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**A journey through structured populations
and the numerics for their linear stability
analysis**

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*A journey through structured populations
and the numerics for their linear
stability analysis*

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*“Ma sai, ti dico che
forse ci penserò domani
davanti ad un caffè”*

“Domani”, by No Good (2025).

Abstract

The aim of this thesis is to present the main results obtained during the author's PhD studies, devoted to the development of numerical tools for the linear stability analysis of some classes of deterministic continuously structured population models [METZ, DIEKMANN, *The Dynamics of Physiologically Structured Populations*, Springer, 1986]. Structured populations associate the individuals with their i -state, i.e., the set of all those characteristics that fully determine the system's present and future dynamics, and whose evolution in time only depends on the past history (e.g., age, size, spatial position) [DIEKMANN, HEESTERBEEK, BRITTON, *Mathematical Tools for Understanding Infectious Disease Dynamics*, Princeton University Press, 2013]. For continuously structured population models, when the aim is to assess the local stability of equilibria or other invariants, one is typically led to investigate the spectrum of linear(ized) infinite-dimensional operators. This target can rarely be achieved analytically. Consequently, numerical methods are often required in practical computations.

The fundamental idea underlying the approximation schemes presented in this thesis is that of discretizing the relevant infinite-dimensional operators through matrices obtained by suitable projection techniques, based on (pseudo)spectral methods. (Pseudo)spectral methods rely on approximating functions through algebraic or trigonometric polynomials obtained via either collocation (pseudospectral method) or projection (spectral method). The main advantage of these methods is that their convergence order depends on the smoothness of the involved functions. In particular, infinite order of convergence is attained when the approximated functions are of class C^∞ , while for continuous functions with limited regularity (e.g., absolutely or Lipschitz continuous), the convergence order is typically algebraic. This allows to obtain accurate approximations with relatively low dimensions of the discretization, thus reducing the overall computational cost in view of possible bifurcation analysis. Furthermore, discontinuities in the model coefficients may be easily addressed by resorting to suitable piecewise approaches.

The first part of the thesis is devoted to the numerical computation of the reproduction numbers (e.g., basic and type reproduction number) of some population models, with particular attention to the case of models from epidemiology. Reproduction numbers are key quantities in population dynamics, as they are usually related to population persistence or extinction, while in epidemiology they are typically related to concepts such as the occurrence of an epidemic outbreak, the existence of endemic equilibria/periodic solutions, the herd immunity level and the final size. In [DIEKMANN, HEESTERBEEK, METZ, *J. Math. Biol.* 7, 1990], the authors "reduce" the computation of the reproduction numbers to the computation of the spectral radius of a Next Generation Operator (NGO) which, typically, turns out to be an infinite-dimensional operator in the case of continuously structured population models.

In this thesis we consider three different classes of models. First, we consider a large class of age-structured population models (e.g., demographic/infection/disease age-structured models) with finite age-span formulated as Integro-Partial Differential Equations (IPDEs) with nonlocal boundary conditions [INABA, *Age-Structured Population Dynamics in Demography and Epidemiology*, Springer, 2017]. For this class of models, we extend the method presented [BREDI, FLORIAN, RIPOLL, VERMIGLIO, *J. Comput. Appl. Math.* 384, 2021] to allow for complete flexibility in the computation of the reproduction numbers.

Then, we consider population models formulated as Ordinary Differential Equations (ODEs)

with time-periodic coefficients. As shown in [BACAER, GUERNAOUI, J. Math. Biol. 69, 2006] and discussed in [DIEKMANN, HEESTERBEEK, BRITTON, *Mathematical Tools for Understanding Infectious Disease Dynamics*, Princeton University Press, 2013], the time-periodicity introduces a structure in the population that is the instant of time in the time-period interval at which an individual is generated (becomes infective in the case of the basic reproduction number in infectious disease dynamics).

Lastly, we consider epidemic models with mass testing strategies, where at fixed intervals of times the infected individuals are tested and isolated if positive. The class of interest is that of SIR (Susceptible, Infectious, Removed) and SEIR (Susceptible, Exposed, Infectious, Removed) models formulated as impulsive ODEs. Here, to compute the (control) reproduction number, one must take into account the heterogeneity introduced by the mass testing events, which is the time elapsed since last testing.

The relevant operators are discretized by suitable pseudospectral collocation methods, and the reproduction numbers are approximated through the spectral radius of matrices.

The second part of the thesis is devoted to the study of numerical methods for the stability analysis of linear age-structured population models with finite age-span, formulated as IPDEs with nonlocal boundary conditions, in which the continuous age-variable is coupled with an additional structure. At first, we consider models where the additional structure is given by a spatial variable, and the spread of individuals is modeled by a nonlocal diffusion (convolution) operator [KANG, RUAN, XI, J. Dyn. Diff. Eq. 34, 2022]. Secondly, we consider models where the additional structure is another age variable [KANG, RUAN, XI, Ann. di Mat. Pura 200, 2021]. For both of these classes of models, the stability of the null equilibrium is determined by the spectrum of the infinitesimal generator associated to the solution semigroup. To approximate those spectra, we discretize the relevant generators through combinations of pseudospectral and spectral methods.

The methods are presented alongside convergence proofs and numerical results attesting the validity of the approaches. An additional novelty of this thesis is the use of interpolation error bounds in L^1 -spaces for the convergence proofs. This choice is motivated by the biological interpretation attached to the L^1 norm in the context of structured populations. This approach is not common in the literature, as the convergence of (pseudo)spectral methods typically rely on interpolation error bounds in Hilbert spaces or in spaces of continuous functions [CANUTO, HUSSANI, QUARTERONI, ZANG, *Spectral Methods in Fluid Dynamics*, Springer, 1988].

To sum up, the main novel contributions of the thesis are: the development of a general class of numerical methods for the computation of the reproduction numbers for a large variety of age-structured population models with finite age-span; the development of a new numerical method for the approximation of the basic reproduction number in compartmental models with time-periodic coefficients; the development of a numerical method for the computation of the control reproduction number in compartmental epidemic models with mass testing and isolation; the development of a numerical method to assess the linear stability analysis of age-structured population models with nonlocal (convolution diffusion) and finite age-span; and the development of numerical methods for the linear stability analysis of age-structured population models with an additional age and finite age-span. The hope is that these new approaches can help researchers in advancing the knowledge and understanding of population dynamics with an increased ability to tackle advanced and complex models for a realistic portrait of epidemics and ecology.

MATLAB implementations of the methods presented in this thesis are provided at <http://cdlab.uniud.it/software>.

Sommario

Lo scopo di questa tesi è quello di presentare i principali risultati ottenuti durante gli studi di dottorato dell'autore, dedicati allo sviluppo di metodi numerici per l'analisi di stabilità lineare di alcune classi di modelli di popolazione deterministici con struttura continua [METZ, DIEKMANN, *The Dynamics of Physiologically Structured Populations*, Springer, 1986]. Le popolazioni strutturate associano agli individui il loro i -state, ovvero l'insieme di tutte quelle caratteristiche che determinano univocamente la dinamica presente e futura del sistema e la cui evoluzione nel tempo dipende solo dalla storia passata (ad esempio, età, dimensione, posizione spaziale) [DIEKMANN, HEESTERBEEK, BRITTON, *Mathematical Tools for Understanding Infectious Disease Dynamics*, Princeton University Press, 2013]. Per i modelli di popolazione con struttura continua, quando l'obiettivo è valutare la stabilità locale degli equilibri o di altri invarianti, si è tipicamente portati a investigare lo spettro di operatori infinito-dimensionali lineari (zzati). Questo obiettivo può raramente essere raggiunto analiticamente. Di conseguenza, i metodi numerici sono spesso necessari in pratica.

L'idea fondamentale alla base degli schemi di approssimazione presentati in questa tesi è quella di discretizzare tali operatori infinito-dimensionali tramite matrici ottenute da tecniche di proiezione idonee, basate su metodi (pseudo)spettrali. I metodi (pseudo)spettrali si fondano sull'approssimazione di funzioni tramite polinomi algebrici o trigonometrici ottenuti tramite collocazione (metodo pseudospettrale) o proiezione (metodo spettrale). Il vantaggio principale di questi metodi è che il loro ordine di convergenza dipende dalla regolarità delle funzioni coinvolte. In particolare, ordine infinito di convergenza è raggiunto quando le funzioni approssimate sono di classe C^∞ , mentre per funzioni continue con regolarità limitata (ad esempio, assolutamente continue o lipschitziane), l'ordine di convergenza è tipicamente algebrico. Ciò consente di ottenere approssimazioni accurate con dimensioni relativamente basse della discretizzazione, riducendo così il costo computazionale complessivo in vista di una possibile analisi di biforcazione. Inoltre, discontinuità nei coefficienti del sistema possono essere agevolmente trattate ricorrendo ad approcci a tratti.

La prima parte della tesi è dedicata al calcolo numerico dei numeri di riproduzione (ad esempio, basic e type reproduction numbers) in alcuni modelli di popolazione, con particolare attenzione al caso dei modelli per la diffusione di malattie infettive. I numeri di riproduzione sono grandezze chiave nello studio delle dinamiche di popolazione, in quanto sono solitamente correlati alla persistenza o all'estinzione della popolazione stessa, mentre in epidemiologia sono tipicamente correlati a concetti quali il verificarsi di un'epidemia, l'esistenza di equilibri endemici/soluzioni periodiche, il livello di immunità di gregge e la final size. In [DIEKMANN, HEESTERBEEK, METZ, *J. Math. Biol.* 7, 1990], gli autori "riducono" il calcolo dei numeri di riproduzione al calcolo del raggio spettrale di un Next Generation Operator (NGO) che, tipicamente, risulta essere un operatore di dimensione infinita nel caso di modelli di popolazione con strutture continue.

In questa tesi consideriamo tre diverse classi di modelli. In primo luogo, consideriamo una vasta classe di modelli di popolazione strutturati per età (ad esempio, modelli strutturati per età demografica/d'infezione) con intervallo d'età finito e formulati come Equazioni Integro-Differenziali alle Derivate Parziali (IPDEs) con condizioni al bordo non locali [INABA, *Age-Structured Population Dynamics in Demography and Epidemiology*, Springer, 2017]. Per questa classe di modelli, estendiamo il metodo presentato [BRED, FLORIAN, RIPOLL, VERMIGLIO, *J. Comput. Appl. Math.* 384,

2021] per consentire completa flessibilità nel calcolo dei numeri di riproduzione.

In seguito, consideriamo modelli di popolazione formulati come Equazioni Differenziali Ordinarie (ODEs) con coefficienti periodici nel tempo. Come mostrato in [BACAER, GUERNAOUI, J. Math. Biol. 69, 2006] e discusso in [DIEKMANN, HEESTERBEEK, BRITTON, *Mathematical Tools for Understanding Infectious Disease Dynamics*, Princeton University Press, 2013], la periodicità introduce una struttura nella popolazione che è l'istante di tempo nel periodo in cui un individuo viene generato (diventa infettivo nel caso del numero di riproduzione di base nelle dinamiche delle malattie infettive).

Infine, consideriamo modelli epidemici con strategie di test di massa, in cui a intervalli di tempo fissati gli individui infetti vengono testati e isolati se positivi. La classe di interesse è quella dei modelli SIR (Suscettibili, Infettivi, Rimossi) and SEIR (Suscettibili, Esposti, Infettivi, Rimossi) formulati come ODEs impulsive. Qui, per calcolare il numero di riproduzione (di controllo), si deve tenere conto dell'eterogeneità introdotta dagli eventi di test di massa, che è il tempo trascorso dall'ultimo test.

L'operatore risultante viene dunque discretizzato tramite metodi di collocazione pseudospettrale adatti, e i numeri di riproduzione vengono approssimati attraverso il raggio spettrale di matrici.

