est naturel de représenter les exploitations bovines liées par des échanges sous la forme d'un réseau, en considérant les exploitations (fermes et opérateurs commerciaux, tels les centres de rassemblement ou les marchés) comme des nœuds et les relations commerciales comme des arêtes orientées. Le réseau ainsi obtenu est pondéré en fonction du nombre d'animaux échangés *via* les différentes arêtes. Il est également dynamique, car les arêtes actives sur une période donnée ainsi que leur poids varient au fil du temps du fait de la variabilité des relations commerciales. Compte tenu des dynamiques démographiques particulières aux exploitations bovines, qui impliquent un renouvellement rapide de la population et donc une arrivée constante de nouveaux individus susceptibles d'être contaminés, le développement d'une épidémie sur un réseau de bovins est susceptible de présenter des caractéristiques d'endémicité — c'est-à-dire de persistance de l'infection à un niveau modéré sur des échelles de temps longues. La modélisation épidémique sur un réseau d'échanges de bovins doit donc tenir compte des importations, naissances, morts et transferts d'animaux intervenant sur la même échelle de temps que les dynamiques épidémiques. On doit donc chercher à modéliser de façon unifiée des dynamiques de métapopulations et de propagation épidémique au sein de populations structurées en réseau.

Avant de présenter les modèles à l'étude, décrivons brièvement le contexte pratique et scientifique dans lequel ils s'inscrivent.

7.1.1 Analyse des réseaux d'échanges de bovins et données empiriques

On évoque dans cette section quelques-unes des problématiques examinées lors de l'étude des réseaux d'échanges de bovins, avant de présenter la base de données sur laquelle est construite l'analyse numérique présentée au chapitre 4.

7.1.1.1 Analyse des réseaux d'échanges de bovins

La grande quantité de données collectées par les autorités européennes suite à la crise de l'ESB dans les années 1990 permet de connaître la position au fil du temps de n'importe quel bovin présent sur les territoires nationaux concernés [Ver11, DEV14]. Une telle précision permet une description détaillée des propriétés du réseau d'échanges marchands observé sur des fenêtres de temps arbitrairement petites [VK09, Ver11, DEV14], mais rend aussi possible la construction et la calibration de modèles de propagation épidémique [PGPSV12, BVE15, HGM⁺16] susceptibles de mener à l'élaboration de stratégies de contrôle [BVJE17].

Un premier pas en direction de l'évaluation de la vulnérabilité d'un réseau d'échanges empirique à la propagation d'une maladie infectieuse est l'étude de sa connectivité (voir [RDD11] pour une analyse de la taille des composantes connexes d'un réseau réel, ou [HS12] pour un article de synthèse sur la question du *reachability ratio*, mesure plus sophistiquée rendant compte des caractéristiques dynamiques du réseau). Une telle étude permet de mettre en place des stratégies d'endiguement [DEV14] tout en limitant la disruption des mécanismes de marché [MGM⁺16]. La structure du réseau elle-même peut être prédite grâce à des modèles microéconomiques adaptés [HGM⁺16] ou plus généralement grâce à des modèles fondés sur l'activité observée sur le réseau [PGPSV12].

Une autre approche, que nous adopterons dans la suite de ce manuscrit, consiste à interpréter les caractéristiques du réseau observable comme des réalisations d'un processus markovien de métapopulations. On peut alors obtenir des résultats théoriques en considérant une potentielle dynamique épidémique couplée avec ce processus, et évaluer des quantités associées à la vulnérabilité du réseau induite par les différentes exploitations qui le constituent. Parmi ces quantités d'intérêt se trouvent la probabilité d'occurrence d'un épisode épidémique majeur, la taille totale de l'épidémie ou le nombre moyen de nœuds atteints par l'infection, lorsque l'épidémie est initiée par un unique individu infectieux dans un nœud donné.

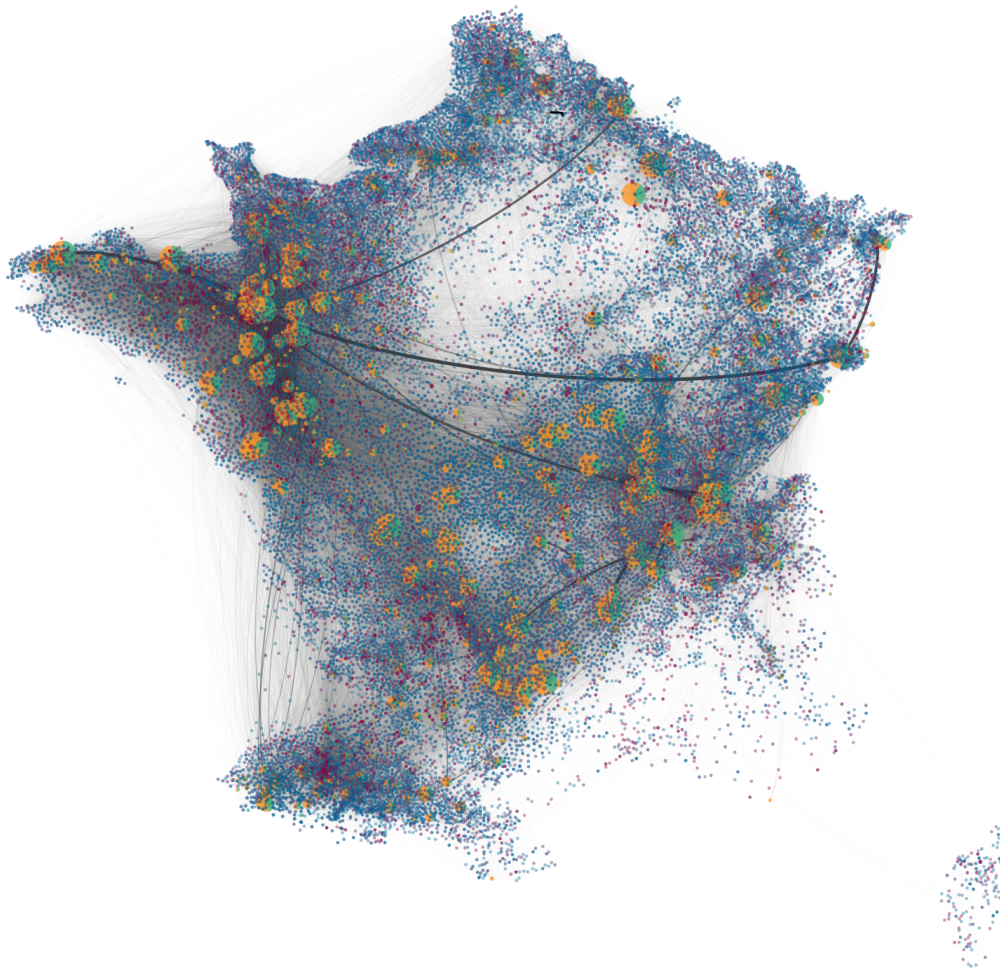


Figure 7.1: Représentation du réseau d'échanges de bovins en France en 2008. Les exploitations sont agrégées au niveau de la commune. La taille d'un nœud représente sa population moyenne au cours de l'année. La couleur des nœuds représente la part d'achats (en orange pour les opérateurs et en rouge pour les fermes) et de ventes (en vert pour les opérateurs et en bleu pour les fermes) dans le volume total d'échanges. Les arêtes représentent l'existence d'un mouvement de bétail sur la période entre deux exploitations des communes concernées, leur largeur étant indicative du volume d'échanges observé. Crédit graphique : Gaël Beaunée.

7.1.1.2 La Base de Données Nationale d'Identification (BDNI)

Les partis-pris de modélisation et l'évaluation des stratégies de contrôle dans les chapitres 2 à 4 sont guidés par les observations empiriques issues de la Base de Données Nationale d'Identification (BDNI) construite par le Ministère de l'Agriculture. Cette base retrace l'itinéraire de chaque bovin sur le territoire français entre 2005 et 2015 [RDD11, DEV14], et a été utilisée au cours des dernières années pour calibrer des modèles paramétriques ainsi que pour élaborer et évaluer des stratégies de contrôle [BVE15, QVDE17, BVJE17].

Les données brutes consistent en cinq strates d'informations [DEV14]. La première est le registre des détentions d'animaux par les différentes exploitations au fil du temps; il y figure notamment le numéro d'identification des animaux détenus, leur date et cause d'entrée dans l'exploitation (naissance ou achat), ainsi que leur date et cause de sortie de l'exploitation (mort ou vente). La seconde strate d'informations contient l'histoire de vie de chaque animal, qui consiste en son numéro d'identification, ses date et lieu de naissance, son sexe, sa race et la date de son premier vêlage (dans le cas d'une femelle). Les trois autres strates sont constituées d'informations sur les marchés et les centres de rassemblement (appelés *opérateurs*) d'une part, et sur les abattoirs d'autre part. Lors du traitement des données on a, à l'instar de [DEV14], considéré les abattoirs comme des puits épidémiologiques ne jouant aucun rôle dans la propagation des pathogènes, si bien que les transferts à l'abattoir et les morts ont été considérées comme des mouvements de même nature. À partir des données brutes, il est possible de reconstituer un registre complet des échanges de bovins sur le territoire français entre 2005 et 2015, faisant figurer pour chaque mouvement sa date, son origine, sa destination et le numéro d'identification des animaux concernés. Ce registre peut être utilisé pour construire et représenter le réseau d'échanges empirique sur une période de temps choisie (voir Figure 7.1).

7.1.2 Contexte de modélisation

L'approche modélisatoire adoptée dans le présent travail, ainsi que ses contributions mathématiques, appartiennent au champ des modèles de métapopulations et des modèles épidémiologiques sur des graphes. Les paragraphes suivants donnent un aperçu succinct (et loin d'être exhaustif) de la littérature existante dans ces domaines.

7.1.2.1 Modèles de métapopulations

Les modèles de métapopulations décrivent le comportement d'une population divisée de façon naturelle ou artificielle en sous-groupes distants (appelés *patches*) connectés à travers des migrations d'individus. Bien que les biologistes aient étudié des populations distantes mais connectées dès les années 1950 [AB54, Huf58, MW67], le terme « métapopulation » en tant que tel ne fut introduit qu'en 1969 par Levins, dans le cadre de l'étude d'un modèle déterministe décrivant l'évolution du nombre total de patches occupé par une espèce au cours du temps [Lev69, Lev70]. D'importantes variations sur ce modèle furent introduites, identifiant par exemple certains patches comme des *sources* de populations capables de subsister grâce à leur propre croissance démographique et d'autres comme des *puits* susceptibles de s'éteindre en l'absence de dispersion de population [Pul88], incorporant l'*effet de sauvetage* par lequel de petites populations sont alimentées par une immigration en provenance de patches plus importants [Han83, HMG96, Eti00], ou l'effet de la distribution spatiale explicite des patches [Pul88,

Kar90, KW95, Rit97]. Les modèles de métapopulations se retrouvent aujourd’hui dans de nombreux contextes biologiques, et en particulier dans la modélisation de la biodiversité, grâce à leur capacité à prendre en compte à la fois des informations spatiales et des typologies individuelles [JS03, BWG⁺09, WCC⁺16]. Des panoramas plus complets sur les diverses extensions du modèle de Levins originel et leurs applications sont proposés dans [HG91, HS97, Han99, Eti02].

Dans le cadre du présent manuscrit, nous nous intéressons particulièrement à des modèles de métapopulations stochastiques. Le modèle de *fonction d’incidence* de Hanski [Han94, VtN00] fut le premier à intégrer un degré de stochasticité dans le processus de dispersion des individus entre les patches. Cependant, il décrit l’état d’une métapopulation par un vecteur d’indicatrices d’occupation à valeurs binaires et ne considère pas les dynamiques démographiques internes aux patches (voir aussi [GS94, EN02]). D’autres modèles, utilisant des processus de Markov, prennent en compte les dynamiques de population locales (naissances et morts) et/ou les transferts entre les patches survenant à des instants aléatoires, avec des taux de transition estimés directement à partir des données disponibles [VLM91] ou déduits d’un modèle paramétrique (voir [PDGM00] pour un modèle de métapopulations à dynamiques logistiques, à comparer avec le modèle déterministe [Ayd17]). Les modèles de population introduits dans la section suivante et étudiés dans le chapitre 2 appartiennent à cette dernière catégorie. C’est aussi le cas des processus de branchement multitype, qui jouissent de nombreuses propriétés théoriques résultant de la contraignante hypothèse de branchement [Ath68, Mod71, AN72] et peuvent être utilisés pour décrire des métapopulations [GL00, BL13, HJK16, Ada16], sans toutefois être limités à cet usage ainsi que le présent travail l’illustre à plusieurs reprises.

7.1.2.2 Processus stochastiques SIR sur des réseaux

Les modèles compartimentaux SIR (Susceptible – Infecté – Rétabli), introduits en tant que systèmes d’EDO par Kermack et MacKendrick [KM27] et sous forme stochastique par Bartlett [Bar49, Ken56], sont couramment utilisés en épidémiologie pour décrire l’évolution de maladies contre lesquelles les individus atteints puis rétablis conservent une immunité à vie (par exemple la rougeole, la rubéole, les oreillons ou la coqueluche dans le cas humain). Dans ces modèles, les individus vivants possèdent un statut de santé parmi trois possibles : ils sont soit Susceptibles (S) et jamais encore atteints par la maladie, soit Infectés (I) et potentiellement à l’origine de contacts infectieux qui transforment des individus susceptibles en individus infectés, soit Rétablis (R) après s’être remis d’une infection et immunisés de façon permanente. Pendant leur vie, les individus peuvent se déplacer entre les différents compartiments dans le sens $S \rightarrow I$ (dans le cas d’une infection) et dans le sens $I \rightarrow R$ (dans le cas d’une rémission). Dans les modèles SIR d’origine, on suppose que la population est *uniformément mélangeante*, c’est-à-dire que chaque individu infectieux est uniformément en contact avec tous les autres membres de la population. De très nombreuses variantes du modèles SIR ont été développées, prenant par exemple en compte d’autres statuts de santé, la perte de l’immunité, la structure d’âge de la population ou le mélange non-uniforme de la population. Nous référons à la monographie [KR07] pour une présentation complète de ces modèles, généralement développés spécifiquement en vue de contextes applicatifs précis.