La seconda parte della tesi è dedicata allo studio di metodi numerici per l'analisi di stabilità di modelli di popolazione lineari, strutturati per età, con intervallo di età finito, formulati come IPDEs con condizioni al bordo non locali, in cui la variabile continua d'età è accoppiata a una struttura aggiuntiva. In primo luogo, consideriamo modelli in cui la struttura aggiuntiva è data da una variabile spaziale e la diffusione degli individui è modellata da un operatore di diffusione (convoluzione) non locale [KANG, RUAN, XI, J. Dyn. Diff. Eq. 34, 2022]. In secondo luogo, consideriamo modelli in cui la struttura aggiuntiva è un'altra variabile d'età [KANG, RUAN, XI, Ann. di Mat. Pura 200, 2021]. Per entrambe queste classi di modelli, la stabilità dell'equilibrio nullo è determinata dallo spettro del generatore infinitesimale associato al semigruppone soluzione. Per approssimare tali spettri, discretizziamo i generatori associati attraverso combinazioni di metodi pseudospettrali e spettrali.

I metodi sono presentati insieme a dimostrazioni di convergenza e risultati numerici che attestano la validità degli approcci. Un'ulteriore novità di questa tesi è l'uso di stime per l'errore di interpolazione in spazi L^1 per le dimostrazioni di convergenza. Questa scelta è motivata dall'interpretazione biologica associata alla norma L^1 nel contesto delle popolazioni strutturate. Questo approccio non è comune in letteratura, in quanto la convergenza dei metodi (pseudo)spettrali viene tipicamente studiata usando risultati di interpolazione in spazi di Hilbert o in spazi di funzioni continue [CANUTO, HUSSANI, QUARTERONI, ZANG, *Spectral Methods in Fluid Dynamics*, Springer, 1988].

Per riassumere, i principali nuovi contributi della tesi sono: lo sviluppo di una classe generale di metodi numerici per il calcolo dei numeri di riproduzione per una grande varietà di modelli di popolazione strutturati per età con intervallo di età finito; lo sviluppo di un nuovo metodo numerico per l'approssimazione del numero di riproduzione di base nei modelli compartimentali con coefficienti periodici nel tempo; lo sviluppo di un metodo numerico per il calcolo del numero di riproduzione di controllo in una classe di modelli epidemici compartimentali con test di massa e isolamento; lo sviluppo di un metodo numerico per valutare l'analisi della stabilità lineare dei modelli di popolazione strutturati per età con non locale (diffusione di convoluzione) e intervallo di età finito; e lo sviluppo di metodi numerici per l'analisi della stabilità lineare dei modelli di popolazione strutturati per età con un'età aggiuntiva e un intervallo di età finito. La speranza è che questi nuovi approcci possano aiutare i ricercatori a far progredire la conoscenza e la comprensione delle dinamiche della popolazione con una maggiore capacità di affrontare modelli avanzati e complessi per un ritratto realistico di epidemie ed ecologia.

Implementazioni in MATLAB dei metodi presentati in questa tesi sono disponibili all'indirizzo <http://cdlab.uniud.it/software>.

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Notation

Spaces of functions

In this section, a, b denote two real numbers such that $a < b$, d, m, s denote nonnegative integers, $p, \tau \in (0, +\infty]$, $\tau < +\infty$, and X, Y are real/complex (Banach) vector spaces. In this thesis:

- $\mathcal{I}_X$ denotes the identity element of X ;
- for $X = \mathbb{R}^d$ or $X = \mathbb{C}^d$, $|\cdot|$ denotes any finite-dimensional norm on X ;
- for a Banach space Y and $\mathcal{A}: X \rightarrow Y$ linear, $\|\mathcal{A}\|_{Y \leftarrow X}$ denotes the operator norm;
- $C([a, b], X)$ denotes the space of continuous functions on $[a, b]$ taking values in X ;
- $AC([a, b], X)$ denotes the space of absolutely continuous functions on $[a, b]$ taking values in X ;
- $\text{Lip}^s([a, b], X)$ denotes the space of Lipschitz continuous functions on $[a, b]$ taking values in X , with s -th Lipschitz continuous derivative, with $\text{Lip}^0([a, b], X)$ the space of Lipschitz continuous functions;
- $L^p([a, b], X)$ denotes the space of L^p -integrable functions on $[a, b]$ taking values in X ;
- $C_\tau(\mathbb{R}, X) := \{\phi: \mathbb{R} \rightarrow X \mid \phi(t) = \phi(t + \tau) \text{ for all } t \in \mathbb{R} \text{ and } \phi \in C([0, \tau], X)\}$;
- $AC_\tau(\mathbb{R}, X) := \{\phi: \mathbb{R} \rightarrow X \mid \phi(t) = \phi(t + \tau) \text{ for all } t \in \mathbb{R} \text{ and } \phi \in AC([0, \tau], X)\}$;
- $\text{Lip}_\tau^s(\mathbb{R}, X) := \{\phi: \mathbb{R} \rightarrow X \mid \phi(t) = \phi(t + \tau) \text{ for all } t \in \mathbb{R} \text{ and } \phi \in \text{Lip}^s([0, \tau], X)\}$;
- $L_\tau^p(\mathbb{R}, X) := \{\phi: \mathbb{R} \rightarrow X \mid \phi(t) = \phi(t + \tau) \text{ for a.a } t \in \mathbb{R} \text{ and } \phi \in L^p([0, \tau], X)\}$.

Unless otherwise indicated:

- $C([a, b], X)$ is equipped with the supremum norm, denoted by $\|\cdot\|_\infty$;
- $L^p([a, b], X)$ is equipped with the standard L^p -norm.

Symbols

- For a Banach space X and $\mathcal{A}: D(\mathcal{A}) \subset X \rightarrow X$ linear:

- $\sigma(\mathcal{A})$ denotes the spectrum of $\mathcal{A}$, i.e.,

$$\sigma(\mathcal{A}) := \mathbb{C} \setminus \left\{ \lambda \in \mathbb{C} \mid (\lambda \mathcal{I}_X - \mathcal{A})^{-1}: X \rightarrow D(\mathcal{A}) \text{ exists and is bounded} \right\};$$

- $\sigma_p(\mathcal{A})$ denotes the point spectrum of $\mathcal{A}$, i.e.,¹

$$\sigma_p(\mathcal{A}) := \{\lambda \in \mathbb{C} \mid \lambda \mathcal{I}_X - \mathcal{A}: D(\mathcal{A}) \rightarrow X \text{ is not injective}\};$$

- $\rho(\mathcal{A})$ denotes the spectral radius of $\mathcal{A}$, i.e.,

$$\rho(\mathcal{A}) := \sup_{\lambda \in \sigma(\mathcal{A})} |\lambda|;$$

¹The elements of $\sigma_p(\mathcal{A})$ are called eigenvalues of $\mathcal{A}$. Note that $\sigma_p(\mathcal{A}) \subseteq \sigma(\mathcal{A})$.

- $s(\mathcal{A})$ denotes the spectral bound of $\mathcal{A}$, i.e.,

$$s(\mathcal{A}) := \sup_{\lambda \in \sigma(\mathcal{A})} \Re(\lambda),$$

- for $\Omega \subset \mathbb{C}^d$, χ_Ω denotes the characteristic (or indicator) function of Ω , i.e.,

$$\chi_\Omega(x) := \begin{cases} 1, & \text{if } x \in \Omega, \\ 0, & \text{otherwise.} \end{cases}$$

Matrix and vector notation

- We use the MATLAB-like notation according to which elements of a column vector are separated by “;” while elements of a row vector are separated by “,”;
- for $A_1, \dots, A_N \in \mathbb{C}^{d \times d}$, d, N positive integers, we use the MATLAB-like notation

$$\text{blkdiag}(A_1, \dots, A_N) = \begin{pmatrix} A_1 & 0 & \dots & 0 \\ 0 & A_2 & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & A_N \end{pmatrix} \in \mathbb{C}^{dN \times dN};$$

- for $A \in \mathbb{C}^{d \times d}$ and $B \in \mathbb{C}^{N \times N}$, d, N positive integers, $A \otimes B$ denotes the Kronecker product

$$A \otimes B = \begin{pmatrix} a_{1,1}B & \dots & a_{1,d}B \\ \vdots & \ddots & \vdots \\ a_{d,1}B & \dots & a_{d,d}B \end{pmatrix} \in \mathbb{C}^{dN \times dN}.$$

Abbreviations

- DDE - Delay Differential Equation
- DFE - Disease-Free Equilibrium
- IDDE - Integro-Delay Differential Equation
- IPDE - Integro-Partial Differential Equation
- IBVP - Initial-Boundary Value Problem
- NGO - Next Generation Operator
- ODE - Ordinary Differential Equation
- PBVP - Periodic Boundary Value Problem
- PDE - Partial Differential Equation
- PMS - Principal Matrix Solution
- RE - Renewal Equation

Introduction

I.1 Structured populations in mathematical modeling

Mathematical modeling plays a fundamental role in understanding population and infectious diseases dynamics. Euler, Bernoulli, Ross, Lotka, Kermack, McKendrick, Volterra..., these are just a few examples of visionary scientists who recognized the potentiality of mathematical approaches in the study of biological and epidemiological phenomena, giving fundamental contributions to the development of mathematical biology, see [10] for an historical overview. In particular, the work of McKendrick [109] is fundamental, as it contains a key observation that ended up being the cornerstone of the philosophy of structured populations: in a given population, individuals are not all equals. Indeed, they can be distinguished by characteristics that affect, e.g., birth, death and interactions with the environment [57]. Consequently, to obtain more accurate portraits of the dynamics of a given population or infectious disease, many mathematical models account for individuals heterogeneity introducing variable, called “structures”.

The basic concept in structured populations is that of i-state, i.e., the set of all those individual characteristics that fully determine the systems present and future dynamics, and whose evolution in time only depends on the past history. Think for example at the demographic age, which in fact affects the vital rates of the individuals (younger individuals may not be fertile, but they may have longer life expectancy if compared to older individuals), and whose future values depend only on the current value (if the age is $a \geq 0$ at time $t_1 = 0$, the age at time $t_2 > 0$ is given by $a + t_2$). Then, given this state representation of the individuals, the population is thought as a frequency distribution over the set of all possible states [110].

When considering epidemic models, more attention must be paid in the definition of the i-state, as one has to deal with both population dynamics and infection transmission [57]. Indeed, one must distinguish, among all the variables in the i-state, those describing the development of the infection within an individual (e.g., the infection age, that is the time elapsed since infection), to which we refer as the d-state. The complement of the d-state is called the h-state, and collects all the variables describing heterogeneities in the population, e.g., age, sex, spatial position, stage development of an infection. In particular, the h-state may contain both discrete and continuous variables.

Eventually, note that often models describing population or infectious disease dynamics are formulated in terms of ODEs. Yet, this is not possible in general for models involving continuous structuring variables, which instead are often formulated either as (I)DDEs, REs or (I)PDEs [110], although the reduction to ODEs models is possible under certain assumptions [56, 79].

I.2 Age-structured population models

Age-structured models are an important class of structured population models, as they have applications in many fields such as demography, ecology, epidemiology, and genetics [88, 135]. In this context, individuals are structured by an age, i.e., the time elapsed since a certain (fixed) initial moment, whose interpretation may vary depending on the context.

In this thesis, we will dedicate much attention to this class of models and to their applications to epidemiology. Hence, to help the reader in going through the details of the content of the following chapters, in this section we present some well-known examples of age-structured population models, and we introduce notions that will be useful throughout the manuscript. For the content of this section, we refer to [22, 57, 81, 82, 88].