Compte tenu de notre cadre applicatif, nous nous pencherons spécifiquement sur des modèles rendant compte de la propagation d’une épidémie de type SIR sur des réseaux de contact.

De tels modèles ont été abondamment abordés dans la littérature ces trois dernières décennies. Si certains d'entre eux considèrent les individus eux-mêmes comme des nœuds du graphe (voir par exemple [BN08, DF15]), d'autres représentent par des nœuds des sous-populations correspondant à différents *types* [Bal86, BC93, Cla94, BC95, Cla96, Nea12]. Ces types peuvent être vus comme des catégories biologiquement distinctes coexistant au sein du même espace, mais aussi comme des groupes d'individus localisés dans des patches géographiquement éloignés. Cette interprétation fait apparaître les modèles SIR multitypes comme des couplages de modèles épidémiologiques et de modèles de métapopulations. Néanmoins, même lorsqu'ils se placent dans ce cadre modélisateur, relativement peu de travaux prennent en compte les dynamiques de populations liées aux naissances et aux morts d'individus, ce qui donne lieu à des modèles à taille fixe dans lesquelles les individus infectieux peuvent se déplacer [BC93, Cla94, Cla96, Nea12] ou non [Bal86, BC95, AB00a]. Selon les cas, ils peuvent [Bal86, BC95, AB00a] ou non [BC93, Cla94, Cla96, Nea12] entreprendre des contacts infectieux avec des individus situés dans d'autres nœuds. Dans l'étude de tels modèles, l'accent est généralement mis sur la description des premières étapes de propagation de l'épidémie ainsi que sur son bilan final. [Cla96, Nea12] approchent le processus épidémique par un processus de branchement multitype au cours des premières phases de l'épidémie lorsque que la taille typique de la population, représentée par un paramètre d'échelle N , tend vers l'infini. Ils distinguent deux types d'événements épidémiques selon que le processus de branchement survit (ce qui donne lieu à un *épisode épidémique majeur*) ou s'éteint (*épisode épidémique mineur*). Dans certains modèles à taille fixe, des résultats exacts sur la *taille finale de l'épidémie*, c'est-à-dire le nombre total d'individus infectés durant l'évolution de l'épidémie, sont obtenus en utilisant la *construction de Sellke*, qui consiste à associer à chaque individu un seuil critique d'exposition à l'infection en-deçà duquel son statut est Susceptible et au-delà duquel il adopte le statut Infecté (voir [Sel83] et le chapitre 6 de [AB00a]). Dans [BC93, Cla94, BC95], des estimations asymptotiques de la taille totale de l'épidémie sont obtenues lorsque $N \rightarrow +\infty$, généralisant au cas multitype les preuves de [Sca85, Sca90]. Nous nous efforçons de tendre vers des résultats similaires dans l'étude des modèles épidémiques au chapitre 3.

Parmi les cadres théoriques que nous venons d'évoquer, le *modèle épidémique dynamique* présenté dans [Nea12] est le plus proche équivalent à population fixe des modèles épidémiques étudiés dans ce manuscrit. Il représente une épidémie SIR évoluant au sein d'une population divisée en sous-groupes entre lesquels les individus se déplacent suivant une matrice de transition, indépendamment de leur statut de santé. Dans ce modèle, les individus infectieux sont uniquement en contact avec les membres du patch dans laquelle ils se trouvent. Neal calcule la fonction génératrice de la progéniture directe d'un individu infectieux pour un processus de branchement approchant le processus épidémique sur des intervalles de temps finis (voir [Cla96]). Connaître l'expression analytique de cette fonction permet de calculer numériquement la probabilité d'occurrence d'un épisode épidémique majeur, mais aussi d'estimer un paramètre épidémiologique important, le *nombre de reproduction de base* R_0 , qui décrit approximativement le nombre moyen d'infections causées par un individu infectieux dans une population totalement susceptible au cours de sa vie. Nous adaptons cette approche à nos modèles avec renouvellement de population au chapitre 3.

Au cours des dernières décennies, la pertinence du paramètre R_0 dans le contexte des réseaux de sous-populations de petites tailles et uniformément mélangeantes (aussi connus sous le

nom de *modèles de ménages*) a fait débat [BN08, BST09, BST10, PBT11, BBH⁺15, BPT16, BS18]. Une recherche active a mené à la définition de nombreux paramètres alternatifs permettant de discriminer le comportement du processus épidémique sur de tels réseaux [BPT16]. Ces paramètres inspirent notre recherche d'indicateurs de vulnérabilité du réseau au chapitre 4.

7.1.2.3 Modèles SIR stochastiques avec démographie

Nous souhaitons définir des modèles rendant compte d'une part de l'évolution de la population par l'immigration, les naissances, les morts et les migrations entre les patches pour permettre de générer des dynamiques plausibles et en conformité avec les observations empiriques, et d'autre part d'une dynamique SIR locale, interne à chaque patch. Il a été montré [VHG95, VH97, Nâ99, AB00b] que de tels modèles *ouverts* diffèrent de leurs analogues à population fixe par le fait qu'ils permettent d'observer un phénomène d'endémicité, si bien que l'épidémie persiste au-delà d'un seuil donné sur des échelles de temps relativement longues lorsqu'un épisode épidémique majeur survient ([Bar56]; sur l'importance de l'endémicité en tant qu'objet d'étude pour l'épidémiologie, voir [Bri10]). La probabilité d'occurrence d'un épisode épidémique majeur (chapitre 4 de [AB00a], [Cla96, Nea12]), de même que le temps d'extinction et la taille totale de l'épidémie conditionnellement à un tel événement, apparaissent donc comme des quantités d'intérêt essentielles pour étudier le processus épidémique, en particulier dans une optique de contrôle. Cependant, la construction de Sellke et les techniques utilisées dans [Sca85, Sca90, BC93, BC95, AB00a] pour obtenir des résultats explicites sur la taille totale de l'épidémie dans le cas sans démographie se transposent mal au cas multitype ouvert, dans lequel l'exposition des individus à l'infection débute à des temps variables, évolue avec les mouvements de population sur le réseau, et s'arrête à la mort des individus, qui survient à des temps aléatoires. Par conséquent, une grande partie de la littérature sur les modèles SIR ouverts concentre ses efforts sur l'estimation du temps d'extinction de l'épidémie [AB00b, O'N96] et la description de son comportement qualitatif après un épisode épidémique majeur [VHG95, VH97].

Certains auteurs considèrent des dynamiques démographiques ouvertes couplées avec des processus épidémiques, mais se limitent au cas unitype, c'est-à-dire à une population unique et uniformément mélangée. La plupart de ces modèles sont construits autour d'un processus de population avec des taux d'entrée affines [O'N96, CG07] ou constants [Nâ99, AB00b]. Dans ce cadre, l'ensemble des états sans individus infectieux est absorbant et l'extinction de l'épidémie en temps finie est presque sûre. [AB00b] et [Nâ99] étudient la *distribution quasi-stationnaire* (QSD) du processus épidémique, c'est-à-dire la limite en temps long de sa loi conditionnellement à la non-extinction de l'épidémie, ainsi que la loi du temps d'extinction d'un processus épidémique ayant cette QSD pour distribution initiale. [O'N96] obtient une approximation du temps d'extinction de l'épidémie par celui d'un processus de naissance et de mort lorsque le paramètre d'échelle de la population N tend vers l'infini, sans toutefois estimer la distribution du temps d'extinction de l'épidémie à N fixé. Nous consacrons une partie du chapitre 3 à étudier l'échelle de temps nécessaire à l'épidémie pour s'éteindre dans notre modèle SIR ouvert, et montrons que dans le régime endémique, le temps d'extinction est au moins égal à une fonction exponentielle de N avec probabilité tendant vers 1.

Dans les chapitres 3 et 4, nous étudions un modèle SIR multitype couplé avec des dynamiques de métapopulations dans lesquelles les taux de transition sont affines ou logistiques. Un modèle

SI multitype avec des taux affines proches de ceux considérés ici est étudié dans [BS16] par une approche principalement numérique. On peut par ailleurs trouver divers analogues déterministes de notre modèle SIR stochastique à taux affines dans [MA07, LS09, MEK13, TL15, TIK18]. Les modèles SIR incorporant des dynamiques de population logistiques sont, quant à eux, plus rares dans la littérature. Quelques sources récentes existent dans un cadre déterministe [WZJ10, LTW⁺17, MMZB17, GS18] ou avec stochasticité brownienne [ZH15]. Toutefois, il n'existe pas à notre connaissance d'étude portant sur un modèle similaire au modèle SIR stochastique à dynamiques de populations logistiques considéré dans le présent manuscrit.

7.2

Modélisation

Notre premier objectif est de définir un modèle de métapopulations sur un réseau. Différentes approches de modélisation peuvent être retenues pour représenter l'évolution des populations selon leur taille et les intervalles de temps sur lesquelles elle sont observées. Nous considérons un processus de métapopulations markovien déterministe par morceaux décrivant des dynamiques locales déterministes pour des populations contrôlées et des transferts stochastiques entre les patches (section 7.2.1). En assouplissant les hypothèses sur le contrôle déterministe des populations au niveau du patch, on obtient ensuite des processus markoviens de sauts purs à valeurs dans \mathbb{N}^n (section 7.2.2) que l'on couple avec un modèle SIR stochastique (section 7.2.3).

7.2.1 Processus de métapopulations déterministes par morceaux

Lorsque les populations étudiées sont de grande taille, que leur évolution est contrôlée de façon déterministe (ce qui est *a priori* le cas dans les exploitations bovines) et que les transferts de population entre les nœuds du réseau surviennent à des temps aléatoires (du fait par exemple de déterminants économiques exogènes), il est naturel de représenter la population du système sous la forme d'un processus markovien $X = (X_1, \dots, X_n)$ à valeurs dans \mathbb{R}_+^n , conduit à la fois par un flot continu et par un ensemble de processus de sauts. L'objet mathématique ainsi obtenu est connu sous le nom de *processus de Markov déterministe par morceaux* (PDMP).

Dans ce modèle de métapopulations, on considère que la population de chaque patch i est associée à une fonction de croissance autonome ϕ_i (au sens où $dX_i(t) = \phi_i(X(t))dt$ en l'absence de sauts), et qu'un transfert instantané de population du patch i au patch j à partir d'un état x survient à taux $\theta_{i,j}(x)$, avec une amplitude distribuée selon une loi $\mu_{i,j}(x, \cdot)$ à support dans $[0, x_i]$.

Ce modèle est défini de façon générale dans la section 2.1. On se borne ici à considérer les deux exemples illustratifs suivants, qui émergent naturellement de la modélisation de dynamiques de populations sur des réseaux d'échanges de bovins. Soient $n \geq 1$, $\mathcal{G} = ([1, n], \mathcal{A})$

un graphe orienté fortement connexe et $(c_1, \dots, c_n) \in \mathbb{R}^n \setminus \{0\}$. On considère les deux modèles à croissance constante définis de la façon suivante :

Modèle multiplicatif uniforme

$$\phi_i(x) = \begin{cases} c_i & \text{si } c_i \geq 0 \\ c_i 1_{x_i > 0} & \text{si } c_i < 0 \end{cases} \quad \text{et} \quad \begin{cases} \theta_{i,j}(x) = \theta_{i,j} \\ \mu_{i,j}(x, \cdot) = \mathcal{U}([0, x_i]) \end{cases} \quad (1.1)$$

où $\theta_{i,j} > 0$ si $(i, j) \in \mathcal{A}$ et $\theta_{i,j} = 0$ sinon, ou :

Modèle puissance unitaire

$$\phi_i(x) = \begin{cases} c_i & \text{si } c_i \geq 0 \\ c_i 1_{x_i > 0} & \text{si } c_i < 0 \end{cases} \quad \text{et} \quad \begin{cases} \theta_{i,j}(x) = (1 \vee x_i)^\alpha \\ \mu_{i,j}(x, \cdot) = \delta_{1 \wedge x_i} \end{cases} \quad (1.2)$$

pour un certain $\alpha \in]0, 1]$.

Le modèle (1.1) correspond au cas de patches échangeant une fraction aléatoire de leur population à un taux temporel constant. Il correspond aux données empiriques sur des réseaux d'échanges observés à des intervalles de temps importants, mais n'est pas réaliste d'un point de vue mécanistique dans la mesure où l'amplitude des transferts réels de population est bornée par des contraintes logistiques associées aux moyens de transport utilisés. Le modèle (1.2) correspond à des transferts de population unitaires réalisés à des taux temporels d'autant plus élevés que la population du patch d'origine est élevée ; il constitue un cadre naturel de modélisation des échanges de bovins observés de façon journalière. Notons que ce dernier modèle est proche d'un réseau de Jackson ouvert [Jac57, MD94, Dai95], dont il ne diffère que par son espace d'états continu et l'existence du flot déterministe défini par les ϕ_i .

7.2.2 Processus de métapopulations markoviens à sauts

Lorsque les populations considérées sont de taille réduite ou que leur évolution locale n'est pas suffisamment contrôlée pour pouvoir être modélisée par un flot déterministe, il est intéressant de les représenter sous la formule d'un processus markovien à sauts unitaires. Cette approche interdit les sauts macroscopiques instantanés et ignore une partie du contrôle effectué sur les populations, pourtant bien réel dans le cadre applicatif que nous considérons. Cependant, il est improbable d'observer des transferts de population très importants entre des exploitations bovines lorsque celles-ci sont observées sur des échelles de temps suffisamment courtes. Par ailleurs, la modélisation des métapopulations considérées par des processus markoviens de sauts permet de considérer des populations à valeurs entières, ce qui est évidemment plus réaliste et facilite l'analyse de stabilité. Comme nous le verrons dans la section 7.2.3, un tel point de vue permet par ailleurs un couplage naturel avec un processus épidémique défini en fonction de mesures ponctuelles de Poisson.

Les sauts des processus de population considérés étant unitaires, on s'attend à voir émerger une limite déterministe continue pour les processus convenablement renormalisés lorsque la population des différents patches est élevée. Cette remarque justifie l'introduction d'un paramètre d'échelle N dans les modèles ci-dessous.

Dans les deux paragraphes suivants, on suppose les processus à valeurs dans \mathbb{N}^n ou $(\mathbb{N}^n)^3$ définis à l'aide d'une unique famille de mesures ponctuelles de Poisson. Des constructions explicites de ces processus sont données aux chapitres 2 et 3.

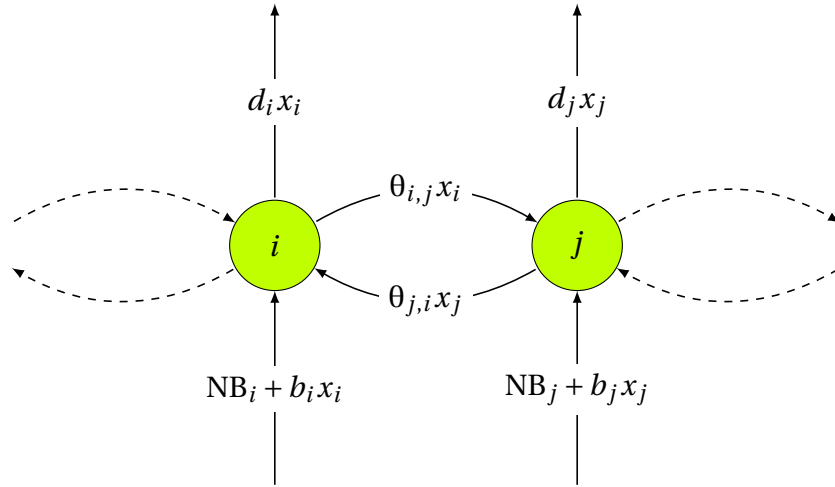


Figure 7.2: Représentation schématique du processus de population branchant. Les coefficients figurant sur les flèches sont les taux de transition.

7.2.2.1 Le processus de population branchant

Il est possible de modéliser les populations observées à l'aide d'un processus de branchement multitype à temps continu avec immigration à valeurs dans \mathbb{N}^n , auquel nous faisons référence dans le reste de ce manuscrit en utilisant la dénomination de *processus de population branchant*. Pour tout $N \geq 1$, on définit $(X^N(t))_{t \geq 0}$ comme un processus de sauts à valeurs dans \mathbb{N}^n ayant pour valeur initiale $X^N(0) = \lfloor Nx(0) \rfloor$ pour un certain $x(0) \in \mathbb{R}_+^n$ et avec les taux de transition suivants sous \mathbb{P} :

Transition	Taux de saut à partir de x	
$x \rightarrow x + e_i$	$NB_i + b_i x_i$	(7.1)
$x \rightarrow x - e_i$	$d_i x_i$	
$x \rightarrow x - e_i + e_j$	$\theta_{i,j} x_i$	

Table 7.1: Taux de saut du processus de population branchant.

où $\theta_{i,j}, b_i, B_i, d_i \in \mathbb{R}_+$.

Il est possible d'interpréter les $b_i x_i$ comme des taux de naissance malthusiens et les NB_i comme des taux d'immigration constants. Les différents taux sont représentés sur la figure 7.2.

Pour ne pas s'embarrasser de cas triviaux non pertinents pour l'application considérée, nous supposons que $B = (B_1, \dots, B_n) \neq 0$, de sorte que 0 n'est pas un état absorbant pour le processus de population, et que le graphe orienté de sommets $\llbracket 1, n \rrbracket$ et d'arêtes $\{(i, j) : \theta_{i,j} > 0\}$ est fortement connexe, de sorte qu'un individu né dans un nœud i a une probabilité non nulle de rejoindre le nœud j au cours de sa vie.

Enfin, on définit

$$A = \begin{pmatrix} b_1 - d_1 - \sum_{j \neq 1} \theta_{1,j} & \theta_{2,1} & \cdots & \theta_{n,1} \\ \theta_{1,2} & b_2 - d_2 - \sum_{j \neq 2} \theta_{2,j} & \ddots & \vdots \\ \vdots & \ddots & \ddots & \theta_{n,n-1} \\ \theta_{1,n} & \cdots & \theta_{n-1,n} & b_n - d_n - \sum_{j \neq n} \theta_{n,j} \end{pmatrix}, \quad (1.4)$$

et on suppose que toutes les valeurs propres de A ont une partie réelle strictement négative.

Dans ce cadre, des individus immigreront dans le patch i à taux NB_i , et ceux présents dans ce patch donneront naissance à taux b_i , meurent à taux d_i et immigreront vers le patch j à taux $\theta_{i,j}$, indépendamment des autres individus présents dans le réseau. La lignée initiée par un individu donné est un processus de branchement multitype à valeurs dans \mathbb{N}^n et à taux de transition donnés par (7.1) en remplaçant les B_i par 0. Après leur entrée dans le système, les individus donnent naissance à des lignées indépendantes qui n'interagissent pas, donc le nombre de telles lignées, et par conséquent la taille typique du processus de population, est proportionnelle au taux d'immigration par unité de temps, c'est-à-dire à N .

La théorie des processus de branchement multitypes à temps continu présentée dans la section 1.3.2 donne un grand nombre d'informations sur le comportement asymptotique des processus X^N . Les valeurs propres de A ayant toutes des parties réelles strictement négatives, X^N apparaît comme la superposition de processus de branchement sous-critiques initiés à taux NB , ce qui implique des propriétés de stabilité. Par ailleurs, on verra dans la section 7.3.3 que la limite d'échelle du processus renormalisé X^N/N lorsque N tend vers l'infini est un processus déterministe x très simple, solution de l'équation différentielle $\dot{x} = Ax + B$.

7.2.2.2 Le modèle de population logistique

Malgré ses propriétés mathématiques agréables, le modèle de population branchant que nous venons de présenter manque de réalisme compte tenu de l'objectif applicatif poursuivi. En effet, il ne prend pas en compte les phénomènes de saturation liés à des contraintes techniques et spatiales qui limitent naturellement la population des exploitations bovines. On introduit donc un second modèle de métapopulations markovien à sauts sur \mathbb{N}^n , le *modèle de population logistique*. On associe à chaque nœud i une capacité $NK_i > 0$ intervenant à la fois dans les taux logistiques d'importation vers le nœud i , son taux de croissance locale logistique et les taux « pseudo-logistiques » des transferts de population dirigés vers i .

Pour tout $N \geq 1$, on définit $(X^N(t))_{t \geq 0}$ comme un processus de sauts à valeurs dans \mathbb{N}^n ayant pour valeur initiale $X^N(0) = \lfloor Nz(0) \rfloor$ pour un certain $z(0) \in \mathbb{R}_+^n$, ainsi que les taux de transition suivants sous \mathbb{P} :

Transition	Taux de saut à partir de x	
$x \rightarrow x + e_i$	$\left(B_i + \frac{b_i}{N} x_i \right) (NK_i - x_i)_+$	(7.2)
$x \rightarrow x - e_i$	$d_i x_i$	
$x \rightarrow x - e_i + e_j$	$\frac{\theta_{i,j}}{N} x_i (NK_j - x_j)_+$	

Table 7.2: Taux de saut du processus de population logistique.

Les taux correspondant au processus de population logistique sont représentés sur la figure 7.3. Remarquons que le paramètre d'échelle N n'intervient plus ici dans les taux d'importation, car la taille typique du système est désormais déterminée par les capacités des nœuds plutôt que par les entrées de population. Nous le faisons figurer dans les taux de naissance et les taux de transfert dans le bus d'obtenir des limites d'échelle dans la section 1.3.3.

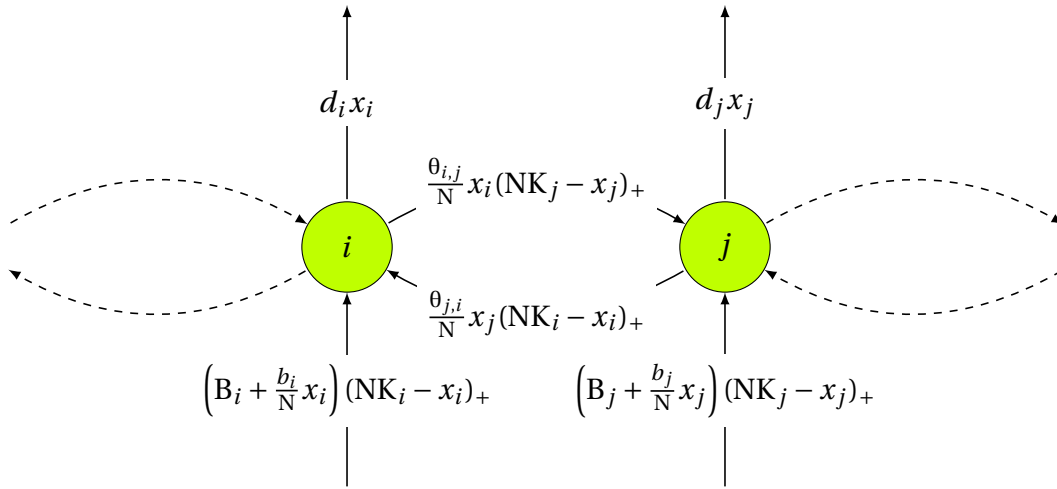


Figure 7.3: Représentation schématique du processus de population logistique. Les coefficients figurant sur les flèches sont les taux de transition.

On suppose cette fois encore que $B = (B_1, \dots, B_n) \neq 0$ et que le graphe de sommets $\llbracket 1, n \rrbracket$ et d'arêtes $\{(i, j) : \theta_{i,j} > 0\}$ est fortement connexe. On suppose aussi que $d \neq 0$, de sorte que $NK = N(K_1, \dots, K_n)$ n'est pas un état absorbant pour le processus. Sous ces hypothèses, X^N est un processus markovien de sauts irréductible à valeurs dans $\prod_{i=1}^n \llbracket 0, \lceil NK_i \rceil \rrbracket$. Il est donc ergodique.

7.2.3 Le processus épidémique

On définit à présent le modèle épidémiologique couplé avec les processus de population à sauts que nous venons d'introduire.

Pour tous N , i et t , on divise la population $X_i^N(t)$ du patch i au temps t en trois sous-populations : $S_i^N(t)$ individus susceptibles, $I_i^N(t)$ infectés et $R_i^N(t)$ rétablis. Les mouvements entre les nœuds, les naissances et les morts sont supposés indépendants du statut de santé, et sont donc décrits par le processus de population (branchant ou logistique, voir le tableau ci-dessous ainsi que les figures 7.4 et 7.5). On ne considère aucune transmission verticale du pathogène, ce qui revient à dire que les individus nés dans le système sont supposés susceptibles. Cependant, des individus infectieux peuvent en général entrer dans le système *via* l'immigration, et on suppose que chaque animal importé dans le nœud i est susceptible avec probabilité p_i , infecté avec probabilité q_i et rétabli avec probabilité $r_i = 1 - p_i - q_i$.

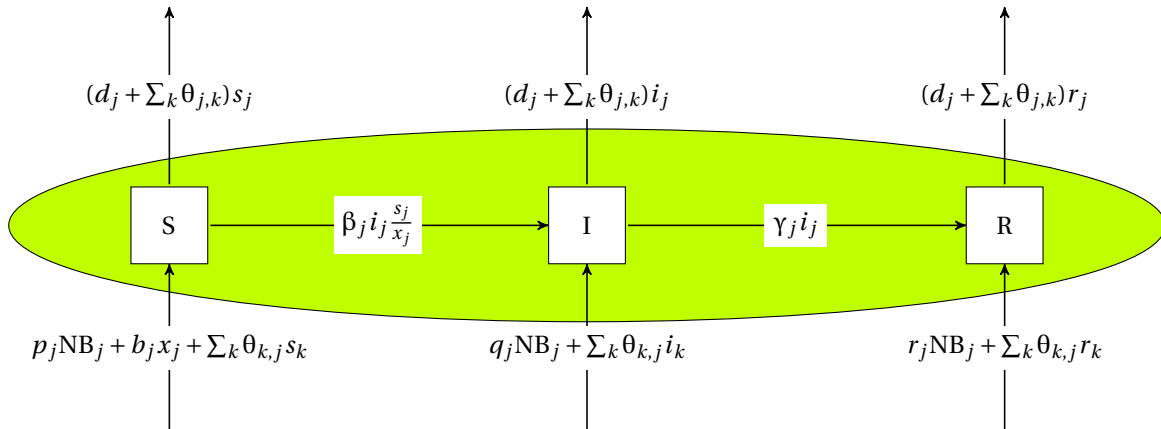


Figure 7.4: Représentation schématique d'un modèle compartimental SIR couplé avec un processus de population branchant. Les trois compartiments représentés sont à l'intérieur d'un même nœud j (ellipse verte). Les coefficients sur les flèches sont les taux de transition. Les flèches horizontales représentent des transferts de population entre compartiments à l'intérieur du nœud j , tandis que les flèches verticales représentent des flux de population vers et depuis le nœud j .