I.2.1 The Lotka-McKendrick age-structured population model

Here we refer to [81, 88]. The Lotka-McKendrick population model (also known as the stable population model, or the Lotka-McKendrick-von Foerster model) describes the dynamics of an aging population in an isolated and invariant habitat, where individuals are structured only by their demographic age (i.e., we assume there are no other heterogeneities relevant to the dynamic among the individuals), and evolve in time only according to birth and mortality processes. The model takes the form of an IBVP for a PDE that was introduced by McKendrick in [109]. In this section, we present the derivation of such a model, alongside some important results on its asymptotic behavior. Note that, in age-structured population models the maximum age of individuals may be either finite or infinite. Here, we assume that it is finite, as in the following chapters we will always work under this assumption. We refer to [88, Chapter I] for the case with infinite maximum age.

Derivation of the model

Let us denote by $a^+ \in (0, +\infty)$ the maximal age of individuals in the population, and let us denote by $P(t, a)$ the age-density of the population at time $t \geq 0$ and age $a \in [0, a^+]$, i.e., for $0 \leq a_1 < a_2 < a^+$, the integral

$$\int_{a_1}^{a_2} P(t, a) da, \quad t \geq 0, \quad (I.2.1)$$

gives the total number of individuals with age in the interval $[a_1, a_2]$ at time $t \geq 0$. Note that (I.2.1) must be nonnegative and finite for all $a_1, a_2 \in [0, a^+]$. Hence, we assume that $P(t, \cdot) \in L^1([0, a^+], \mathbb{R})$ and is nonnegative for any $t \geq 0$.

Let $B(t)$ denote the total birth rate of the population at time $t \geq 0$, which gives the total number of newborns per unit of time, and let $\mu(a)$ denote the age-specific death rate of the population, which gives the death rate of people with age in $[a, a + da]$. We assume that $\mu \in L^1_{loc}([0, a^+], \mathbb{R})$ is nonnegative and satisfies

$$\int_0^{a^+} \mu(a) da = +\infty, \quad (I.2.2)$$

so that the survival probability function²

$$\Pi(a) := e^{-\int_0^a \mu(\xi) d\xi}, \quad a \in [0, a^+], \quad (I.2.3)$$

satisfies $\Pi(a^+) = 0$. Under the assumptions made at the beginning of this section, it is easy to see that the cumulative age-distribution

$$F(t, a) := \int_0^a P(t, \xi) d\xi, \quad t \geq 0, \quad a \in [0, a^+],$$

satisfies the balance equation

$$F(t + h, a + h) = F(t, a) + \int_t^{t+h} B(\xi) d\xi - \int_0^h \int_0^a \mu(\xi) P(t + \xi, \xi + \zeta) d\xi d\zeta, \quad (I.2.4)$$

for $t \geq 0$, $a \in [0, a^+]$ and $h \in [a, a^+]$. Supposing that F is sufficiently smooth, we differentiate (I.2.4) with respect to h , and by setting $h = 0$ we get

$$P(t, a) + \int_0^a \partial_t P(t, \xi) d\xi = B(t) - \int_0^a \mu(\xi) P(t, \xi) d\xi. \quad (I.2.5)$$

Note that $P(t, 0) = B(t)$, for $t \geq 0$. Hence, differentiating (I.2.5) with respect to a , we get

$$\begin{cases} \mathcal{D}P(t, a) = -\mu(a)P(t, a), & t \geq 0, \quad a \in (0, a^+), \\ P(t, 0) = B(t). & t \geq 0, \end{cases}$$

²That is, the probability of still being alive at age $a \in [0, a^+]$.

where

$$\mathcal{D}P(t, a) := \partial_t P(t, a) + \partial_a P(t, a). \quad (\text{I.2.6})$$

Finally, by assuming that

$$B(t) := \int_0^{a^+} f(a)P(t, a) \, da, \quad t \geq 0,$$

for $f(a)$ the age-specific per-capita fertility rate of the population, we get

$$\begin{cases} \mathcal{D}P(t, a) = -\mu(a)p(t, a), & t \geq 0, \quad a \in (0, a^+), \\ P(t, 0) = \int_0^{a^+} f(a)P(t, a) \, da, & t \geq 0. \end{cases} \quad (\text{I.2.7})$$

This is the famous Lotka-McKendrick model, which represents a generalization of the Malthus model to the case of age-dependent dynamics [81, 88].

Solution of the model and asymptotic behavior

In order to solve (I.2.7), we need to specify the initial age-density of the population, i.e., $P(0, \cdot) = \phi$, where $\phi \in L^1([0, a^+], \mathbb{R})$ is nonnegative and non identically zero. Then, integrating (I.2.7) along the characteristic lines, we obtain³

$$P(t, a) = \begin{cases} \phi(a-t) \frac{\Pi(a)}{\Pi(a-t)}, & a > t, \\ B(t-a; \phi) \Pi(a), & a < t, \end{cases} \quad (\text{I.2.8})$$

where $B(t; \phi) \geq 0$ is the unique solution of the RE

$$B(t) = B_0(t; \phi) + \int_0^t f(a) \Pi(a) B(t-a) \, da, \quad (\text{I.2.9})$$

for

$$B_0(t; \phi) := \int_0^{a^+} f(a+t) \frac{\Pi(a+t)}{\Pi(a)} \phi(a) \, da, \quad t \geq 0.$$

The following result holds [81, Theorem 5.2].

Theorem I.2.1 (Fundamental theorem of demography). *Let $\phi \in L^1([0, a^+], \mathbb{R})$ be nonnegative and non identically zero. Let $B(t; \phi)$, for $t \geq 0$, denote the unique solution of (I.2.9), and let r_0 denote the unique real solution of the Euler-Lotka equation*

$$1 = \int_0^{a^+} f(a) \Pi(a) e^{-\lambda a} \, da, \quad \lambda \in \mathbb{C}. \quad (\text{I.2.10})$$

Then there exists $b_0 > 0$ and a continuous function $g(t)$ such that

$$B(t; \phi) = b_0 e^{r_0 t} (1 + g(t)), \quad t \geq 0.$$

and $g(t) \rightarrow 0$ as $t \rightarrow +\infty$.

The previous theorem states that the solution $B(t; \phi)$ of (I.2.9) asymptotically behaves as an exponential function, with exponential rate given by the *Malthusian parameter* (or growth bound) r_0 . Now, we introduce the persistent age-profile

$$w_0(a) := \frac{e^{-r_0 a} \Pi(a)}{\int_0^{a^+} e^{-r_0 \xi} \Pi(\xi) \, d\xi}, \quad a \in [0, a^+]. \quad (\text{I.2.11})$$

Then, the following important result follows from Theorem I.2.1 [83, Section 2].

³We would like to emphasize that the Lotka-McKendrick model can be solved by just using the biological interpretation. In fact, if $a > t$, then the individuals who are alive at time $t \geq 0$ and age $a \in [0, a^+]$ are exactly those who were alive at age $a-t$ and survived up to age a . On the other hand, if $a < t$, then the individuals who are alive at age $a \in [0, a^+]$ and time $t \geq 0$ are exactly those who were born at age $t-a$ and survived up to age a .

Corollary I.2.2. Let $\phi \in L^1([0, a^+], \mathbb{R})$ be nonnegative and non identically zero. Let $P(t, a)$, for $t \geq 0$ and $a \in [0, a^+]$, denote the unique solution of (I.2.8), and let r_0 denote the unique real solution of (I.2.10). Then there exists $P_0 > 0$ and a function $\eta(t, a)$ such that

$$P(t, a) = P_0 e^{r_0(t-a)} \Pi(a) (1 + \eta(t, a)), \quad t \geq 0,$$

where $\eta(t, a) \rightarrow 0$ uniformly in a as $t \rightarrow +\infty$. Moreover, it holds

$$\lim_{t \rightarrow +\infty} \frac{P(t, a)}{\int_0^{a^+} P(t, \xi) d\xi} = w_0(a), \quad a \in [0, a^+],$$

where w_0 is defined as in (I.2.11).

Theorem I.2.2 implies that all the solutions of (I.2.8) asymptotically behave as exponential functions in time, no matter what the initial age-density is. This phenomenon is called *asynchronous exponential growth*, and is often observed in reproducing populations in the absence of effects due to crowding or limited resources [133].

Remark I.2.3. The persistent age-profile w_0 in (I.2.11) is also known as the stable age-distribution.

We conclude this section with an important observation: the sign of r_0 is uniquely determined by the threshold parameter

$$R_0 := \int_0^{a^+} f(a) \Pi(a) da. \quad (\text{I.2.12})$$

This quantity is the *basic reproduction number* of the population, i.e., the average number of newborns produced by an individual during its entire life [73]. In fact, the following relation hold

$$\text{sign}(R_0 - 1) = \text{sign}(r_0). \quad (\text{I.2.13})$$

This relation was first discovered by Lotka, and then discussed by him and Dublin in their famous paper [64]. To be fair, Dublin and Lotka did not use the term basic reproduction number, nor they used the symbol R_0 , which was introduced much later. Instead, they referred to this quantity as the *net reproductive ratio*, and used the letter R to denote it [73].

I.2.2 Demographic age-structured epidemic models

The demographic age of individuals plays a fundamental role in trying to understand the dynamics of many infectious diseases. One may think for example at sexually transmitted diseases, for which the transmission mechanism generally involves only individuals that are mature enough, or at childhood diseases, in which the age-dependent contact pattern plays a fundamental role in the transmission processes. Not only, also the design of efficient vaccination programs needs to take into consideration the age structure, as some individuals may be more or less susceptible to the disease, or some of them may contribute more than others to the spread of the infection. We refer to [2, 4, 66, 78, 79, 137] and to the monographs [5, 98] for some important examples.

In this thesis, we will often focus on the applications to demographic age-structured epidemic models. To do so, we will consider different assumptions and notions, which are common in the literature.

Hence, to make the reader be familiar with the details of the models presented in the following chapters, in this section we introduce a first example of demographic age-structured epidemic model, and we discuss notions and techniques that will be useful throughout the manuscript. For the content of this section, we refer to [22, 57, 81, 82], and in particular to [88, Chapter 6].

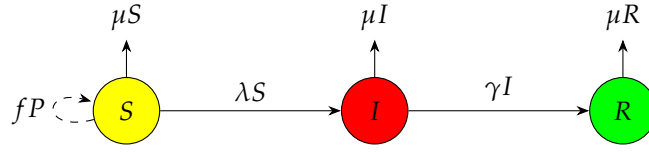


Figure I.2.1: Flow chart for the demographic age-structured SIR model in (I.2.14). The solid lines describe the horizontal dynamics, while the dashed lines describe the vertical dynamics.

A demographic age-structured SIR model

We consider the spread of an infectious disease in a population structured by demographic age. It is assumed that, upon infection, susceptible individuals immediately become infectious (there is no latent period), and once recovered, the disease-conferred immunity is permanent. We denote by $S(t, \cdot), I(t, \cdot), R(t, \cdot) \in L^1([0, a^+], \mathbb{R})$ denote the age-density of individuals who are susceptible, infectious, and removed, respectively, at time $t \geq 0$, where $a^+ < \infty$. We neglect the role of vertical transmission⁴, so that the dynamic is described by the following system of IPDEs with nonlocal boundary conditions (see also Figure I.2.1) The model reads as follows:

$$\begin{cases} \mathcal{D}S(t, a) = -(\lambda(t, a) + \mu(a))S(t, a), \\ \mathcal{D}I(t, a) = \lambda(t, a)S(t, a) - (\gamma(a) + \mu(a))I(t, a), \\ \mathcal{D}R(t, a) = \gamma(a)I(t, a) - \mu(a)R(t, a), \\ S(t, 0) = \int_0^{a^+} f(a)P(t, a) da, \\ I(t, 0) = R(t, 0), \end{cases} \quad (\text{I.2.14})$$

for $t \geq 0$ and $a \in [0, a^+]$, where $\mathcal{D}$ is defined as in (I.2.6),⁵

$$\lambda(t, a) := \int_0^{a^+} k(a, \alpha) \frac{I(t, \alpha)}{\int_0^{a^+} P(t, \xi) d\xi} d\alpha, \quad t \geq 0, \quad a \in [0, a^+],$$

is the force of infection, $k(a, \alpha)$ is the transmission rate between infectious individuals at age α and susceptible individuals at age a , $k \in L^\infty([0, a^+]^2, \mathbb{R})$, $P := S + I + R$ is the age-density of the host population, $\mu \in L^1_{loc}([0, a^+], \mathbb{R})$ is the age-specific mortality rate, $\gamma \in L^\infty([0, a^+], \mathbb{R})$ is the age-specific recovery rate and $f \in L^\infty([0, a^+], \mathbb{R})$ is the per capita birth rate.

Note that the age-density of the host population, P , satisfies the Lotka-McKendrick equation (I.2.7). Hence, its dynamics can be independently determined from the epidemic. In particular, Theorem I.2.2 ensures that P will ultimately behave as an exponential function in time, and its age-profile will tend to the stable age-distribution w_0 in (I.2.11). Consequently, in the literature it is common to assume that the age-profile of P has already reached the stable age-distribution (see for example [43, 83]), so that it can be expressed as

$$P(t, a) = P_0 e^{r_0 t} w_0(a), \quad a \in [0, a^+],$$

for some $P_0 > 0$, where r_0 is the Malthusian parameter introduced in (I.2.1). Moreover, if we assume that the host population is at demographic equilibrium, i.e.,

$$1 = \int_0^{a^+} f(a) \Pi(a) da, \quad (\text{I.2.15})$$

⁴Vertical transmission is the transmission process that occurs from an infective parent to offspring [42].

⁵In this example we are assuming the *true mass action*.

we have

$$P(t, a) = P^*(a) := P_0 w_0(a), \quad a \in [0, a^+]. \quad (\text{I.2.16})$$

Then, one can consider the new variables

$$s(t, a) := \frac{S(t, a)}{P^*(a)}, \quad i(t, a) := \frac{I(t, a)}{P^*(a)}, \quad r(t, a) := \frac{R(t, a)}{P^*(a)}, \quad (\text{I.2.17})$$

and investigate the dynamics of the relevant system

$$\begin{cases} \mathcal{D}s(t, a) = -\lambda(t, a)s(t, a), \\ \mathcal{D}i(t, a) = \lambda(t, a)s(t, a) - \gamma(a)i(t, a), \\ \mathcal{D}r(t, a) = \gamma(a)i(t, a), \\ s(t, 0) = 1, \\ i(t, 0) = r(t, 0) = 0, \end{cases} \quad (\text{I.2.18})$$

for $t \geq 0$ and $a \in [0, a^+]$, where now λ can be expressed as

$$\lambda(t, a) := \int_0^{a^+} k(a, \alpha) w_0(\alpha) i(t, \alpha) d\alpha, \quad t \geq 0, \quad a \in [0, a^+].$$

Note that, under assumption (I.2.15), the two models are equivalent from the point of view of the asymptotic stability, see [88, Chapter 6].

Remark I.2.4. In this thesis we will often work under assumption (I.2.15) for simplicity. Nevertheless, we mention that the method that we will present can be applied also in the general case $r_0 \neq 0$.

Remark I.2.5. In this thesis, we will refer to (I.2.16) as the stationary age-density.

I.3 Reproduction numbers

Here we refer to [54]. Reproduction numbers are threshold parameters that play a fundamental role in mathematical biology, as they determine population persistence or disease invasibility [104, 124]. We already encountered one of these quantities, the *basic reproduction number*, in Section I.2.1. As a matter of fact, reproduction numbers were first (formally) introduced in the context of demography and ecology.⁶ Yet, their notoriety notably increased due to their fundamental role in epidemiology, as they can be related to concepts such as the herd immunity level, the final size, and the endemic equilibrium (or periodic solution) [5, 57].

The most known and used example of reproduction number in epidemiology is the already mentioned R_0 , which in this context describes the average number of secondary cases produced by a typical infected individual during its entire infectious period, in a completely susceptible population [58]. In (I.2.13), we already observed an important property about R_0 : for deterministic models, $R_0 = 1$ is a threshold that determines the stability of the DFE, i.e., it is stable when $R_0 < 1$ and unstable when $R_0 > 1$.

Moreover, in simple models R_0 characterizes the herd immunity threshold (the proportion of population that needs to be immunized to prevent the spread of the disease) via the expression $1 - 1/R_0$.

Variations of R_0 when the population is partially immune or in the presence of control measures are also known as *effective* and *control* reproduction numbers [112].

⁶Although a similar concept had already appeared in Ross' famous work on Malaria [10].

For more complicated models (e.g., with heterogeneity), looking at R_0 alone may not be satisfactory for epidemic control [117]. For instance, if it is possible to apply control measures only to a certain group of individuals (e.g., mosquitoes rather than humans in vector-borne infections) or against certain transmission routes (e.g., vertical rather than horizontal transmission), then a simple and explicit relation between R_0 and the herd immunity level may no longer exist. In this case, the *type reproduction number*, usually denoted by T , may be a more appropriate measure [117]. Indeed, it describes the expected number of secondary cases in individuals of a certain type produced by one infected individual of the same type, either directly or through chains of infection passing through any sequence of the other types [76]. Consequently, T can be directly linked to the amount of control measures to be applied to one specific group of individuals to stop the spread.

In [90], the authors propose an extension of the type reproduction number, the *state reproduction number*, which allows for focus any epidemic state (e.g., asymptomatic and symptomatic phase) [88, Section 5.2]. Finally, [104, 124] consider a further generalization of these quantities, the *target reproduction number*, which focuses on specific interactions between types, rather than on all interactions that involve a given type of individuals. We remark that although different reproduction numbers have different biological interpretations, they typically share the same threshold for epidemic extinction with R_0 [104, 128].

I.3.1 The next generation operator method

The content of this section is taken from [57, Section 7]. We already discussed the considerable importance of reproduction numbers in mathematical epidemiology. But a question is left open: how do we define these quantities? The answer was given in [58].⁷ To be fair, here we shall restrict to R_0 , as that paper originally deals with this quantity. Yet, the same reasoning may be applied to the other reproduction numbers, as we will intensively discuss throughout the thesis. In the meanwhile, we refer the reader to [50, 76, 86, 88, 90, 117, 124].

The basic idea of [58] is simple, but at the same time incredibly clever: an infection processes may be interpreted as a *birth* in the demographic sense. Consequently, one may think about successive infections in terms of *generations*. This observation is fundamental, as in this way R_0 can be related to the demographic interpretation of Dublin and Lotka [64], recall (I.2.12).

With this in mind, we suppose to be looking at the infection processes from its beginning, in a situation where all individuals are susceptibles. Let $\Omega \subset \mathbb{R}^n$, for n a positive integer, denote the h-state set, which we suppose being measurable. We denote by $k(\xi, \eta)$ the expected number of new individuals with state at birth $\xi \in \Omega$ generated by an individual with state at birth $\eta \in \Omega$, during its entire period of fertility. Then we introduce the Next Generation Operator (NGO)

$$(\mathcal{K}\psi)(\xi) = \int_{\Omega} k(\xi, \eta)\psi(\eta) \, d\eta, \quad \xi \in \Omega, \quad (\text{I.3.1})$$

where $\psi \in L^1(\Omega, \mathbb{R}^d)$ for some $d \geq 1$.⁸ The interpretation of $\mathcal{K}$ is clear: if ψ denotes the current generation of infected individuals, described by means of a density over the h-state space, then $\mathcal{K}\psi$ denotes the successive generation of individuals. Hence, the m -th generation is given by $\mathcal{K}^m\psi$, and the per-generation growth factor is given by $\|\mathcal{K}^m\|^{1/m}$. Thus looking at the behavior in the long run, i.e., for $m \rightarrow \infty$, one gets⁹

$$\rho(\mathcal{K}) = \lim_{m \rightarrow \infty} \|\mathcal{K}^m\|^{1/m}, \quad (\text{I.3.2})$$

⁷I ask the reader to apologize myself, as I cannot help expressing my admiration for this incredible work by Diekmann, Heesterbeek and Metz, which, up to date, is my favorite paper. I am always astonished and fascinated by the elegance by which the authors relate a so important biological problem to a very abstract and general framework. I read this paper for the first time in 2020, while I was writing my Master Thesis “Bivariate collocation methods for computing the basic reproduction number of population dynamics with double structure”. Yet, its reading always helps me in having new good insights.

⁸If Ω is a discrete set, the integral is interpreted as a sum [58].

⁹We refer to [84, 89] for an extensive discussion on the biological interpretation of the NGO and the characterization of R_0 as its spectral radius.

where $\rho(\mathcal{K})$ denotes the spectral radius of $\mathcal{K}$. In this sense, by interpreting (I.3.2) as the long term average per generation multiplication number [57], one obtains the characterization

$$R_0 = \rho(\mathcal{K}). \quad (\text{I.3.3})$$

Hence, the computation of R_0 is “reduced” to the computation of the spectral radius of an (infinite-dimensional in general) operator. But now, another question is left open: how do we derive $\mathcal{K}$? The answer is: it depends. Often, one can derive the kernel k in (I.3.1) by means of the useful relation

$$k(\xi, \eta) = \int_0^\infty \mathfrak{A}(a, \xi, \eta) da, \quad \xi \in \Omega,$$

where $\mathfrak{A}(a, \xi, \eta)$ denotes the rate at which an individual that was generated a time ago, with state-at-infection η , produces secondary cases with state-at-birth ξ [57]. See for example Chapter 3. Of course, somehow this requires some modeling skills. Nevertheless, under certain conditions, the computation of R_0 extremely simplifies.

The next generation matrix

To have a better understanding of the NGO method, here we consider deterministic compartmental models in a constant environment, i.e., mathematical models formulated as ODEs, describing the dynamics of an infectious disease, where individuals are divided into *compartments* depending on the stage of infection, and where the coefficients of the systems do not vary in time. For this class of models, we aim at introducing a simple method to compute R_0 (and also other reproduction numbers). We do this by recalling that, in Section I.3.1 we look at the spread of an epidemic from its beginning, when all individuals are susceptible, and we try to capture informations on the long-run behavior of the dynamics. From the point of view of dynamical systems, this corresponds to looking at the linearized stability of the model, where the linearization is performed around the DFE. This reduces the (possibly) nonlinear model to a linear model of the form

$$u'(t) = Au(t), \quad t \geq 0,$$

where $u(t) \in \mathbb{R}^d$ for every $t \geq 0$ and $A \in \mathbb{R}^{d \times d}$ for some positive integer d . We suppose that A can be splitted according to $A = B - M$, where $B \in \mathbb{R}^{d \times d}$ is a nonnegative matrix containing all the entries relevant to the *birth* processes (new infections in the case of R_0 in epidemiology), and $-M \in \mathbb{R}^{d \times d}$ describes the *transition* processes (which include, for instance, changes in the epidemiological state, death, or acquisition of immunity). We assume that, in the absence of the processes described by B , the processes in $-M$ can not sustain the growth of the population (infection) by themselves, but they will lead the population (infectious disease) to die out. Formally, we require that $-M$ is positive off-diagonal, with $s(-M) < 0$. This guarantees that M^{-1} is positive, so that $(M^{-1})_{ij}$, for $i, j = 1, \dots, d$, gives the expected time that an individual will spend in the state i if having currently state j . Alternatively, one can interpret the exponential matrix e^{-Mt} as the probability of having survived the transition processes at time $t \geq 0$ if infected at time 0 [18]. Then, the nonnegative matrix

$$K = BM^{-1} \in \mathbb{R}^{d \times d}$$

is called the next generation matrix (NGM) and, one can show that, the NGO in (I.3.1) reduces to K , being the h-state space is finite-dimensional. Hence, we reduced the computation of R_0 to the computation of the spectral radius of a matrix. Moreover, the following equality holds [59, Theorem A.1]

$$\text{sign}(\rho(K) - 1) = \text{sign}(s(A)). \quad (\text{I.3.4})$$

Note that (I.3.10) is the same relation that we found in (I.2.13). This tells us that, from the point of view of the linear stability analysis, R_0 and the spectral bound of A are equally informative on the stability properties of the DFE. We refer to [50, 58, 59, 63] for further details.