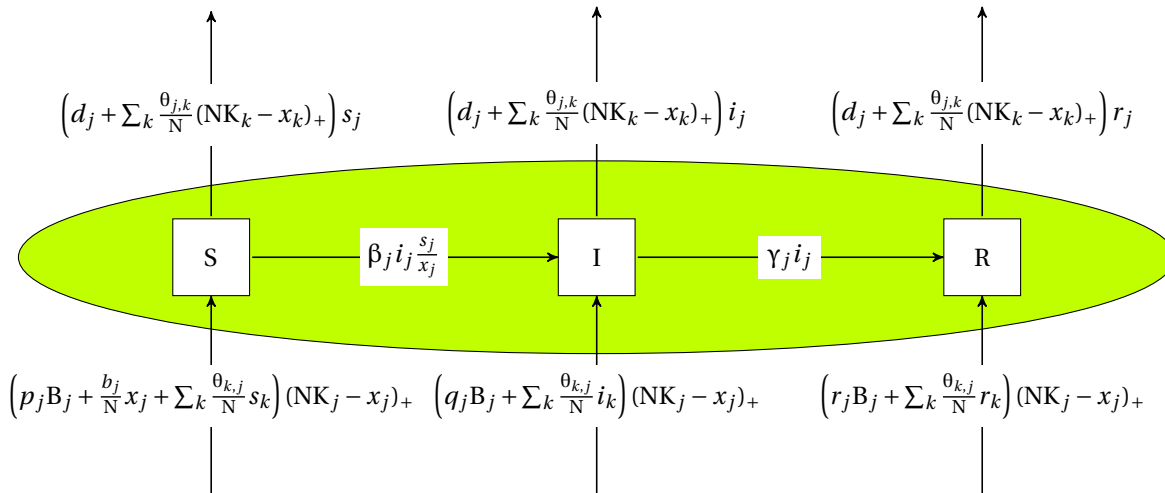


Figure 7.5: Représentation schématique d'un modèle compartimental SIR couplé avec un processus de population logistique. Les trois compartiments représentés sont à l'intérieur d'un même nœud j . Les coefficients sur les flèches sont les taux de transition. Les flèches horizontales représentent des transferts entre compartiments à l'intérieur du nœud j , tandis que les flèches verticales représentent des flux de population vers et depuis le nœud j .

Chaque individu infecté présent dans le nœud i réalise des contacts avec des individus choisis indépendamment et uniformément dans le nœud i à taux β_i . Insistons sur le fait que ces contacts peuvent uniquement être effectués entre des individus situés dans un même nœud. Les individus susceptibles atteints par ces contacts deviennent infectés ; le statut des autres individus atteints ne change pas. Indépendamment, les individus infectés vivant dans le nœud i se rétablissent à taux γ_i et entrent alors dans le compartiment correspondant.

Écrivons la base canonique de \mathbb{R}^{3n} sous la forme $(e_1^s, \dots, e_n^s, e_1^i, \dots, e_n^i, e_1^r, \dots, e_n^r)$. Pour tout $N \geq 1$, on considère un processus markovien de sauts $(S^N(t), I^N(t), R^N(t))_{t \geq 0}$ à valeurs dans $(\mathbb{Z}_+^n)^3$ défini sur (Ω, \mathcal{A}) et décrit par les taux de transition suivants au départ de l'état (s, i, r) , où l'on écrit $x_j = s_j + i_j + r_j$ pour tout $j \in \llbracket 1, n \rrbracket$:

Transition	Taux (cas branchant)	Taux (cas logistique)
$(s, i, r) \rightarrow (s, i, r) + e_j^s$	$p_j N B_j + b_j x_j$	$\left(p_j B_j + \frac{b_j}{N} x_j\right) (N K_j - x_j)_+$
$(s, i, r) \rightarrow (s, i, r) + e_j^i$	$q_j N B_j$	$q_j B_j (N K_j - x_j)_+$
$(s, i, r) \rightarrow (s, i, r) + e_j^r$	$r_j N B_j$	$r_j B_j (N K_j - x_j)_+$
$(s, i, r) \rightarrow (s, i, r) - e_j^s$	$d_j s_j$	$d_j s_j$
$(s, i, r) \rightarrow (s, i, r) - e_j^i$	$d_j i_j$	$d_j i_j$
$(s, i, r) \rightarrow (s, i, r) - e_j^r$	$d_j r_j$	$d_j r_j$
$(s, i, r) \rightarrow (s, i, r) + e_k^s - e_j^s$	$\theta_{j,k} s_j$	$\frac{\theta_{j,k}}{N} s_j (N K_k - x_k)_+$
$(s, i, r) \rightarrow (s, i, r) + e_k^i - e_j^i$	$\theta_{j,k} i_j$	$\frac{\theta_{j,k}}{N} i_j (N K_k - x_k)_+$
$(s, i, r) \rightarrow (s, i, r) + e_k^r - e_j^r$	$\theta_{j,k} r_j$	$\frac{\theta_{j,k}}{N} r_j (N K_k - x_k)_+$
$(s, i, r) \rightarrow (s, i, r) + e_j^i - e_j^s$	$\beta_j \frac{i_j s_j}{x_j}$	$\beta_j \frac{i_j s_j}{x_j}$
$(s, i, r) \rightarrow (s, i, r) + e_j^r - e_j^i$	$\gamma_j i_j$	$\gamma_j i_j$

Table 7.3: Taux de sauts du processus SIR couplé avec un processus de population branchant ou logistique.

L'une des questions abordées dans le cadre du présent travail est le comportement d'une épidémie initiée par un petit nombre d'individus dans le cas où $p_j = 1$ (et donc $q_j = r_j = 0$) pour tout j , c'est-à-dire lorsque l'immigration d'individus infectieux est inexistante. On n'impose donc pas que $I^N(0)$ soit proportionnel à N ; dans le cas évoqué, on prendra plutôt

$$I^N(0) = I(0), \quad S^N(0) = X^N(0) - I^N(0) = X^N(0) - I(0) \quad \text{et} \quad R^N(0) = 0$$

avec un $I(0) \in \mathbb{N}^n$ fixé (typiquement e_i pour un certain i).

7.2.4 Questions soulevées par les modèles étudiés

On démontre dans le chapitre 2 des propriétés de récurrence et d'ergodicité pour les processus de populations introduits dans les paragraphes 7.2.1 et 7.2.2. Dans le cas des processus à sauts, on s'intéresse à deux questions supplémentaires :

- Quelle est la limite déterministe de ces processus lorsque le paramètre d'échelle N tend vers l'infini ?
- Sur quelles échelles de temps peut-on considérer que la population est stable ?

Dans le chapitre 3, on étudie les processus épidémiques définis dans la section 7.2.3. Dans le cas où l'immigration d'individus infectieux n'est pas considérée ($p = \mathbb{1}$) et où l'épidémie est initiée par un nombre fixé d'infectieux introduits accidentellement dans le système, on répond aux questions suivantes :

- Par quel objet mathématique peut-on approcher le processus infectieux durant les premières phases de l'épidémie ?
- Quelle est la probabilité d'occurrence d'un événement épidémique majeur ?
- Sur quelle échelle de temps l'épidémie s'éteint-elle, et quelle est sa taille totale ?

Dans le cas où les individus entrant dans le système sont infectés avec une probabilité non nulle ($q \neq 0$), on s'intéresse à deux autres problématiques :

- Quel est le comportement du processus épidémique lorsque la population est importante ?
- Sur quelles échelles de temps peut-on observer le phénomène d'endémicité et à quel niveau la prévalence de l'infection se stabilise-t-elle ?

On réalise enfin dans le chapitre 4 une application numérique des résultats théoriques obtenus dans le chapitre 3 sur le processus épidémique couplé à des dynamiques de population logistiques. Cette application est construite autour de deux questions centrales :

- Comment définir des indicateurs calculables de la vulnérabilité du réseau à une épidémie grâce aux résultats analytiques obtenus au chapitre 3 ?
- Quelles stratégies de contrôle ciblant les nœuds critiques peut-on mettre en place, comment les évaluer et quelles sont les stratégies les plus efficaces ?

La section 1.3 de l'Introduction générale présente des outils mathématiques permettant de répondre à ces différentes questions et énonce les principaux résultats théoriques de la thèse. Nous nous bornons ici à reproduire lesdits résultats ; le lecteur désireux de rafraîchir ses connaissances relatives à un concept mathématique abordé peut être certain de trouver son bonheur dans la section 1.3 (en anglais).

7.3

Principaux résultats théoriques de la thèse

Cette section est organisée en paragraphes présentant les résultats obtenus à partir de différents cadres théoriques (présentés en détail, on le rappelle, dans la section 1.3).

7.3.1 Stabilité des modèles de population étudiés

Les principaux résultats relatifs à la récurrence et à l'ergodicité des processus de population étudiés sont les suivants :

THÉORÈME 7.3.1 (Ergodicité des modèles multiplicatif uniforme et puissance unitaire). — *Les modèles de métapopulations multiplicatif uniforme et puissance unitaire définis par 1.1 et 1.2 sont récurrents positifs au sens de Harris si et seulement si*

$$\sum_{i=1}^n c_i < 0$$

auquel cas ils sont aussi F-ergodiques, avec

$$F: \begin{cases} \mathbb{R}_+^n & \longrightarrow \mathbb{R}_+ \\ x & \longmapsto e^{\eta \|x\|_1} \end{cases}$$

pour un certain $\eta > 0$.

PROPOSITION 7.3.2 (Ergodicité du processus de population branchant). — *Soit $N \geq 1$. Le processus de population branchant X^N défini dans la section 7.2.2.1 est récurrent positif et $(\|\cdot\|_1 + 1)$ -uniformément exponentiellement ergodique. De plus, pour tout $x(0) \in \mathbb{R}_+^N$,*

$$\lim_{t \rightarrow +\infty} \mathbb{E}(X^N(t)) = \int x d\pi(x) = -NA^{-1}B$$

où A est défini par (1.4) et $B = (B_1, \dots, B_n)$.

Comme évoqué après la définition du processus de population logistique, l'ergodicité (exponentielle) de celui-ci est triviale puisqu'il s'agit d'un processus de Markov irréductible à temps continu à espace d'états fini. Nous énonçons néanmoins le résultat correspondant pour des raisons de symétrie :

PROPOSITION 7.3.3 (Ergodicité du processus de population logistique). — *Soit $N \geq 1$. Le processus de population logistique X^N défini dans la section 1.2.2.2 est récurrent positif et exponentiellement ergodique.*

7.3.2 Approximation des processus épidémiques à l'étude par des processus de branchement

Une seconde série de résultats porte sur l'approximation des processus épidémiques dans les premières phases de l'épidémie par des processus de branchement lorsque la population des différents nœuds tend vers l'infini et lorsque l'épidémie est initiée par un nombre fixé d'individus infectieux et n'est pas alimentée par l'immigration. On suppose donc dans ce paragraphe que $p = 1$, $I^N(0) = I(0) \in \mathbb{Z}_+^n$, $S^N(0) = X^N(0) - I(0)$ et par conséquent $R^N(0) = 0$. Alors :

THÉORÈME 7.3.4 (Convergence vers un processus de branchement (cas branchant)). — On peut définir un processus épidémique $(S^N(t), I^N(t), R^N(t))_{t \geq 0}$ sur \mathbb{N}^{3n} couplé à un processus de population branchant ainsi qu'un processus de branchement multitype $(I'(t))_{t \geq 0}$ sur $(\Omega, \mathcal{A}, \mathbb{P})$ à valeurs dans \mathbb{N}^n avec $I'(0) = I(0)$, décrivant une population d'individus se déplaçant du nœud i au nœud j à taux $\theta_{i,j}$ et, lorsqu'ils sont dans le nœud i , donnant naissance à taux β_i et mourant à taux $d_i + \gamma_i$, tels que pour tout temps $T \geq 0$, \mathbb{P} -presque sûrement on ait :

$$\exists N_0 \in \mathbb{Z}_+^* : \forall N \geq N_0, \forall u \in [0, T], \quad I^N(u) = I'(u).$$

En particulier, si τ^N (resp. Z^N) est le temps d'extinction (resp. la taille totale) de l'épidémie (S^N, I^N, R^N) et τ' (resp. Z') ceux du processus de branchement I' , alors

$$\tau^N \xrightarrow{N \rightarrow +\infty} \tau' \quad \text{et} \quad Z^N \xrightarrow{N \rightarrow +\infty} Z'$$

\mathbb{P} -presque sûrement.