Extension to infinite-dimensional systems

The idea of the next generation matrix presented in the previous section can be extended to the case of models described by functional evolution equations, i.e., models in which the state space has infinite dimension [88, 89, 128]. The aim is to look again at the spread of an epidemic from its beginning, assuming a whole susceptible population. However, in this context the linearization of the model around the DFE is described by an abstract differential equation, and the birth/infection and transition processes are described by operators acting on infinite-dimensional spaces.

To better understand the framework underlying this method, here we first briefly recall some basic facts on linear abstract differential equations and Cauchy problems, making reference to [67, Chapter II]. Let $(X, \|\cdot\|_X)$ be an infinite-dimensional real/complex Banach space and $\mathcal{A}: D(\mathcal{A}) \subset X \rightarrow X$ be a linear operator. A problem of the form

$$x'(t) = \mathcal{A}x(t), \quad t \geq 0, \quad (\text{I.3.5})$$

for $x(t) \in D(\mathcal{A}), t \geq 0$, is called an abstract differential equation, and a problem of the form

$$\begin{cases} x'(t) = \mathcal{A}x(t), & t \geq 0, \\ x(0) = x_0 \in D(\mathcal{A}) \end{cases} \quad (\text{I.3.6})$$

is called an abstract Cauchy problem. If $D(\mathcal{A}) = X$ and $\mathcal{A}$ is bounded, then (I.3.6) admits a unique solution for every $x_0 \in X$, which is explicitly given by $x(t) = T(t)x_0, t \geq 0$, where [67, Section I.3, Proposition 3.5]

$$T(t) := e^{t\mathcal{A}} = \sum_{k=0}^{+\infty} \frac{(t\mathcal{A})^k}{k!}, \quad t \geq 0.$$

In particular, the family $\{T(t)\}_{t \geq 0}$ is a strongly continuous semigroup of bounded linear operators, i.e., it satisfies [67, Section I.5, p.36]:

- (i) $T(t)$ is linear and there exist $\omega \in \mathbb{R}$ and $C \geq 1$ such that $\|T(t)\|_{X \leftarrow X} \leq Ce^{\omega t}$ for all $t \geq 0$,
- (ii) $T(0) = \mathcal{I}_X$,
- (iii) $T(t)T(s) = T(t+s)$ for every $t, s \geq 0$,
- (iv) for all $\phi \in X, T(t)\phi$ is a continuous function of $t \geq 0$.

Definition I.3.1. If $\{T(t)\}_{t \geq 0}$ is a strongly continuous semigroup of bounded linear operators, its growth bound is defined as

$$\omega(T) := \inf\{\tilde{\omega} \in \mathbb{R} \mid \text{there exists } C \geq 1 \text{ such that } \|T(t)\|_{X \leftarrow X} \leq Ce^{\tilde{\omega}t} \text{ for all } t \geq 0\}.$$

Note that if $\mathcal{A}$ is unbounded, $e^{t\mathcal{A}}$ is not well-defined. Nevertheless, one can still derive conditions for the existence and uniqueness of the solutions of (I.3.6) by using for instance the celebrated Hille-Yosida theorem [67, Section II.3, Theorem 3.8].

Theorem I.3.2 (Hille-Yosida). Let $\omega \in \mathbb{R}$ and $C \geq 1$. The following properties are equivalent:

- (i) $\mathcal{A}$ is closed, $D(\mathcal{A})$ is dense in X , and for all $\lambda \in \mathbb{C}$ with $\Re(\lambda) > \omega$ one has $\lambda \notin \sigma(\mathcal{A})$ and

$$\|(\lambda\mathcal{I}_X - \mathcal{A})^{-N}\|_{X \leftarrow X} \leq \frac{C}{(\Re(\lambda) - \omega)^N}, \quad \text{for all } N \in \mathbb{N},$$

- (ii) $\mathcal{A}$ is the infinitesimal generator of a strongly continuous semigroup of bounded linear operators $\{T(t)\}_{t \geq 0}$ satisfying

$$\|T(t)\|_{X \leftarrow X} \leq Ce^{\omega t}, \quad t \geq 0,$$

i.e.,

$$\mathcal{A}\phi := \lim_{t \rightarrow 0^+} \frac{T(t)\phi - \phi}{t}, \quad \phi \in D(\mathcal{A}), \quad (\text{I.3.7})$$

where $D(\mathcal{A}) := \{\phi \in X \mid \text{the limit (I.3.7) exists}\}$.

Note that if $x_0 \in D(\mathcal{A})$, then $x(t) := T(t)x_0$ is a differentiable function of time for every $t \geq 0$. Hence, $x(t)$ is called a *strong* solution of (I.3.6). On the other hand, if $x_0 \in X \setminus D(\mathcal{A})$, then $x(t) = T(t)x_0$ is only continuous for every $t \geq 0$ (it may be differentiable for some $t > 0$). In this case $x(t)$ is called a *mild* solution of (I.3.6).

Remark I.3.3. Let us note that the asymptotic stability of the null-equilibrium of (I.3.5) is determined by the growth bound $\omega(T)$. Then, it is natural to ask whether, as in the finite-dimensional case, $s(\mathcal{A})$ has some relation with $\omega(T)$. Unfortunately, in general one only has that $s(\mathcal{A}) \leq \omega(T)$ holds [67, p. 251, 2.2 Proposition]. Nevertheless, for the models that we consider in this thesis, the equality $s(\mathcal{A}) = \omega(T)$ holds. See for instance [30, 128], [67, Chapter III], [88, Chapter 1 and Chapter 6] and the following example (other examples are discussed later on in the thesis).

Example I.3.4. For the Lotka-McKendrick model (I.2.7) we have that the family of linear operators

$$T(t) : L^1([0, a^+], \mathbb{R}) \rightarrow L^1([0, a^+], \mathbb{R}), \quad t \geq 0, \quad (\text{I.3.8})$$

defined as

$$(T(t)\phi)(a) = \begin{cases} \phi(a-t) \frac{\Pi(a)}{\Pi(a-t)}, & a > t, \\ B(t-a; \phi) \Pi(a), & a < t \end{cases}$$

where $B(t; \phi)$ is the unique solution of the renewal equation (I.2.9), is a C_0 -semigroup of bounded positive linear operators on $L^1([0, a^+], \mathbb{R})$, with infinitesimal generator

$$\mathcal{A}\phi := -\phi'(a) - \mu(a)\phi(a), \quad \phi \in D(\mathcal{A}),$$

where

$$D(\mathcal{A}) := \left\{ \phi \in AC([0, a^+], \mathbb{R}) \mid \phi(0) = \int_0^{a^+} f(a)\phi(a) da, \text{ and } \mu\phi \in L^1([0, a^+], \mathbb{R}) \right\}.$$

Moreover, $T(t)$ is compact for every $t \geq a^+$, i.e., $\{T(t)\}_{t \geq 0}$ is an eventually compact semigroup [88, p. 23, Corollary 1.1]. This implies that $\sigma(\mathcal{A}) = \sigma_p(\mathcal{A})$, i.e., the spectrum of $\mathcal{A}$ consists of eigenvalues only, which are at most countable, and are either isolated or accumulate at $-\infty$ [67, p. 330, Corollary 3.2]. In particular, $s(\mathcal{A}) = \omega(T)$ [67, p. 281, Corollary 3.12].

Now, we are ready to extend the idea of the next generation matrix to infinite-dimensional systems. In particular, here we refer to [16, 18, 128]. Let us suppose that the linearization of a model around the DFE can be recast as in (I.3.5), where X is an ordered Banach space of real functions with a positive cone $X_+ := \{\phi \in X \mid \phi \geq 0_X\}$, and $\mathcal{A} : D(\mathcal{A}) \subset X \rightarrow X$ satisfies the hypotheses of the Hille-Yosida theorem. As we are dealing with population/epidemic models, it is assumed that $\mathcal{A}$ generates a semigroup $\{S(t)\}_{t \geq 0}$ of positive operators on X , i.e., if $u_0 \in X_+$, then $S(t)u_0 \in X_+$ for all $t \geq 0$.

We suppose that $\mathcal{A}$ can be split according to $\mathcal{A} = \mathcal{B} - \mathcal{M}$, where $\mathcal{B} : X \rightarrow X$ accounts for the *birth* processes (new infections in the case of R_0 in epidemiology), and $-\mathcal{M} : D(\mathcal{M}) := D(\mathcal{A}) \rightarrow X$ accounts for the *transition* processes. We assume that $\mathcal{B}$ is positive, and that $-\mathcal{M}$ is the generator of a strongly continuous semigroup of bounded positive linear operators on X , $\{T(t)\}_{t \geq 0}$. As for the case of finite-dimensional systems, we suppose that in the absence of “birth”, the processes in $\mathcal{M}$ can only lead the population (infectious disease) to die out. Thus, we suppose that

$$\omega(T) = s(-\mathcal{M}) < 0,$$

where $\omega(T)$ is the growth bound of $\{T(t)\}_{t \geq 0}$. As a result, $\mathcal{M}^{-1}$ exists bounded and positive, and standard results in semigroup theory ensures that [67, Theorem 1.10]

$$\mathcal{M}^{-1} = \int_0^\infty T(t) dt. \quad (\text{I.3.9})$$

Note that, similarly to the finite-dimensional case, in (I.3.9) $T(t)$ is interpreted as the probability of having survived the transition processes at time $t \geq 0$. Then, the NGO is formally derived as the positive operator

$$\mathcal{K} := \mathcal{B}\mathcal{M}^{-1}.$$

The following equality follows by combining [67, p. 356, Corollary 1.11] with [128, Theorem 3.5 and Theorem 3.12]

$$\text{sign}(\rho(\mathcal{K}) - 1) = \text{sign}(s(\mathcal{A})). \quad (\text{I.3.10})$$

Example I.3.5. For the SIR model (I.2.18), the linearized equation for the infected individuals around the DFE $(s^*, i^*, r^*) = (1, 0, 0)$ reads

$$\begin{cases} \mathcal{D}i(t, a) = \int_0^{a^\dagger} k(a, \alpha) w_0(\alpha) i(t, \alpha) d\alpha - \gamma(a) i(t, a), \\ i(t, 0) = 0. \end{cases} \quad (\text{I.3.11})$$

Let us define birth and transition operators $\mathcal{B}: X \rightarrow X$ and $\mathcal{M}: D(\mathcal{M}) \subset X \rightarrow X$ respectively as

$$\mathcal{B}\phi(a) := \int_0^{a^\dagger} k(a, \alpha) w_0(\alpha) \phi(\alpha) d\alpha, \quad a \in [0, a^\dagger],$$

and

$$\mathcal{M}\phi(a) := \phi'(a) + \gamma(a)\phi(a), \quad a \in [0, a^\dagger],$$

where

$$D(\mathcal{M}) := \{\phi \in AC([0, a^\dagger], \mathbb{R}) \mid \phi(0) = 0\}.$$

Then, (I.2.14) can be recast as in (I.3.5) by taking $\mathcal{A} := \mathcal{B} - \mathcal{M}$ [67, Chapter III, 88, Chapter 1 and Chapter 6]. In particular, thanks to what observed in Example I.3.4, we can apply the above method for the derivation of the NGO. Note in fact that, for every $\psi \in X$, we have

$$\mathcal{M}^{-1}\psi(a) = \int_0^a \frac{\Gamma(a)}{\Gamma(\eta)} \psi(\eta) d\eta, \quad a \in [0, a^\dagger],$$

where

$$\Gamma(a) := e^{-\int_0^a \gamma(z) dz}, \quad a \in [0, a^\dagger] \quad (\text{I.3.12})$$

is the probability of still being infectious at age $a \in [0, a^\dagger]$. Then, the NGO is explicitly given by

$$\mathcal{B}\mathcal{M}^{-1}\psi(a) = \int_0^{a^\dagger} k(a, \alpha) w_0(\alpha) \int_0^\alpha \frac{\Gamma(\alpha)}{\Gamma(\eta)} \psi(\eta) d\eta d\alpha, \quad a \in [0, a^\dagger]. \quad (\text{I.3.13})$$

Note that the NGO is positive and compact (see Theorem 3.1.3). Hence, if $R_0 > 0$, then the Krein–Rutmann theorem ensures that R_0 is an eigenvalue of $\mathcal{B}\mathcal{M}^{-1}$ with associated a nonnegative eigenfunction [99]. Thus R_0 can be computed as the dominant eigenvalue of an infinite-dimensional operator, which is a task that can not be analytically achieved in general. Hence, numerical methods are often needed. Yet, if one considers the (simplifying) separable mixing assumption, i.e., β is the product of a function of only α with a function of only a , then an explicit expression may be derived [88, Chapter 6].