La proposition suivante caractérise le comportement du processus de branchement limitant et fournit une méthode itérative pour estimer sa probabilité de survie, c'est-à-dire la probabilité d'occurrence d'un épisode épidémique majeur :

PROPOSITION 7.3.5 (Probabilité d'occurrence d'un épisode épidémique majeur (cas branchant)). — Pour tous $i, j \in \llbracket 1, n \rrbracket$, soit $W_{i,j}$ la progéniture de première génération dans le nœud j d'un individu né dans le nœud i . On note $\Sigma_i = \gamma_i + d_i + \sum_{j \neq i} \theta_{i,j}$ pour tout $i \in \llbracket 1, n \rrbracket$, et on définit $\Theta \in \mathcal{M}_n(\mathbb{R})$ par $\Theta_{i,j} = \theta_{i,j}$ si $i \neq j$ et par $\Theta_{i,i} = 0$. Alors :

1. La matrice $C = (\mathbb{E}(W_{i,j}))_{1 \leq i, j \leq n}$ est donnée par

$$C = (\text{diag}(\Sigma_1, \dots, \Sigma_n) - \Theta)^{-1} \text{diag}(\beta_1, \dots, \beta_n).$$

2. Soit R_0 la valeur propre dominante de C , que nous appellerons nombre de reproduction de base du processus épidémique. C'est un nombre réel, et le processus de branchement I' est sous-critique si $R_0 < 1$, critique si $R_0 = 1$ et surcritique si $R_0 > 1$.
3. Si le processus de branchement I' est sous-critique ou critique, alors la probabilité d'occurrence d'un épisode épidémique majeur est 0. S'il est surcritique, alors cette

probabilité est strictement positive et vaut $1 - \prod_{k=1}^n \zeta_k^{I_k(0)}$, où ζ est l'unique point fixe dans $[0, 1]^n$ de la fonction génératrice

$$G: [0, 1]^n \longrightarrow [0, 1]^n$$

$$s = (s_1, \dots, s_n) \longmapsto \left(\mathbb{E} \left[\prod_{j=1}^n s_j^{W_{1,j}} \right], \dots, \mathbb{E} \left[\prod_{j=1}^n s_j^{W_{n,j}} \right] \right) .$$

4. La fonction G a pour expression explicite

$$G(s) = (\text{diag}(\lambda_1(s), \dots, \lambda_n(s)) - \Theta)^{-1} (\gamma + d)$$

où $\lambda_i(s) = (1 - s_i)\beta_i + \Sigma_i$.

5. La suite des itérées $(G^k(s))_{k \geq 0}$ converge vers ζ pour tout $s \in [0, 1]^n$.

Le même résultat est valable pour les processus épidémiques couplés à des processus de population logistiques, pour peu que la population totale du système soit initiée à l'équilibre :

THÉORÈME 7.3.6 (Approximation du processus épidémique (cas logistique)). — *Le théorème ?? et la proposition 7.3.5 sont valables dans le cas logistique, sous la condition supplémentaire que $z(0)$ soit un point d'équilibre z^* du système dynamique (\mathcal{S}'_{pop}) défini dans la section 7.3.3 ci-dessous, et en remplaçant les taux de mouvement individuels $\theta_{i,j}$ par $\tilde{\theta}_{i,j} = \theta_{i,j}(K_j - z_j^*)_+$ dans la définition de Θ , Σ_i et λ_i .*

7.3.3 Limites d'échelle des processus étudiés

Le résultat suivant donne une approximation du processus de population branchant mis à l'échelle sur des intervalles de temps finis :

PROPOSITION 7.3.7 (Limite d'échelle du processus de population branchant). — *Soit $(X^N)_{N \geq 1}$ la suite de processus de population branchants définie dans la section 7.2.2. On note x la solution du problème de Cauchy $x' = Ax + B$ ayant pour condition initiale $x(0)$, c'est-à-dire*

$$x: \mathbb{R} \longrightarrow \mathbb{R}^n$$

$$t \longmapsto e^{tA}(A^{-1}B + x(0)) - A^{-1}B .$$

Alors pour tout $T \geq 0$,

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{t \in [0, T]} \left\| \frac{X^N(t)}{N} - x(t) \right\|_{\infty} = 0 \right) = 1 .$$

Considérons à présent le système dynamique sur $(\mathbb{R}_+^n)^3$ défini par

$$\left. \begin{aligned} \dot{s}_j &= p_j B_j + b_j(s_j + i_j + r_j) - d_j s_j + \sum_{k \neq j} \theta_{k,j} s_k - \sum_{k \neq j} \theta_{j,k} s_j - \beta_j i_j \frac{s_j}{s_j + i_j + r_j} \\ \dot{i}_j &= q_j B_j + \beta_j i_j \frac{s_j}{s_j + i_j + r_j} - d_j i_j - \gamma_j i_j + \sum_{k \neq j} \theta_{k,j} i_k - \sum_{k \neq j} \theta_{j,k} i_j \\ \dot{r}_j &= r_j B_j + \gamma_j i_j - d_j r_j + \sum_{k \neq j} \theta_{k,j} r_k - \sum_{k \neq j} \theta_{j,k} r_j \end{aligned} \right\} (\mathcal{S}_{\text{epi}})$$

pour tout $j \in \llbracket 1, n \rrbracket$. Le résultat suivant montre que le processus couplé à un processus de population branchant peut être approché par une solution de $(\mathcal{S}_{\text{epi}})$ sur des intervalles de temps finis :

PROPOSITION 7.3.8 (Limite d'échelle du processus épidémique (cas branchant)). — Soit $((S^N, I^N, R^N))_{N \geq 1}$ la suite de processus épidémiques couplés à des processus de population branchants et définis dans la section 7.2.3. On suppose que $N^{-1}(S^N(0), I^N(0), R^N(0))$ tend vers $(s(0), i(0), r(0)) \in \mathbb{R}_+^3$ lorsque N tend vers $+\infty$. En notant (s, i, r) la solution $(\mathcal{S}_{\text{epi}})$ ayant pour condition initial $(s(0), i(0), r(0))$, on a pour tout $T \geq 0$:

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{t \in [0, T]} \left\| \frac{(S^N(t), I^N(t), R^N(t))}{N} - (s, i, r)(t) \right\|_{\infty} = 0 \right) = 1.$$

Des résultats similaires sont valables pour le processus de population logistique et pour le processus épidémique associé. On introduit le système dynamique sur \mathbb{R}_+^n défini par

$$\dot{z}_i = (B_i + b_i z_i)(K_i - z_i)_+ - d_i z_i + \sum_{j \neq i} \theta_{j,i} z_j (K_i - z_i)_+ - \sum_{j \neq i} \theta_{i,j} z_i (K_j - z_j)_+ \quad (\mathcal{S}'_{\text{pop}})$$

pour tout $i \in \llbracket 1, n \rrbracket$. On peut montrer (voir la section 2.3) que ce système admet un équilibre sur $\prod_{i=1}^n (0, K_i)$ (dont l'unicité n'est pas établie), que nous noterons z^* . On considère à présent le système dynamique sur $(\mathbb{R}_+^n)^3 = \{(s, i, r) \in (\mathbb{R}_+^n)^3\}$ défini par

$$\left. \begin{aligned} \dot{s}_j &= (p_j B_j + b_j z_j)(K_j - z_j^*)_+ - d_j s_j - \beta_j i_j \frac{s_j}{z_j^*} \\ &\quad + \sum_{k \neq j} \theta_{k,j} s_k (K_j - z_j^*)_+ - \sum_{k \neq j} \theta_{j,k} s_j (K_k - z_k^*)_+ \\ \dot{i}_j &= q_j B_j (K_j - z_j^*)_+ + \beta_j i_j \frac{s_j}{z_j^*} - d_j i_j - \gamma_j i_j \\ &\quad + \sum_{k \neq j} \theta_{k,j} i_k (K_j - z_j^*)_+ - \sum_{k \neq j} \theta_{j,k} i_j (K_k - z_k^*)_+ \\ \dot{r}_j &= r_j B_j (K_j - z_j^*)_+ + \gamma_j i_j - d_j r_j + \sum_{k \neq j} \theta_{k,j} r_k (K_j - z_j^*)_+ - \sum_{k \neq j} \theta_{j,k} r_j (K_k - z_k^*)_+ \end{aligned} \right\} (\mathcal{S}'_{\text{epi}})$$

pour tout $j \in \llbracket 1, n \rrbracket$. Les résultats suivants sont les analogues des propositions 7.3.7 et 7.3.8 dans le cas logistique.

PROPOSITION 7.3.9 (Limite d'échelle du processus de population logistique). — Soit $(X^N)_{N \geq 1}$ la suite de processus de population logistiques définis dans la section 7.2.2. On

note z the solution du système dynamique (\mathcal{S}'_{pop}) avec condition initiale $z(0)$. Alors pour tout $T \geq 0$,

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{t \in [0, T]} \left\| \frac{X^N(t)}{N} - z(t) \right\|_{\infty} = 0 \right) = 1.$$

PROPOSITION 7.3.10 (Limite d'échelle du processus épidémique (cas logistique)). — Soit $((S^N, I^N, R^N))_{N \geq 1}$ une suite de processus épidémiques couplés à des processus de population logistiques comme définis dans la section 1.2.3. On suppose que $z(0) = z^*$ et que $N^{-1}(S^N(0), I^N(0), R^N(0))$ tend vers $(s(0), i(0), r(0)) \in \mathbb{R}_+^3$ lorsque N tend vers $+\infty$. En notant (s, i, r) la solution (\mathcal{S}'_{epi}) avec condition initiale $(s(0), i(0), r(0))$, on a pour tout $T \geq 0$:

$$\mathbb{P} \left(\lim_{N \rightarrow +\infty} \sup_{t \in [0, T]} \left\| \frac{(S^N(t), I^N(t), R^N(t))}{N} - (s, i, r)(t) \right\|_{\infty} = 0 \right) = 1.$$

7.3.4 Résultats de grandes déviations pour les processus étudiés

On peut quantifier l'échelle de temps sur laquelle un processus de population branchant mis à l'échelle reste dans le voisinage de sa valeur d'équilibre une fois ce voisinage rejoint :

PROPOSITION 7.3.11 (Temps de sortie d'un processus de population branchant). — Soit $(X^N)_{N \geq 1}$ la suite de processus de population branchants et soit $x^* = -A^{-1}B$. Pour tout $\varepsilon \in (0, \|x^*\|_2)$, on note τ_{ε}^N le temps de sortie de X^N/N de la boule $\mathcal{B}_2(x^*, \varepsilon)$. Alors, pour ε assez petit, il existe $\bar{V}_{\varepsilon}(x^*) > 0$ tel que pour tout $x(0) \in \mathcal{B}_2(x^*, \varepsilon)$ et pour tout $\alpha > 0$:

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(e^{(\bar{V}_{\varepsilon}(x^*) - \alpha)N} < \tau_{\varepsilon}^N < e^{(\bar{V}_{\varepsilon}(x^*) + \alpha)N} \right) = 1.$$

Les résultats de métastabilité présentés dans l'Introduction générale permettent d'obtenir des informations sur le temps d'extinction et la taille de l'épidémie dans le cas endémique lorsque $p = 1$. On a notamment l'énoncé suivant :

THÉORÈME 7.3.12 (Bilan d'un épisode épidémique majeur dans le cas branchant). — Supposons que $p = 1$, que $x(0) = x^*$, que $R_0 > 1$ et que le système dynamique (\mathcal{S}_{epi}) restreint à $\mathbb{R}_+^n \times (\mathbb{R}_+^n \setminus \{0\}) \times \mathbb{R}_+^n$ admet un équilibre endémique globalement asymptotiquement stable (s^*, i^*, r^*) . Soit $((S^N, I^N, R^N))_{N \geq 1}$ la suite de processus épidémiques donnée par le théorème 7.3.4, avec $I^N(0) = I(0) \in \mathbb{Z}_+^n$, $S^N(0) = \lfloor Nx(0) \rfloor - I(0)$ et $R^N(0) = 0$. Alors, en notant τ^N le temps d'extinction de l'épidémie et Z^N sa taille finale, il existe $V > 0$ tel que :

$$\lim_{N \rightarrow +\infty} \mathbb{P} (\tau^N > e^{VN} | Z^N = +\infty) = 1. \tag{7.3}$$

et

$$\lim_{N \rightarrow +\infty} \mathbb{P} (Z^N > e^{VN} | Z^N = +\infty) = 1. \tag{7.4}$$

Lorsque l'immigration d'individus infectieux est possible, on obtient un énoncé en termes de temps d'occupation :

PROPOSITION 7.3.13 (Temps passé par le processus épidémique dans le voisinage d'un équilibre de $(\mathcal{S}_{\text{epi}}^1)$). — Soit $((S^N, I^N, R^N))_{N \geq 1}$ une suite de processus épidémiques couplés à des processus de population branchants comme définis dans la section 1.2.3. Si $q \neq 0$ et si $(\mathcal{S}_{\text{epi}})$ admet un équilibre globalement asymptotiquement stable (s^*, i^*, r^*) , alors $i_j^* > 0$ pour tout $j \in \llbracket 1, n \rrbracket$, et quel que soit $\varepsilon > 0$ il existe $T > 0$ et $V > 0$ tels que:

$$\lim_{N \rightarrow +\infty} \mathbb{P} \left(\int_0^{T+e^{VN}} \mathbf{1}_{\frac{(S^N(t), I^N(t), R^N(t))}{N} \in \mathcal{B}_2((s^*, i^*, r^*), \varepsilon)} dt > e^{VN} \right) = 1.$$

On a une fois encore des résultats similaires dans le cas logistique :

THÉORÈME 7.3.14 (Bilan d'un épisode épidémique majeur dans le cas logistique). — Les conclusions du théorème 7.3.12 et de la proposition 7.3.13 sont exactes dans le cas logistique, en remplaçant $(\mathcal{S}_{\text{epi}})$ par $(\mathcal{S}'_{\text{epi}})$ et $x(0) = x^*$ par $z(0) = z^*$.

Bibliography

- [AB54] H. G. Andrewartha and L. C. Birch. *The Distribution and Abundance of Animals*. Chicago: University of Chicago Press, 1954.
- [AB00a] H. Andersson and T. Britton. *Stochastic Epidemic Models and Their Statistical Analysis*. Springer, 2000.
- [AB00b] H. Andersson and T. Britton. Stochastic epidemics in dynamic populations: quasi-stationarity and extinction. *J. Math. Biol.*, 41:559–580, 2000.
- [Ada16] Etienne Adam. *Persistence et vitesse d'extinction pour des modèles de populations stochastiques multitypes en temps discret*. PhD thesis, Université Paris-Saclay, 2016. Thèse de doctorat dirigée par Chazottes, Jean-René.
- [ADR67] J. Azéma, M. Duflo, and D. Revuz. Mesure invariante sur les classes récurrentes des processus de Markov. *Zeitschrift für Wahrscheinlichkeitstheorie und Verwandte Gebiete*, 1967.
- [ADR69] J. Azéma, M. Duflo, and D. Revuz. Mesure invariante des processus de Markov récurrents. In *Séminaire de probabilités de Strasbourg*, volume 3, pages 24–33, 1969.
- [AK78] Søren Asmussen and Niels Keiding. Martingale central limit theorems and asymptotic estimation theory for multitype branching processes. *Advances in Applied Probability*, 10(1):109–129, 1978.
- [AN72] K. B. Athreya and P. E. Ney. *Branching Processes*. Springer, 1972.
- [ARM98] A. Arkin, J. Ross, and H. McAdams. Stochastic kinetic analysis of developmental pathway bifurcation in phage lambda-infected escherichia coli cells. *Genetics*, 149(4):1633–1648, 1998.
- [Ath68] K. B. Athreya. Some results on multitype continuous time Markov branching processes. *The Annals of Mathematical Statistics*, 39(2):347–357, 1968.
- [Ayd17] O. Aydogmus. Phase transitions in a logistic metapopulation model with nonlocal interactions. *Bulletin of Mathematical Biology*, 80(6), 2017.
- [Bal83] F. G. Ball. The threshold behavior of epidemic models. *Journal of Applied Probability*, 20:227–241, 1983.

- [Bal86] F. Ball. Deterministic and stochastic epidemics with several kinds of susceptibles. *Advances in Applied Probability*, 17(01):1–22, 1986.
- [Bar49] M. S. Bartlett. Some evolutionary stochastic processes. *Journal of the Royal Statistical Society. Series B (Methodological)*, 11(2):211–229, 1949.
- [Bar55] M. S. Bartlett. *An Introduction to Stochastic Processes*. Cambridge Univ. Press, 1955.
- [Bar56] M. S. Bartlett. *Proceedings of the Third Berkeley Symposium on Mathematical Statistics and Probability*, volume 4, chapter Deterministic and stochastic models for recurrent epidemics, pages 81–109. University of California Press, 1956.
- [Bas10] R. F. Bass. The measurability of hitting times. *Electronic communications in Probability*, 10:99–105, 2010.
- [BBH⁺15] Frank Ball, Tom Britton, Thomas House, Valerie Isham, Denis Mollison, Lorenzo Pellis, and Gianpaolo Scalia-Tomba. Seven challenges for metapopulation models of epidemics, including households models. *Epidemics*, 10:63 – 67, 2015. Challenges in Modelling Infectious Disease Dynamics.
- [BBL18] Frank Ball, Tom Britton, Ka Yin Leung, and David Sirl. A stochastic SIR network epidemic model with preventive dropping of edges. *Preprint*, 08 2018.
- [BC93] F. Ball and D. Clancy. The final size and severity of a generalised stochastic multitype epidemic model. *Advances in Applied Probability*, 25(4):721–736, 1993.
- [BC95] F. Ball and D. Clancy. The final outcome of an epidemic model with several different types of infective in a large population. *Journal of Applied Probability*, 32(3):579–590, 1995.
- [BCF⁺16] S. Billiard, P. Collet, R. Ferrière, S. Méléard, and V. C. Tran. The effect of competition and horizontal trait inheritance on invasion, fixation and polymorphism. *Journal of Theoretical Biology*, 411:48–58, 2016.
- [BCG⁺13] J.-B. Bardet, A. Christen, A. Guillin, F. Malrieu, and P.-A. Zitt. Total variation estimates for the TCP process. *Electronic Journal of Probability*, 18, No 10:1–21, 2013.
- [BdRa15] Carla Bravo de Rueda and al. Quantification of transmission of foot-and-mouth disease virus caused by an environment contaminated with secretions and excretions from infected calves. *Veterinary Research*, 46(1):43, 2015.
- [BHL⁺15] Tom Britton, Thomas House, Alun L. Lloyd, Denis Mollison, Steven Riley, and Pieter Trapman. Five challenges for stochastic epidemic models involving global transmission. *Epidemics*, 10:54 – 57, 2015.
- [BJS16] Tom Britton, David Juher, and Joan Saldaña. A network epidemic model with preventive rewiring: Comparative analysis of the initial phase. *Bulletin of Mathematical Biology*, 78:2427–2454, 10 2016.

- [BL13] V. Bansaye and A. Lambert. New approaches of source-sink metapopulations decoupling the roles of demography and dispersal. *Theoretical Population Biology*, 88, 2013.
- [BM15] V. Bansaye and S. Méléard. *Stochastic Models for Structured Populations*. Stochastics in Biological Systems. Springer, 2015.
- [BN08] F. Ball and P. Neal. Network epidemic models with two levels of mixing. *Mathematical Biosciences, Volume 212, Issue 1*, pp. 69-87, 2008.
- [Bov06] Anton Bovier. *Metastability: A potential theoretic approach*. Springer, 04 2006.
- [BP18] T. Britton and E. Pardoux. Stochastic epidemics in a homogeneous community. *arXiv:1808.05350*, 2018.
- [BPT16] Frank Ball, Lorenzo Pellis, and Pieter Trapman. Reproduction numbers for epidemic models with households and other social structures II: Comparisons and implications for vaccination. *Mathematical Biosciences*, 274:108 – 139, 2016.
- [Bra08] F. Brauer. *Mathematical Epidemiology (Lecture Notes in Mathematics)*, chapter Compartmental Models in Epidemiology, pages 19–79. Springer, 2008.
- [Bri10] T. Britton. Stochastic epidemic models: A survey. *Math. Biosci.*, 225(1):24–35, 2010.
- [BS05] Mogens Bladt and Michael Sørensen. Statistical inference for discretely observed Markov jump processes. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 67:395 – 410, 06 2005.
- [BS16] H. Baumann and W. Sandmann. Structured modeling and analysis of stochastic epidemics with immigration and demographic effects. *PLOS One*, 11(3), 2016. <https://doi.org/10.1371/journal.pone.0152144>.
- [BS18] Frank Ball and David Sirl. Evaluation of vaccination strategies for SIR epidemics on random networks incorporating household structure. *Journal of Mathematical Biology*, 76(1):483–530, Jan 2018.
- [BS19] S. Billiard and C. Smadi. Stochastic dynamics of three competing clones: Conditions and times for invasion, coexistence and fixation. *Submitted*, 2019.
- [BST09] F. Ball, D. Sirl, and P. Trapman. Threshold behaviour and final outcome of an epidemic on a random network with household structure. *Advances in Applied Probability*, 41(3):765–796, 2009.
- [BST10] Frank Ball, David Sirl, and Pieter Trapman. Analysis of a stochastic SIR epidemic on a random network incorporating household structure. *Mathematical Biosciences*, 224(2):53 – 73, 2010.
- [BT14] T. Britton and P. Trapman. Stochastic epidemics in growing populations. *Bulletin of Mathematical Biology*, 76:985–996, 2014.

- [BVE15] G. Beaunée, E. Vergu, and P. Ezanno. Modelling of paratuberculosis spread between dairy cattle farms at a regional scale. *Veterinary Research* 46:111, 2015.
- [BVJE17] G. Beaunée, E. Vergu, A. Joly, and P. Ezanno. Controlling bovine paratuberculosis at a regional scale: Towards a decision modelling tool. *Journal of Theoretical Biology*, 435, 09 2017.
- [BWG⁺09] Sarah Bekessy, Brendan Wintle, Ascelin Gordon, Ryan Chisholm, Lisa Venier, and Jennie Pearce. Chapter 18 - dynamic landscape metapopulation models and sustainable forest management. In Joshua J. Millspaugh and Frank R. Thompson, editors, *Models for Planning Wildlife Conservation in Large Landscapes*, pages 473 – 499. Academic Press, San Diego, 2009.
- [CBBV06] Vittoria Colizza, Alain Barrat, Marc Barthélemy, and Alessandro Vespignani. The role of the airline transportation network in the prediction and predictability of global epidemics. *Proceedings of the National Academy of Sciences*, 103(7):2015–2020, 2006.
- [CFM05] N. Champagnat, R. Ferrière, and S. Méléard. *Seminar on Stochastic Analysis, Random Fields and Applications V*, chapter Individual-Based Probabilistic Models of Adaptive Evolution and Various Scaling Approximations, pages 75–113. Springer, 11 2005.
- [CG07] A. J. K. Conlan and B. T. Grenfell. Seasonality and the persistence and invasion of measles. *Proceedings of the Royal Society B*, 274:1133–1141, 2007.
- [CGP06] Y. Cao, D. Gillespie, and L. R. Petzold. Efficient step size selection for the tau-leaping simulation method. *The Journal of Chemical Physics*, 124(044109), 2006.
- [CL07] C. G. Cassandras and J. Lygeros. *Stochastic Hybrid Systems*. Taylor & Francis, 2007.
- [Cla94] D. Clancy. Some comparison results for multitype epidemic models. *Journal of Applied Probability*, 31(1):9–21, 1994.
- [Cla96] D. Clancy. Strong approximations for mobile population epidemic models. *Annals of Applied Probability*, 6(3):883–895, 1996.
- [CMP10] D. Chafaï, F. Malrieu, and K. Paroux. On the long time behavior of the TCP window size process. *Stochastic Process. Appl.*, 120(8):1518–1534, 2010.
- [CPJEJG06] Ben Cooper, Richard Pitman, W John Edmunds, and Nigel J Gay. Delaying the international spread of pandemic influenza. *PLoS medicine*, 3:e212, 07 2006.
- [CV14] Nicolas Champagnat and Denis Villemonais. Exponential convergence to quasi-stationary distribution and q -processes. *Probability Theory and Related Fields*, 164, 04 2014.
- [CV15] Nicolas Champagnat and Denis Villemonais. Quasi-stationary distribution for multi-dimensional birth and death processes conditioned to survival of all coordinates. arXiv:1508.03161v1, 08 2015.

- [CV16] Nicolas Champagnat and Denis Villemonais. Population processes with unbounded extinction rate conditioned to non-extinction. Preprint. Available at arXiv:1611.03010v1, 11 2016.
- [CV17] Nicolas Champagnat and Denis Villemonais. General criteria for the study of quasi-stationarity. Preprint. Available at arXiv:1712.08092v2, 12 2017.
- [Dai95] J. G. Dai. On positive harris recurrence of multiclass networks: A unified approach via fluid limits models. *The Annals of Applied Probability*, 5(1):49–77, 1995.
- [Dav93] M.H.A. Davis. *Markov Models and Optimization*. Springer, 1993.
- [DEV14] B.L. Dutta, P. Ezanno, and E. Vergu. Characteristics of the spatio-temporal network of cattle movements in France over a 5-year period. *Preventive Veterinary Medicine(1)*:79-94, 2014.
- [DF15] M. Dottori and G. Fabricius. SIR model on a dynamical network and the endemic state of an infectious disease. *Physica A: Statistical Mechanics and its Applications*, 434:25–35, September 2015.
- [DGLO16] A. Duarte, A. Galves, E. Löcherbach, and G. Ost. Estimating the interaction graph of stochastic neural dynamics. *arXiv:1604.00419*, 2016.
- [DGR02] V. Dumas, F. Guillemin, and P. Robert. A Markovian analysis of additive-increase multiplicative-decrease (AIMD) algorithms. *Advances in Applied Probability*, 2002.
- [DH00] Odo Diekmann and Johan Andre Peter Heesterbeek. *Mathematical epidemiology of infectious diseases: model building, analysis and interpretation*, volume 5. John Wiley & Sons, 2000.
- [DHB12] O. Diekmann, H. Heesterbeek, and T. Britton. *Mathematical Tools for Understanding Infectious Disease Dynamics*. Princeton University Press, 2012.
- [DHM90] O Diekmann, J.A.P. Heesterbeek, and Johan Metz. On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations. *Journal of mathematical biology*, 28:365–82, 02 1990.
- [DHR09] O Diekmann, J.A.P. Heesterbeek, and M.G. Roberts. The construction of next-generation matrices for compartmental epidemic models. *Journal of the Royal Society, Interface / the Royal Society*, 7:873–85, 11 2009.
- [DM68] J.N. Darroch and K.W. Morris. Passage-time generating functions for continuous-time finite Markov chains. *Journal of Applied Probability*, 5(2):414–426, Aug. 1968.
- [DM00] B. Durand and O. Mahul. An extended state-transition model for foot-and-mouth disease epidemics in France. *Preventive Veterinary Medicine*, 47:121–139, 2000.
- [DMT95] D. Down, Sean P. Meyn, and R. L. Tweedie. Exponential and uniform ergodicity of Markov processes. *The Annals of Probability*, 23:1671–1691, 1995.