Let us remark that, in this section, we assumed that $\mathcal{A}$ is the infinitesimal generator of a strongly continuous semigroup of bounded positive linear operators on the Banach space X , and we assumed that $\mathcal{B}$ is a bounded operator with range contained in X . However, there may be cases in which the above framework cannot be applied. For instance, this is the case of the demographic

age-structured SIR model with vertical transmission [83, 88, Chapter 6]

$$\begin{cases} \mathcal{D}S(t, a) = -(\lambda(t, a) + \mu(a))S(t, a), \\ \mathcal{D}I(t, a) = \lambda(t, a)S(t, a) - (\gamma(a) + \mu(a))I(t, a), \\ \mathcal{D}R(t, a) = \gamma(a)I(t, a) - \mu(a)R(t, a), \\ S(t, 0) = \int_0^{a^+} (1 - q)f(a)P(t, a) da, \\ I(t, 0) = \int_0^{a^+} qf(a)P(t, a) da, \\ R(t, 0) = 0, \end{cases}$$

for $t \geq 0$ and $a \in [0, a^+]$, where $\lambda, \mathcal{D}, \mu, \gamma, f, k$ and P are defined as in Section I.2.2, and $q \in [0, 1]$ is the proportion of vertically infected newborns.

Again, we assume that the host population is at demographic equilibrium, see (I.2.15), and that P has already reached the stationary density (I.2.16). Thus, by considering the variables s, i, r defined as in (I.2.17) and linearizing the equation for infected individuals around the DFE $(s^*, i^*, r^*) = (1, 0, 0)$ we obtain

$$\begin{cases} \mathcal{D}i(t, a) = \int_0^{a^+} k(a, \xi)w_0(\xi)i(t, \xi) d\xi - \gamma(a)i(t, a), \\ i(t, 0) = q \int_0^{a^+} f(a)\Pi(a)i(t, a) da, \end{cases}$$

where w_0 is defined as in (I.2.11) and Π is defined as in (I.2.3). Note that, in this case the term in the boundary condition describes an infection process, which then shall be included in the “birth” operator for computing R_0 . However, the operator $\hat{\mathcal{B}}: X \rightarrow Y \simeq \mathbb{R}$ accounting for the processes in the boundary condition is formally defined as [18]

$$(\hat{\mathcal{B}}\phi)(a) = q\delta_0(a) \int_0^{a^+} f(\alpha)\Pi(\alpha)\phi(\alpha) d\alpha,$$

where δ_0 is the Dirac delta concentrated in zero. Thus, in this case we cannot apply the framework described in this section to compute R_0 . Nevertheless, an alternative approach is to work in the extended space of the density function and its boundary value $\mathbb{R} \times L^1([0, a^+], \mathbb{R})$, and to develop the relevant theory in this context by using the theory of nondensely defined Cauchy problems [107, 127] and the concept of resolvent positive operator [128]. We mention that the numerical method presented in Chapter 2 is actually built on the extended space framework, for which we refer the reader to [88, Chapter 6, Chapter 10.1.2] and [83, 86, 127, 128] for the details.

I.4 Aims, contents and organization of the thesis

The aim of this thesis is to assess the linear stability of some population models with continuous structuring variables. We consider different types of models and, for each of them, we develop numerical methods to approximate the spectra of suitable operators that determine either persistence or extinction of a given population/infectious disease.¹⁰ In the first part of this work, we consider the numerical computation of reproduction numbers for different classes of models for which the relevant (next generation) operator turns out to be infinite-dimensional. In the second part, we develop numerical methods for the linear stability analysis of linear age-structured population/epidemic models in which the age-variable is coupled with an additional structuring variable. Alongside the numerical methods, convergence proofs and/or numerical results attesting

¹⁰For the methods developed in this thesis, we assume that the eigenvalues of matrices can be exactly computed.

the validity of the approaches are presented, and applications in the context of infectious disease dynamics are discussed.

The thesis is organized as follows. In Chapter 1, we collect some results on approximation theory, which are used in the following chapters. In Chapter 2, we propose a general numerical method to approximate the reproduction numbers of a large class of age-structured population models with finite age-span. In Chapter 3, we develop an efficient and general numerical method to approximate reproduction numbers in time-periodic compartmental models formulated as ODEs. In Chapter 4, we derive a characterization for the control reproduction number in compartmental models of SIR and SEIR type with mass testing strategies formulated as impulsive ODEs, and we develop a numerical method for its computation. Chapter 5 contains a numerical method to assess the linear stability analysis of age-structured population models with nonlocal diffusion of convolution type. In Chapter 6, a numerical method for the linear stability analysis of age-structured population models with an additional age is proposed. Finally, in Chapter 7 we present some conclusions and we discuss some possible future developments.

A brief summary of the content of each chapter is given below.

- Chapter 1: we summarize some results on approximation theory, which may help the reader in going through the details of the manuscript.
- Chapter 2: we develop a general numerical method to approximate the reproduction numbers of a large class of age-structured population models with finite age-span formulated as IPDEs with nonlocal boundary conditions. With respect to previous works on the topic [25, 29, 31, 72, 102], we take one step forward allowing for complete flexibility in the definition of the birth/infection and transition processes by reformulating the problem on a space of absolutely continuous functions, via an integral mapping. This permits us to see processes described by boundary conditions as perturbations of an operator with trivial domain condition, and it allows us to work with polynomial interpolation. Then, we identify birth(/infection) and transition operators, and we discretize the resulting operators via pseudospectral collocation [25, 29, 31, 72, 102]. The convergence of the method is proved using the well-established spectral approximation theory of [45]. We prove that the convergence order of the approximating reproduction number depends on the regularity of the model coefficients. Numerical results and applications to infectious disease dynamics are discussed.
- Chapter 3: we develop an efficient and general numerical method to approximate R_0 in time-periodic compartmental models formulated as ODEs. In this context, the infected individuals are explicitly structured by the instant in the time period interval at which they become infected. As a result, the NGO becomes an infinite-dimensional operator acting on a space of periodic functions [57, Section 7.9]. The numerical method takes advantage of the characterization of the NGO via its connection with the theory of evolution semigroups [48, 89, 128], which allows us to identify two operators acting on a space of periodic functions, accounting for birth and transition, respectively. The relevant operators are discretized by using pseudospectral collocation methods based on either trigonometric or algebraic polynomial approximation. The two approaches require different convergence proofs. For the former, the convergence is investigated using the spectral approximation theory of [45]. As for the latter, the convergence is proved by adapting the results of [31]. For both methods, we prove that the convergence order of the approximating reproduction number depends on the regularity of the model coefficients, and we present numerical tests confirming the theoretical results. Finally, we discuss how the method can be adapted to compute also the type reproduction number.
- Chapter 4: we consider compartmental models of SIR and SEIR type with mass testing strategies and isolation, which are formulated as impulsive ODEs [105, 120]. For these, we derive a characterization of the control reproduction numbers starting from the general definition in (I.3.1). The NGO turns out to be an infinite-dimensional operator, as newly

infected individuals are structured by the time since last testing at the moment of infection. Hence, we present a method to approximate R_c based on the pseudospectral discretization of the NGO. We rigorously investigate the convergence of the method using the spectral approximation theory of [45] and we prove that the convergence order of the approximating reproduction number depends on the regularity of the model coefficients. Finally, we present numerical results showing that $R_c = 1$ is a threshold for the stability of the DFE.

- Chapter 5: we consider age-structured population models with finite age-span and nonlocal (convolution) diffusion formulated as IPDEs with nonlocal boundary conditions. For these models, the asymptotic stability of the null equilibrium is determined by the spectrum of the infinitesimal generator associated with the semigroup [65, 94, 95, 96]. We propose a numerical method to approximate the leading part of this spectrum. To conveniently deal with the boundary condition in the domain of the generator, we first reformulate the problem via integration of the age-state, and then we discretize the generator combining a spectral projection in space with a pseudospectral collocation in age. A rigorous convergence analysis proving spectral accuracy is provided in the case of separable model coefficients. Results are confirmed experimentally and numerical tests are presented also for the more general instance. The content of this chapter extend previous works on age-structured models with no or Laplace diffusion [7, 23, 28, 30, 35, 37].
- Chapter 6: we consider age-structured population models with an additional age and finite life span (for both the ages), formulated as IPDEs with nonlocal boundary conditions. As in the case of models with nonlocal diffusion (see Chapter 5), for these models, the asymptotic stability of the null equilibrium is determined by the spectrum of the infinitesimal generator associated with the semigroup [91, 134]. We propose a numerical method to approximate the leading part of this spectrum. To conveniently deal with the boundary conditions in the domain of the generator, we first reformulate the problem in a space of absolutely continuous functions, via integration of the state in both the structuring variables. This allows us to work with polynomial interpolation. Hence, we discretize the generator via bivariate pseudospectral collocation. Although a rigorous convergence analysis is still lacking, numerical results attest the validity of the approach.
- Chapter 7: We present some conclusions and discuss future developments.

All the numerical tests presented in this thesis are performed with MATLAB R2020b on a machine with Intel Core i3-1005G1 CPU and 8 Gb of RAM, running Windows 10.

MATLAB implementations for the methods presented in this thesis are available at <http://cdlab.uniud.it/software>.

I.5 Publications, preprints and papers in preparation

The content of this thesis are mostly based on the following works (some of them are currently under revision or in preparation).

- A. Andò, S. De Reggi, D. Liessi, and F. Scarabel. “A pseudospectral method for investigating the stability of linear population models with two physiological structures.” In: *Math. Biosci. Eng.* 20.3 (2023), pp. 4493–4515. DOI: [10.3934/mbe.2023208](https://doi.org/10.3934/mbe.2023208).
- D. Breda, S. De Reggi, and J. Ripoll. *On the numerical computation of R_0 in periodic environments*. In preparation.
- D. Breda, S. De Reggi, and R. Vermiglio. “A numerical method for the stability analysis of linear age-structured models with nonlocal diffusion.” In: *SIAM J. Sci. Comput.* 46.2 (2024), A953–A973. DOI: [10.1137/23M1568971](https://doi.org/10.1137/23M1568971).

- S. De Reggi, F. Scarabel, and R. Vermiglio. “Approximating reproduction numbers: a general numerical method for age-structured models.” In: *Math. Biosci. Eng.* 21.4 (2024), pp. 5360–5393. DOI: [10.3934/mbe.2024236](https://doi.org/10.3934/mbe.2024236).
- S. De Reggi, F. Scarabel, and R. Vermiglio. *On the convergence of the pseudospectral approximation of reproduction numbers for age-structured models*. 2024. Submitted. eprint: [2409.01520](https://arxiv.org/abs/2409.01520) (math.NA).
- M. Sabbatino, S. De Reggi, and A. Pugliese. “A Theoretical Analysis of Mass Testing Strategies to Control Epidemics.” In: *Bull. Math. Biol.* 87.2 (2025), p. 22. DOI: [10.1007/s11538-024-01387-w](https://doi.org/10.1007/s11538-024-01387-w).