- [DO16] A. Duarte and G. Ost. A model for neural activity in the absence of external stimuli. *Markov Processes and Related Fields*, 22(1):37–52, 2016.
- [Doo42] J.L. Doob. Topics in the theory of markoff chains. *Transactions of the American Mathematical Society*, 52(1):37–64, 1942.
- [Doo45] J.L. Doob. Markoff chains — denumerable case. *Transactions of the American Mathematical Society*, 58(3):455–473, 1945.
- [EK86] S. N. Ethier and T. G. Kurtz. *Markov Processes: Characterization and Convergence*. Wiley Series in Probability and Statistics, 1986.
- [EN02] R.S. Etienne and C. J. Nagelkerke. Non-equilibria in small metapopulations: Comparing the deterministic Levins model with its stochastic counterpart. *Journal of Theoretical Biology*, 219:463–478, 2002.
- [Eti00] R. S. Etienne. Local populations of different sizes, mechanistic rescue effect and patch preference in the Levins metapopulation model. *Bulletin of Mathematical Biology*, 62:943–958, 2000.
- [Eti02] Rampal S. Etienne. A scrutiny of the Levins metapopulation model. *Comments on Theoretical Biology*, 7:257–281, 2002.
- [FAO99] Food and United Nations Agriculture Organization. *Manual on the preparation of national animal disease emergency preparedness plans*. Rome, 1999.
- [FCF⁺06] Neil Ferguson, Derek Cummings, Christophe Fraser, James C Cajka, Philip Cooley, and Samuel Burke. Strategies for mitigating an influenza pandemic. *Nature*, 442:448–52, 08 2006.
- [FKMP95] P.A. Ferrari, H. Kesten, S. Martinez, and P. Picco. Existence of quasi-stationary distributions. a renewal dynamical approach. *The Annals of Probability*, 23(2):501–521, 1995.
- [FW84] M.I. Freidlin and A.D. Wentzell. *Random Perturbations of Dynamical Systems*, volume Grundlehren der mathematischen Wissenschaften 260 of *A Series of Comprehensive Studies in Mathematics*. Springer-Verlag, 1984.
- [GH60] F. W. Gehring and P. R. Halmos. *Finite Markov Chains*, chapter 3 : Absorbing Markov Chains, page 224. Springer-Verlag, 1960.
- [Gil76] D. Gillespie. A general method for numerically simulating the stochastic time evolution of coupled chemical reactions. *Journal of Computational Physics*, 22(4):403–434, December 1976.
- [Gil77] D. Gillespie. Exact stochastic simulation of coupled chemical reactions. *The Journal of Physical Chemistry*, 81(25):2340–2361, December 1977.
- [Gil01] D. Gillespie. Approximate accelerated stochastic simulation of chemically reacting systems. *The Journal of Chemical Physics*, 115:1716–1733, July 2001.

- [GL00] F. Gosselin and J.-D. Lebreton. *Quantitative Methods for Conservation Biology*, chapter Potential of Branching Processes as a Modeling Tool for Conservation Biology, pages 199–225. Springer, 2000.
- [GP03] D. Gillespie and L. Petzold. Improved leap-size selection for accelerated stochastic simulation. *Journal of Chemical Physics*, 119(16):8229–8234, 2003.
- [GS94] M. Gyllenberg and D. S. Silvestrov. Quasi-stationary distributions of a stochastic metapopulation model. *Journal of Mathematical Biology*, 33:35–70, 1994.
- [GS18] Uttam Ghosh and Susmita Sarkar. Global stability analysis of logistically grown SIR model with loss of immunity, inhibitory effect, crowding effect and its protection measure. *Computational Methods in Science and Technology*, 24, 05 2018.
- [Han83] I. Hanski. Coexistence of competitors in a patchy environment. *Ecology*, 64:493–500, 1983.
- [Han94] I. Hanski. A practical model of metapopulation dynamics. *Journal of Animal Ecology*, 63:151–162, 1994.
- [Han99] I. Hanski. *Metapopulation Ecology*. Oxford University Press, New York, 1999.
- [HBG04] L. Hufnagel, D. Brockmann, and T. Geisel. Forecast and control of epidemics in a globalized world. *Proceedings of the National Academy of Sciences*, 101(42):15124–15129, 2004.
- [HD00] S. C. Howard and C. A. Donnelly. The importance of immediate destruction in epidemics of foot-and-mouth disease. *Research in Veterinary Science*, 69:189–196, 2000.
- [HG91] I. Hanski and M. Gilpin. Metapopulation dynamics: brief history and conceptual domain. *Biological Journal of the Linnean Society*, 42(1-2):3–16, 1991.
- [HGM⁺16] P. Hoscheit, S. Geeraert, H. Monod, C.A. Gilligan, J. Filipe, E. Vergu, and M. Moslonka-Lefebvre. Dynamical network models for cattle trade: Towards economy-based epidemic risk assessment. *Journal of Complex Networks*, 5(4):604–624, August 2016.
- [HJK16] Kais Hamza, Peter Jagers, and Fima C Klebaner. On the establishment, persistence, and inevitable extinction of populations. *Journal of Mathematical Biology*, 72(4):797–820, 2016.
- [HK96] A. M. Hutber and R. P. Kitching. The use of vector transition in the modelling of intraherd foot-and-mouth disease. *Environnemental and Ecological Statistics*, 3:245–255, 1996.
- [HL01] D. Hong and D. Lebedev. Many TCP user asymptotic analysis of the AIMD model. *Rapport de recherche INRIA*, 4229, 2001.

- [HMG96] I. Hanski, A. Moilanen, and M. Gyllenberg. Minimum viable metapopulation size. *American Naturalist*, 147:527–541, 1996.
- [HR76] J. M. Harrison and S. I. Resnick. The stationary distribution and first exit probabilities of a storage process with general release rule. *Mathematics of Operations Research*, 1:347–358, 1976.
- [HS97] I. Hanski and D. Simberloff. *Metapopulation Biology: Ecology, Genetics, and Evolution*. Academic Press, Elsevier, 1997.
- [HS12] Petter Holme and Jari Saramäki. Temporal networks. *Physics Reports*, 519(3):97 – 125, 2012. Temporal Networks.
- [Huf58] C.B. Huffaker. Experimental studies on predation: Dispersion factors and predator-prey oscillations. *Hilgardia*, 27(343):83, 1958.
- [HW73] Herbert W. Hethcote and Paul Waltman. Optimal vaccination schedules in a deterministic epidemic model. *Mathematical Biosciences*, 18(3):365 – 381, 1973.
- [HWK97] D. T. Haydon, M. E. J. Woolhouse, and R. P. Kitching. An analysis of foot-and-mouth-disease epidemics in the UK. *IMA Journal of Mathematics Applied in Medicine and Biology*, 14:1–9, 1997.
- [Jac57] J.R. Jackson. Networks of waiting lines. *Operations Research* 5 (4): pp.518-521, 1957.
- [Jag78] P. Jagers. *Branching Processes with Biological Applications*. Wiley Series in Probability and Mathematical Statistics, 1978.
- [JS03] Karin Johst and Katrin Schöps. Persistence and conservation of a consumer–resource metapopulation with local overexploitation of resources. *Biological Conservation*, 109(1):57 – 65, 2003.
- [Kar59] S. Karlin. Positive operators. *J. Math. Mech.*, 8:907–937, 1959.
- [Kar90] P. Kareiva. Population dynamics in spatially complex environments: theory and data. *Philosophical Transactions of the Royal Society, London B*, 330:175–190, 1990.
- [KDGK06] R. R. Kao, L. Danon, D. M. Green, and I. Z. Kiss. Demographic structure and pathogen dynamics on the network of livestock movements in Great Britain. *Proceedings of the Royal Society B: Biological Sciences*, 273:1999–2007, 2006.
- [Kee05] M. J. Keeling. Models of foot-and-mouth disease. *Proceedings of the Royal Society B*, 272:1195–1202, 2005.
- [Ken50] D. G. Kendall. An artificial realization of a simple "birth-and-death" process. *Journal of the Royal Statistical Society. Series B (Methodological)*, 12(1):116–119, 1950.
- [Ken56] D. G. Kendall. Deterministic and stochastic epidemics in closed populations. *Proc. Third Berkeley Symp. Math. Statist. Probab.*, 4:149–165, 1956.

- [KM27] W. O. Kermack and A. G. McKendrick. A contribution to the mathematical theory of epidemics. *Proceedings of the Royal Society of London*, 115(772):700–721, 1927.
- [KP18] P. Kratz and E. Pardoux. *Séminaire de Probabilités XLIX*, chapter Large Deviations for Infectious Diseases Models, pages 221–327. Springer Verlag, 2018.
- [KPSK15] P. Kratz, E. Pardoux, and B. Samegni-Kepgnou. Numerical methods in the context of compartmental models in epidemiology. *Ensaïm: proceedings and surveys*, 48:169–189, 2015.
- [KR07] M. J. Keeling and P. Rohani. *Modeling Infectious Diseases in Humans and Animals*. Princeton University Press, 2007.
- [KS67] 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.
- [KW95] P. Kareiva and U. Wennergren. Connecting landscape patterns to ecosystem and population processes. *Nature*, 373:299–302, 1995.
- [Lev69] R. Levins. Some demographic and genetic consequences of environmental heterogeneity for biological control. *Bulletin of the Entomological Society of America*, 15:237–240, 1969.
- [Lev70] R. Levins. Extinction. *Lecture Notes in Mathematics*, 2:75–107, 1970.
- [LM01] D. Liberzon and A. S. Morse. Basic problems in stability and design of switched systems. *IEEE Control Systems Magazine*, 19:59–70, 2001.
- [Löc18] E. Löcherbach. Absolute continuity of the invariant measure in piecewise deterministic Markov processes having degenerate jumps. *Stochastic Processes and their Applications*, 128:1797–1829, 2018.
- [LS09] Michael Y. Li and Zhisheng Shuai. Global stability of an epidemic model in a patch environment. *Canadian Applied Mathematics Quarterly*, 17(1):175–187, 2009.
- [LTW⁺17] J. Li, Z. Teng, G. Wang, L. Zhang, and C. Hu. Stability and bifurcation analysis of an SIR epidemic model with logistic growth and saturated treatment. *Chaos, Solitons & Fractals*, 99:63–71, 2017.
- [MA97] H. McAdams and A. Arkin. Stochastic mechanisms in gene expression. *Proceedings of the National Academy of Science of the United States of America*, 94:814–819, 1997.
- [MA07] Robert K. McKormack and Linda J.S. Allen. Multi-patch deterministic and stochastic models for wildlife diseases. *Journal of Biological Dynamics*, 1(1):63–85, October 2007.
- [Mal90] R. Malhamé. A jump-driven Markovian electric load model. *Advances in Applied Probability*, 22:564–586, 1990.

- [MD94] S. P. Meyn and D. Down. Stability of generalized Jackson networks. *The Annals of Applied Probability*, 4(1):124–148, 1994.
- [MEK13] Y. Muroya, Y. Enatsu, and T. Kuniya. Global stability of extended multi-group SIR epidemic models with patch through migration and cross-patch infection. *Acta Mathematica Scientia*, 33:341–361, 2013.
- [MGM⁺16] M. Moslonka-Lefebvre, C.A. Gilligan, H. Monod, C. Belloc, P. Ezanno, J.A.N. Filipe, and E. Vergu. Market analyses of livestock trade networks to inform the prevention of joint economic and epidemiological risks. *Journal of The Royal Society Interface*, 2016.
- [Mil76] W. M. Miller. A state-transition model of epidemic foot-and-mouth disease. In University of Reading, editor, *Proceedings of Symposium New Techniques in Veterinary Epidemiology and Economics*, pages 56–72, 1976.
- [MK85] D. Mollison and K. Kuulasmaa. *Spatial epidemic models: theory and simulations*, pages 291–309. Academic Press, 1985.
- [MMZB17] Wenjun Mei, Shadi Mohagheghi, Sandro Zampieri, and Francesco Bullo. On the dynamics of deterministic epidemic propagation over networks. *Annual Reviews in Control*, 44, 01 2017.
- [Mod71] C. J. Mode. *Multitype Branching Processes*. Elsevier Publishing Co. Ltd., London, 1971.
- [Mol77] D. Mollison. Spatial contact models for ecological and epidemic spread. *Journal of the Royal Statistical Society Series B*, 39:283–326, 1977.
- [Mon19a] P. Montagnon. Stability of piecewise deterministic Markovian metapopulation processes on networks. *Submitted*, 2019.
- [Mon19b] Pierre Montagnon. A stochastic SIR model on a graph with epidemiological and population dynamics occurring over the same time scale. *Journal of Mathematical Biology*, Apr 2019.
- [MT92a] S. P. Meyn and R. L. Tweedie. Generalized resolvents and harris recurrence of Markov processes. In *50 years after Doebelin: Developments in the Theory of Markov Chains, Markov Processes and Sums of Random Variables.*, 1992.
- [MT92b] S. P. Meyn and R. L. Tweedie. Stability of Markovian processes I: Criteria for discrete-time chains. *Advances in Applied Probability*, 24:542–574, 1992.
- [MT93a] S. P. Meyn and R. L. Tweedie. Stability of Markovian processes II: Continuous-time processes and sampled chains. *Advances in Applied Probability*, 25:487–517, 1993.
- [MT93b] S. P. Meyn and R. L. Tweedie. Stability of Markovian processes III: Foster-lyapunov criteria for continuous-time processes. *Advances in Applied Probability*, 25:518–548, 1993.

- [MT94] S. P. Meyn and R. L. Tweedie. State-dependent criteria for convergence of Markov chains. *The Annals of Applied Probability*, 1994.
- [MW67] R. MacArthur and E. O. Wilson. *The Theory of Island Biogeography*. Princeton University Press, 1967.
- [MW74] R. Morton and K. H. Wickwire. On the optimal control of a deterministic epidemic. *Advances in Applied Probability*, 6(4):622–635, 1974.
- [Mye88] G. H. Myers. Strategies to Control Internal Parasites in Cattle and Swine. *Journal of Animal Science*, 66(6):1555–1564, 06 1988.
- [Nå99] I. Nåsell. On the time to extinction in recurrent epidemics. *Journal of the Royal Statistical Society*, 61(2):309–330, 1999.
- [Nea12] P. Neal. The basic reproduction number and the probability of extinction for a dynamic epidemic model. *Mathematical Bioscience*, 236(1):31–35, 2012.
- [NT19] Peter Neal and Thitiya Theparod. The basic reproduction number, R_0 , in structured populations. *Submitted*, 03 2019.
- [O’N96] P. O’Neill. Strong approximations for some open population epidemic models. *Journal of Applied Probability*, 33(2):448–457, 1996.
- [PBT11] Lorenzo Pellis, Frank Ball, and Pieter Trapman. Reproduction numbers for epidemic models with households and other social structures. I. definition and calculation of R_0 . *Mathematical biosciences*, 235:85–97, 11 2011.
- [PCVV15] Romualdo Pastor-Satorras, Claudio Castellano, Piet Van Mieghem, and Alessandro Vespignani. Epidemic processes in complex networks. *Rev. Mod. Phys.*, 87:925–979, Aug 2015.
- [PDGM00] K. Parvinen, U. Dieckmann, M. Gyllenberg, and J. A. Metz. Evolution of dispersal in metapopulations with local density dependence and demographic stochasticity, 2000.
- [PGPSV12] N. Perra, B. Gonçalves, R. Pastor-Satorras, and A. Vespignani. Activity driven modeling of time varying networks. *Nature Scientific Reports* 2, 469, 2012.
- [PSK17] E. Pardoux and B. Samegni-Kepgnou. Large deviation principle for epidemic models. *Journal of Applied Probability*, 54(3):905–920, September 2017.
- [Pul88] H. R. Pulliam. Sources, sinks and population regulation. *The American Naturalist*, 132(5):652–661, 1988.
- [QVDE17] Luyuan Qi, Elisabeta Vergu, Bhagat Dutta, and Pauline Ezanno. Modelling bovine viral diarrhoea virus spread between dairy cattle farms on a regional scale: relative contribution of two between-herd transmission pathways. In *SVEPM2017 Conference Proceedings*, March 2017.

- [RCCM14] J R. Chazottes, P Collet, and S Méléard. Sharp asymptotics for the quasi-stationary distribution of birth-and-death processes. *Probability Theory and Related Fields*, 164, 06 2014.
- [RDD11] S. Rautureau, B. Dufour, and B. Durand. Vulnerability of animal trade networks to the spread of infectious diseases: A methodological approach applied to evaluation and emergency control strategies in cattle, France, 2005. *Transboundary and Emerging Diseases*, 58(2):110–120, 2011.
- [REI⁺15] Steven Riley, Ken Eames, Valerie Isham, Denis Mollison, and Pieter Trapman. Five challenges for spatial epidemic models. *Epidemics*, 10:68 – 71, 2015.
- [Rit97] M.E. Ritchie. *Wildlife and Landscape Ecology*, chapter Populations in a Landscape Context: Sources, Sinks, and Metapopulations, pages 160–184. Springer, New York, 1997.
- [Sca85] Gianpaolo Scalia-Tomba. Asymptotic final size distribution for some chain-binomial processes. *Advances in Applied Probability*, 17:477–495, 1985.
- [Sca90] Gianpaolo Scalia-Tomba. On the asymptotic final size distribution of epidemics in heterogeneous populations. *Stochastic Processes in Epidemic Theory*, 86, 01 1990.
- [Sel83] Thomas Sellke. On the asymptotic distribution of the size of a stochastic epidemic. *Journal of Applied Probability*, 20(2):390–394, 1983.
- [TBKW09] Michael J. Tildesley, Paul R. Bessell, Matt J. Keeling, and Mark E.J. Woolhouse. The role of pre-emptive culling in the control of foot-and-mouth disease. *Proceedings of the Royal Society B: Biological Sciences*, 276(1671):3239–3248, 2009.
- [TIK18] Nagatani T., Genki I., and Tainaka K. Epidemics of random walkers in metapopulation model for complete, cycle, and star graphs. *Journal of Theoretical Biology*, 450:66–75, April 2018.
- [TL15] T. Takagushi and R. Lambiotte. Analysis of metapopulation epidemic process on arbitrary networks. *IFAC Conference Paper Archive*, 48(18):141–145, 2015.
- [Var62] R. S. Varga. *Matrix Iterative Analysis*. Prentice Hall, Englewood Cliffs, 1962.
- [VBE10] E. Vergu, H. Busson, and P. Ezanno. Impact of the infection period distribution on the epidemic spread in a metapopulation model. *PLOS ONE*, 5(2):1–16, 02 2010.
- [VD91] A. Van Doorn. Quasi-stationary distributions and convergence to quasi-stationarity of birth-death processes. *Advances in Applied Probability*, 23(4):683–700, Dec. 1991.
- [VDP13] E. A. Van Doorn and P. K. Pollett. Quasi-stationary distributions for discrete-state models. *European Journal of Operational Research*, 230:1–14, 2013.
- [Ver38] P-F Verhulst. *Correspondance mathématique et physique, No 10*, chapter Notice sur la loi que la population poursuit dans son accroissement, pages 113–121. 1838.

- [Ver11] M. C. Vernon. Demographics of cattle movements in the United Kingdom. *BMC Veterinary Research*, 7(31), 2011.
- [VH97] O. A. Van Herwaarden. Stochastic epidemics: the probability of extinction of an infectious disease at the end of a major outbreak. *Journal of Mathematical Biology*, 35:793–813, 1997.
- [VHG95] Onno A. Van Herwaarden and J. Grasman. Stochastic epidemics: major outbreaks and the duration of the endemic period. *Journal of Mathematical Biology*, 33:581–601, 1995.
- [VK09] Matthew C Vernon and Matt J Keeling. Representing the UK’s cattle herd as static and dynamic networks. *Proceedings of the Royal Society B: Biological Sciences*, 276(1656):469—476, February 2009.
- [VLM91] J. Verboom, K. Lankester, and J. A. Metz. Linking local and regional dynamics in stochastic metapopulation models. *Biological Journal of the Linnean Society*, 42(1-2):39–55, 1991.
- [VO05] E. Vares and E. Olivieri. *Large Deviations and Metastability*. Cambridge University Press, 2005.
- [Vol28] Vito Volterra. Variations and fluctuations of the number of individuals in animal species living together. *ICES Journal of Marine Science*, 3:3–51, 1928.
- [VtN00] C. C. Vos, C. J. F. ter Braak, and W. Nieuwenhuizen. Incidence function modelling and conservation of the tree frog *Hyla arborea* in the Netherlands. *Ecological Bulletins*, 48:165–180, 2000.
- [WCC⁺16] Maxwell C. Wilson, Xiao-Yong Chen, Richard T. Corlett, Raphael K. Didham, Ping Ding, Robert D. Holt, Marcel Holyoak, Guang Hu, Alice C. Hughes, Lin Jiang, William F. Laurance, Jiajia Liu, Stuart L. Pimm, Scott K. Robinson, Sabrina E. Russo, Xingfeng Si, David S. Wilcove, Jianguo Wu, and Mingjian Yu. Habitat fragmentation and biodiversity conservation: key findings and future challenges. *Landscape Ecology*, 31(2):219–227, Feb 2016.
- [WMZ10] William Webber, Alistair Moffat, and Justin Zobel. A similarity measure for indefinite rankings. *ACM Trans. Inf. Syst.*, 28:20, 11 2010.
- [WS18] Anuwat Wiratsudakul and Satoshi Sekiguchi. The implementation of cattle market closure strategies to mitigate the foot-and-mouth disease epidemics: A contact modeling approach. *Research in Veterinary Science*, 121:76 – 84, 2018.
- [WSKM03] J. W. Wilesmith, M. A. Stevenson, C. B. King, and R. S. Morris. Spatio-temporal epidemiology of foot-and-mouth disease in two counties of Great Britain in 2001. *Preventive Veterinary Medicine*, 61:157–170, 2003.
- [WV80] J. Walrand and P. Varaiya. Sojourn times and the overtaking condition in Jacksonian networks. *Advances in Applied Probability*, 12(4):1000–1018, 1980.

-
- [WW90] C. Z. Wei and J. Winnicki. Estimation of the means in the branching process with immigration. *Ann. Statist.*, 18(4):1757–1773, 12 1990.
- [WZJ10] J.-J. Wang, J.-Z. Zhang, and Z. Jin. Analysis of an SIR model with bilinear incidence rate. *Nonlinear Analysis: Real World Applications*, 11:2390–2402, 2010.
- [ZH15] Ling Zhu and Hongxiao Hu. A stochastic SIR epidemic model with density dependent birth rate. *Advances in Difference Equations*, 2015(1):330, Oct 2015.

Titre : Dynamiques de populations et processus épidémiques sur des réseaux d'échanges

Mots clés : Réseaux, métapopulations, processus épidémiques

Résumé : On s'intéresse à la modélisation mathématique de dynamiques de populations sur des réseaux d'échanges de bovins couplées avec des processus épidémiques.

On discute tout d'abord de modèles de métapopulations prenant en compte des dynamiques démographiques locales (immigration, naissances, morts et mouvements d'animaux dus aux échanges entre les nœuds du réseau). Des critères de stabilité sont établis pour des modèles markoviens dans lesquels les dynamiques locales sont déterministes et les transferts entre nœuds sont stochastiques, pour un processus de branchement multitype avec immigration et pour un processus de sauts à espace d'états finis à taux logistiques. Dans les deux derniers cas, on étudie les limites d'échelle des processus en temps fini ainsi que leur stabilité sur des échelles de temps exprimées comme fonctions exponentielles du paramètre d'échelle.

Dans une deuxième partie, on réalise un couplage des modèles de sauts considérés avec un processus épidémique SIR (Susceptible — Infecté — Rétabli), rendant compte de contacts infectieux locaux et de la propagation d'un pathogène dans le réseau au gré des mouvements d'animaux entre les nœuds. On établit une approximation du processus épidémique par un pro-

cessus de branchement multitype sur des intervalles de temps fini, puis l'on fournit une méthode de calcul approché de la probabilité d'un épisode épidémique majeur, défini comme l'événement de survie du branchement approchant. On montre ensuite que dans le cas d'un événement épidémique majeur et sous contrainte de stabilité d'un équilibre endémique pour un système déterministe associé, le temps d'extinction de l'épidémie et sa taille totale évoluent de façon au moins exponentielle par rapport au paramètre d'échelle du modèle.

On effectue enfin une application numérique des résultats théoriques obtenus sur le modèle SIR couplé avec des dynamiques de population logistiques. On calibre les paramètres démographiques de ce modèle sur le réseau d'échanges de bovins du Finistère observé sur l'année 2015, puis l'on calcule plusieurs indicateurs de la vulnérabilité du réseau induite par les différentes exploitations. Une procédure est détaillée afin de comparer l'efficacité relative de trois types de stratégies de contrôle (dépistage à l'importation, isolation et vaccination) ciblant les exploitations identifiées comme critiques vis-à-vis des indicateurs calculés.

Title: Population dynamics and epidemic processes on trade networks

Keywords: Networks, metapopulations, epidemic processes

Abstract: This thesis discusses the mathematical modeling of population dynamics on cattle trade networks coupled with epidemic processes.

We first consider metapopulation models taking into account local demographic dynamics (immigration, births, deaths and animal movements due to trade between the nodes of the network). Recurrence and ergodicity criteria are stated for Markovian models with deterministic local dynamics and stochastic inter-nodal transfers, for a multitype branching process with immigration and for a jump process with logistic rates on a finite state space. In these last two cases, we study scaling limits of processes over finite time intervals and their stability over time scales that are exponentials of the scaling parameter.

In a second part, we define a coupling of the jump population models considered with an SIR (Susceptible — Infected — Removed) epidemic dynamics. The resulting process accounts for local infectious contacts and pathogen propagation on the network due to movements of infective animals. We approximate the epidemic process by a

multitype branching process on finite time intervals, then provide an iterative method to compute the probability of a *major epidemic outbreak*, defined as the event of survival of the approximating branching process. We then show that conditionally on a major epidemic outbreak and under a stability condition for an endemic equilibrium of the associated dynamical system, the extinction time and final size of the epidemic grow at least exponentially with respect to the scaling parameter of the model.

We finally perform a numerical application of the theoretical results obtained on the SIR model coupled with logistic population dynamics. Calibrating the demographic model parameters on the 2015 Finistère cattle trade network, we compute indicators of the epidemic vulnerability of the network induced by individual holdings. We detail a protocol to assess the relative efficiency of three types of control strategies (screening at importation, isolation and vaccination) targeting the holdings identified as critical for the computed indicators.