1

Theoretical results in approximation theory

(Pseudo)spectral methods rely on discretizing infinite-dimensional problems by either algebraic or trigonometric polynomial collocation or projection [21, 130]. Thus, it is clear that polynomial approximation plays a fundamental role in these techniques. Hence, in this chapter we review some (non)standard results in approximation theory, with particular attention to Lagrange polynomial interpolation.

In the following, N, n and d will always denote a positive integer. For the following results, we refer to [52, 108, 116].

1.1 Algebraic polynomial approximation

In this section we recall some results on algebraic polynomial approximation. Although here we present all the results for the case $[a, b] = [-1, 1]$, these can be extended to generic intervals by suitable mappings.

Definition 1.1.1. Let $\alpha_0, \dots, \alpha_N \in \mathbb{C}^d$. An algebraic polynomial of degree at most N on $[-1, 1]$ is a function of the form

$$p_N(x) := \sum_{i=0}^N \alpha_i x^i, \quad x \in [-1, 1].$$

1.1.1 Best polynomial approximation for continuous functions

Theorem 1.1.2. [52, Corollary 7.4.2 and Theorem 7.5.6] Let $f \in C([-1, 1], \mathbb{C}^d)$. Then there exists a unique algebraic polynomial of degree at most N , p_N^* , such that, for every algebraic polynomial of degree at most N , p_N , it holds

$$\|f - p_N^*\|_\infty \leq \|f - p_N\|_\infty,$$

where $\|\cdot\|_\infty$ is the supremum norm in $C([-1, 1], \mathbb{C}^d)$.

Definition 1.1.3 (Best approximation error). Let $f \in C([-1, 1], \mathbb{C}^d)$. The polynomial p_N^* in Theorem 1.1.2 is the best approximation of f on $[-1, 1]$ as a polynomial of degree at most N , and the best approximation error $\mathcal{E}_N(f)$ is defined as

$$\mathcal{E}_N(f) := \|f - p_N^*\|_\infty. \quad (1.1.1)$$

For $a, b \in \mathbb{R}$ with $a < b$, let us define the modulus of continuity of a function $f: [a, b] \rightarrow \mathbb{R}$ as

$$\omega(\delta; f) := \sup_{\substack{x_1, x_2 \in [a, b] \\ |x_1 - x_2| \leq \delta}} |f(x_1) - f(x_2)|.$$

Theorem 1.1.4 (Jackson). [116, Theorem 1.4] Let $f \in C([-1, 1], \mathbb{C}^d)$. Then

$$\mathcal{E}_N(f) \leq 6\omega\left(\frac{1}{N}; f\right). \quad (1.1.2)$$

Remark 1.1.5. Note that in (1.1.2), the error depends on the length of the interval $[-1, 1]$ through $\omega(1/N; f)$. For a general bounded interval $[a, b]$, with $a < b$, the term on the right-hand side of (1.1.6) becomes [116, Corollary 1.4.1]

$$\omega\left(\frac{b-a}{2N}; f\right).$$

Theorem 1.1.6. [116, Theorem 1.5] Let $f \in \text{Lip}^k([-1, 1], \mathbb{C}^d)$, and let $N > k$. Then

$$\mathcal{E}_N(f) \leq C \frac{L(f^{(k)})}{(N-k)N^k},$$

where $C := (6^{k+1}e^k)(1+k)^{-1}$ and $L(f^{(k)})$ denotes the Lipschitz constant of $f^{(k)}$.

Theorem 1.1.7. [8, Theorem 1.12] Let $f: [-1, 1] \rightarrow \mathbb{C}^d$ be analytic. Then there exists $p > 1$ and $C > 0$ such that

$$\mathcal{E}_N(f) \leq Cp^{-N}.$$

1.1.2 Interpolation and Lagrange representation

In this section, $x_0, \dots, x_N$ will denote a mesh of $N+1$ distinct points in $[-1, 1]$, and $f_0, \dots, f_N \in \mathbb{C}^d$.

Definition 1.1.8. An algebraic polynomial p_N of degree at most N interpolates $f_0, \dots, f_N$ at $x_0, \dots, x_N$ if

$$p_N(x_i) = f_i, \quad i = 0, \dots, N.$$

The unique polynomial p_N of degree at most N interpolating $f_0, \dots, f_N$ at $x_0, \dots, x_N$ [116, Chapter 4] can be expressed in its Lagrange form [20]

$$p_N(x) = \sum_{i=0}^N \ell_i(x) f_i, \quad x \in [-1, 1],$$

where $\{\ell_i\}_{i=0}^N$ is the Lagrange algebraic polynomial basis defined as

$$\ell_i(x) := \prod_{\substack{j=0 \\ j \neq i}}^N \frac{x - x_j}{x_i - x_j}, \quad x \in [-1, 1], \quad i = 0, \dots, N. \quad (1.1.3)$$

Note that the Lagrange polynomials in (1.1.3) satisfy the cardinal property

$$\ell_j(x_i) = \begin{cases} 1 & \text{if } i = j, \\ 0 & \text{otherwise,} \end{cases} \quad i, j = 0, \dots, N, \quad (1.1.4)$$

Definition 1.1.9. The Lebesgue constant relevant to the nodes $x_0, \dots, x_N$ in $[-1, 1]$ is

$$\Lambda_N := \max_{x \in [-1, 1]} \sum_{i=0}^N |\ell_i(x)|.$$

Theorem 1.1.10. [116, Theorem 4.1] Let $f \in C([-1, 1], \mathbb{C}^d)$ and let $\mathcal{L}_N f$ denote the unique algebraic polynomial interpolating f at $x_0, \dots, x_N$. Then

$$\|f - \mathcal{L}_N f\|_\infty \leq (1 + \Lambda_N) \mathcal{E}_N(f).$$

1.1.3 Orthogonal polynomials, Jacobi zeros and Chebyshev nodes

For the content of this section, we refer to [108].

Definition 1.1.11 (Orthogonal polynomials). Let $w: (-1, 1) \rightarrow \mathbb{R}$ be a positive function, and let $\{p_M\}_{M=0}^\infty$ be a sequence of algebraic polynomials. $\{p_M\}_{M=0}^\infty$ is a family of orthogonal polynomials with respect to w if

$$\int_{-1}^1 p_M(x) p_K(x) dx = 0, \quad \text{for all } M \neq K.$$

Definition 1.1.12 (Jacobi weights). Let $\alpha, \beta \in (-1, +\infty)$. A weight-function of the form $w^{(\alpha, \beta)}(x) = (1-x)^\alpha (1+x)^\beta$, $x \in (-1, 1)$, is called a Jacobi weight.

Definition 1.1.13 (Jacobi polynomials). Let $w^{(\alpha, \beta)}$ be a Jacobi weight and let $\{p_M^{(\alpha, \beta)}\}_{M=0}^\infty$ be the family of orthogonal polynomials with respect to $w^{(\alpha, \beta)}$. Then, $\{p_M^{(\alpha, \beta)}\}_{M=0}^\infty$ is called a family of Jacobi polynomials.

The Chebyshev polynomials of the first kind are the family of orthogonal polynomials relevant to the Jacobi weight $w^{(-\frac{1}{2}, -\frac{1}{2})}$, and they explicitly read

$$T_N(x) := \cos(N \arccos(x)), \quad x \in [-1, 1], \quad N \in \mathbb{N}.$$

For N a positive integer, the zeros of T_N are called the N Chebyshev zeros of the first kind, and are explicitly given by

$$x_{I,N,i} = \cos\left(\frac{(2(N-i)-1)\pi}{2N}\right), \quad i = 0, \dots, N-1.$$

The Chebyshev polynomials of the second kind are the family of orthogonal polynomials relevant to the Jacobi weight $w^{(\frac{1}{2}, \frac{1}{2})}$, and they explicitly read

$$U_N(x) := \frac{\sin((N+1) \arccos(x))}{\sin(\arccos(x))}, \quad x \in [-1, 1], \quad N \in \mathbb{N}.$$

For N a positive integer, the zeros of U_N are called the N Chebyshev zeros of the second kind, and are explicitly given by

$$x_{II,N,i} = \cos\left(\frac{(N-i)\pi}{N+1}\right), \quad i = 0, \dots, N-1.$$

The N Chebyshev extremal points are the extrema of T_{N-1} , and are obtained by adding the endpoints -1 and 1 to the $N-2$ Chebyshev zeros of the second kind, i.e., they are given by

$$x_{ext,N,i} = \cos\left(\frac{(N-i-1)\pi}{N-1}\right), \quad i = 0, \dots, N-1.$$

1.1.4 Nonstandard results on algebraic Lagrange interpolation

Theorem 1.1.14. [114, Theorem 1] Let $f \in BV([-1, 1], \mathbb{C}^d)$, $\mathcal{L}_{N-1}f$ denote the polynomial interpolating f at the roots of the N -th orthogonal polynomial associated with the Jacobi weight $w^{(\alpha, \beta)}$, $a, b \in (-1, +\infty)$, and $p \in [1, +\infty)$. Then there exists a positive constant C depending only on α, β, a, b and p such that

$$\|(f - \mathcal{L}_{N-1}f)w^{(a,b)}\|_{L^p([-1,1], \mathbb{C}^d)} \leq C \cdot V(f) \cdot \left(N^{d(p,a,\alpha)} D(p, a, \alpha, N) + N^{d(p,b,\beta)} D(p, b, \beta, N) \right),$$

where $V(f)$ denotes the total variation of f , $d(p, a, \alpha) := \max\left(\alpha - \frac{1}{2} - \frac{2a+2}{p}, -\frac{2a+2}{p}, -\frac{1}{p}\right)$, and

$$D(p, a, \alpha, N) := \begin{cases} (\log N)^2, & \text{if } p = 1, \alpha = \frac{1}{2}, a = -\frac{1}{2}, \\ \log N, & \text{if } (p = 1, \alpha \neq \frac{1}{2}, a \geq -\frac{1}{2}, \alpha \leq 2a + \frac{3}{2}), \text{ or} \\ & \text{if } (p = 1, \alpha = \frac{1}{2}, a \neq -\frac{1}{2}), \text{ or} \\ & \text{if } (p > 1, \alpha = \frac{1}{2}, a \leq -\frac{1}{2}), \\ 1, & \text{otherwise.} \end{cases}$$

Then we have the following corollary.

Corollary 1.1.15. *Let $f \in BV([-1, 1], \mathbb{C}^d)$ and let $\mathcal{L}_{N-1}f$ denote the polynomial interpolating f at the N Chebyshev zeros of the first kind in $[-1, 1]$. Then there exists a positive constant C independent of f and N such that*

$$\|f - \mathcal{L}_{N-1}f\|_{L^1([-1, 1], \mathbb{C}^d)} \leq C \cdot V(f) \cdot \frac{\log N}{N}.$$

The following results concern the mean convergence of derivatives of Lagrange interpolants. As they hold for general w and it is not necessary to specify α, β , we omit to write them.

Theorem 1.1.16. *[125, Theorem 1] Let r be a nonnegative integer. Let $f^{(r)} \in C([-1, 1], \mathbb{C}^d)$ and let $\mathcal{L}_{N-1}f$ denote the polynomial interpolating f at the roots of the N -th orthogonal polynomial associated with the Jacobi weight w . Then there exists a positive constant C depending only on p and r such that*

$$\begin{aligned} \int_{-1}^1 |f^{(r)}(x) - \mathcal{L}_{N-1}f^{(r)}(x)|^p (1-x^2)^{rp/2} w(x) dx \\ \leq C \left(N^{rp} \int_{-1}^1 |f(x) - \mathcal{L}_{N-1}f(x)|^p w(x) dx + E_{N-r-1}(f^r)^p \right). \end{aligned}$$

Corollary 1.1.17. *[125, Corollary 1] Let r be a nonnegative integer. Let $f^{(r)} \in C([-1, 1], \mathbb{C}^d)$ and let $\mathcal{L}_{N-1}f$ denote the polynomial interpolating f at the roots of the N -th orthogonal polynomial associated with the Jacobi weight w . If w satisfies*

$$w(x)^{\frac{1}{p}-\frac{1}{2}} (1-x^2)^{-\frac{1}{4}} \in L^p([-1, 1], \mathbb{C}),$$

Then there exists a positive constant C depending only on p and r such that

$$\int_{-1}^1 |f^{(r)}(x) - \mathcal{L}_{N-1}f^{(r)}(x)|^p (1-x^2)^{rp/2} w(x) dx \leq C E_{N-r-1}(f^r)^p.$$

1.2 Trigonometric polynomial approximation

In this section we recall some results on trigonometric polynomial approximation. Although here we present all the results for the case $[a, b] = [0, 2\pi]$, these can be extended to generic intervals by suitable mappings.

Definition 1.2.1. *Let $a_0, \dots, a_n, b_1, \dots, b_n \in \mathbb{C}^d$. A trigonometric polynomial of degree at most n on $[0, 2\pi]$ is a periodic function of the form*

$$p_n(x) = a_0 + \sum_{h=1}^n a_h \cos(hx) + \sum_{h=1}^n b_h \sin(hx), \quad x \in \mathbb{R}.$$

1.2.1 Best polynomial approximation for continuous functions

Theorem 1.2.2. [52, Corollary 7.4.8, 116, Exercise I.8] Let $f \in C_{2\pi}(\mathbb{R}, \mathbb{C}^d)$. Then there exists a unique trigonometric polynomial of degree at most n , p_n^* , such that, for every trigonometric polynomial of degree at most n , p_n , it holds

$$\|f - p_n^*\|_\infty \leq \|f - p_n\|_\infty,$$

where $\|\cdot\|_\infty$ is the supremum norm in $C_{2\pi}(\mathbb{R}, \mathbb{C}^d)$.

Definition 1.2.3 (Best approximation error). Let $f \in C_{2\pi}(\mathbb{R}, \mathbb{C}^d)$. The polynomial p_n^* in Theorem 1.2.2 is the best approximation of f on $[0, 2\pi]$ as a trigonometric polynomial of degree at most n , and the best approximation error $\mathcal{E}_n(f)$ is defined as

$$\mathcal{E}_n(f) := \|f - p_n^*\|_\infty. \quad (1.2.1)$$

Theorem 1.2.4. [116, Theorem 1.3] Let $f \in C_{2\pi}(\mathbb{R}, \mathbb{C}^d)$. Then

$$\mathcal{E}_n(f) \leq 6\omega\left(\frac{1}{n}; f|_{[0, 2\pi]}\right). \quad (1.2.2)$$

Remark 1.2.5. Note that in (1.2.2), the error depends on the length of the period interval $[0, 2\pi]$ through $\omega(1/n; f)$. For a general bounded interval $[a, b]$, with $a < b$, the term on the right-hand side of (1.2.2) becomes

$$\omega\left(\frac{b-a}{2\pi n}; f|_{[a, b]}\right).$$

Theorem 1.2.6. [138, Theorem 4.2] Let $f \in \text{Lip}_{2\pi}^k(\mathbb{R}, \mathbb{C}^d)$, and let $n > k$. Then

$$\mathcal{E}_n(f) \leq C \frac{L(f^{(k)})}{2(n-k)n^k}, \quad (1.2.3)$$

where $C := (6^{1+k}e^{1+k})(1+k)^{-1}$ and $L(f^{(k)})$ denotes the Lipschitz constant of $f^{(k)}$.

Theorem 1.2.7. [8, Theorem 1.11] Let $f: \mathbb{R} \rightarrow \mathbb{C}^d$ be 2π -periodic and analytic. Then there exists $p > 1$ and $C > 0$ such that

$$\mathcal{E}_n(f) \leq Cp^{-n}. \quad (1.2.4)$$

1.2.2 Interpolation and Lagrange representation

In this section, $x_0, \dots, x_N$ will denote a mesh of $N+1$ distinct points in $[0, 2\pi]$, and $f_0, \dots, f_N \in \mathbb{C}^d$, for $N = 2n$.

Definition 1.2.8. A trigonometric polynomial p_n of degree at most n interpolates $f_0, \dots, f_N$ at the nodes $x_0, \dots, x_N$ if

$$p_n(x_i) = f_i, \quad i = 0, \dots, N.$$

The unique polynomial p_n of degree at most n interpolating $f_0, \dots, f_N$ at $x_0, \dots, x_N$ [138, Section 3] can be expressed in its Lagrange form [15, 108, p. 42, eq. 1.3.10]

$$p_n(x) = \sum_{i=0}^N \ell_i(x) f_i, \quad x \in \mathbb{R},$$

where $\{\ell_i\}_{i=0}^N$ is the Lagrange trigonometric polynomial basis defined as

$$\ell_i(x) := \prod_{\substack{j=0 \\ j \neq i}}^N \frac{\sin\left(\frac{x-x_j}{2}\right)}{\sin\left(\frac{x_i-x_j}{2}\right)}, \quad x \in \mathbb{R}, \quad i = 0, \dots, N. \quad (1.2.5)$$

Note that the Lagrange polynomials in (1.2.5) satisfy the cardinal property

$$\ell_j(x_i) = \begin{cases} 1 & \text{if } i = j, \\ 0 & \text{otherwise,} \end{cases} \quad i, j = 0, \dots, N, \quad (1.2.6)$$

The Lebesgue constant relevant to the nodes $x_0, \dots, x_N$ is

$$\Lambda_N := \max_{x \in [0, 2\pi]} \sum_{i=0}^N |\ell_i(x)|.$$

Theorem 1.2.9. [108, Theorem 3.2.4] Let $f \in C_{2\pi}(\mathbb{R}, \mathbb{C}^d)$ and let $\mathcal{L}_N f$ denote the unique polynomial interpolating f at $x_0, \dots, x_N$. Then

$$\|f - \mathcal{L}_N f\|_\infty \leq (1 + \Lambda_N) \mathcal{E}_N(f).$$

1.3 Spectra of operators and their approximation

Proposition 1.3.1. [36, Proposition 4.1] Let X, Y be linear spaces and let $\mathcal{A}: X \rightarrow X$, $\mathcal{R}: Y \rightarrow X$, and $\mathcal{P}: X \rightarrow Y$ be linear operators. If

$$\mathcal{R}\mathcal{P} = \mathcal{I}_X,$$

then $\mathcal{A}$ has the same nonzero eigenvalues, with the same geometric and partial multiplicities, as

$$\mathcal{B} := \mathcal{P}\mathcal{A}\mathcal{R}: Y \rightarrow Y.$$

Proposition 1.3.2. [36, Proposition 4.3] Let X be a linear space, $\mathcal{A}: X \rightarrow X$ be a linear operator, and $\lambda \in \mathbb{C}$. If $Y \subset X$ is such that

$$1 \quad \mathcal{A}(Y) \subseteq Y,$$

$$2 \quad \text{for any } x, y \in X,$$

$$(\lambda \mathcal{I}_X - \mathcal{A})x = y, \quad \text{and} \quad y \in Y \Rightarrow x \in Y,$$

then λ is an eigenvalue of geometric multiplicity g of $\mathcal{A}$ if and only if λ is an eigenvalue of geometric multiplicity g of $\mathcal{A}|_Y: Y \rightarrow Y$. Moreover, the eigenvectors relevant to λ are the same for $\mathcal{A}$ and $\mathcal{A}|_Y$, and also the partial multiplicities of λ are the same.

The proof of the following result is adapted from the proof of [32, Proposition 4.9].

Theorem 1.3.3. Let $(X, \|\cdot\|_X)$, $(Y, \|\cdot\|_Y)$ be real (complex) Banach spaces with $\dim X = M < +\infty$. Let $\mathcal{A}: X \rightarrow Y$ be linear, $\{\mathcal{A}_N\}_{N=0}^\infty$ be a sequence of linear operators from X to Y such that

$$\|\mathcal{A}_N - \mathcal{A}\|_{Y \leftarrow X} \rightarrow 0, \quad N \rightarrow \infty,$$

and let $\phi_1, \dots, \phi_M$ be a basis for X . If there exists a sequence $\{\rho_N\}_{N=0}^\infty \subset [0, +\infty)$ such that $\rho_N \rightarrow 0$ as $N \rightarrow \infty$, and $\max_{i=1, \dots, M} \|(\mathcal{A}_N - \mathcal{A})\phi_i\|_Y = O(\rho_N)$ for every $i = 1, \dots, M$, then

$$\|\mathcal{A}_N - \mathcal{A}\|_{Y \leftarrow X} = O(\rho_N).$$

Proof. Let $\phi \in X$. Then there exist $\alpha_1(\phi), \dots, \alpha_M(\phi) \in \mathbb{R}$ (or $\mathbb{C}$) such that $\phi = \sum_{i=1}^M \alpha_i(\phi) \phi_i$. Hence

$$\|(\mathcal{A}_N - \mathcal{A})\phi\|_Y \leq \sum_{i=1}^M |\alpha_i(\phi)| \|(\mathcal{A}_N - \mathcal{A})\phi_i\|_Y.$$

Now, note that the function $\phi \rightarrow \max_{i=1, \dots, M} |\alpha_i(\phi)|$ determines a norm on X . Thus, there exists a positive constant C independent of ϕ such that $\max_{i=1, \dots, M} |\alpha_i(\phi)| \leq C \|\phi\|_X$ for every $\phi \in X$, and

$$\|(\mathcal{A}_N - \mathcal{A})\|_{Y \leftarrow X} \leq \sup_{\phi \in X, \|\phi\|_X \leq 1} \frac{\sum_{i=1}^M \alpha_i(\phi) \|(\mathcal{A}_N - \mathcal{A})\phi_i\|_Y}{\|\phi\|_X}$$

$$\begin{aligned}
&\leq M \max_{i=1,\dots,M} \|(\mathcal{A}_N - \mathcal{A})\phi_i\|_Y \sup_{\phi \in X, \|\phi\|_X \leq 1} \frac{\max_{i=1,\dots,M} |\alpha_i(\phi)|}{\|\phi\|_X} \\
&\leq M \cdot C \cdot \max_{i=1,\dots,M} \|(\mathcal{A}_N - \mathcal{A})\phi_i\|_Y \\
&= O(\rho_N).
\end{aligned}$$

The thesis follows. □

A general numerical method to approximate reproduction numbers for age-structured models

The aim of this chapter, is to present a general numerical method to approximate the reproduction numbers of a large class of age-structured population models with finite age span, i.e., with $a^+ < +\infty$. The content of this chapter is mainly taken from the works [54, 55] (the latter currently under revision) by the author, F. Scarabel and R. Vermiglio.

For age-structured population models formulated as IPDEs with nonlocal boundary conditions, reproduction numbers are characterized as the spectral radius of linear, compact, positive operators [58, 88, 128], which are obtained by linearizing the model around an equilibrium and then splitting the linearization into birth and transition [18, 59, 63]. As the resulting operators are typically infinite-dimensional, numerical methods are often needed in practical computations.

In [25, 29, 31, 72, 102], numerical methods to approximate the reproduction numbers for age-structured models with finite age span are proposed. The underlying idea of these methods is that of separately discretizing the birth and transition operators, and then to approximate the reproduction numbers through the spectral radius of a matrix. In [72, 102], the discretization is obtained via a Theta and a Backward Euler method, respectively, while in [25, 29, 31], the discretization is obtained via Chebyshev pseudospectral collocation. However, all these methods rely on the assumption that the birth and transition operators are defined on a subspace of the state space (which typically is assumed to be an L^1 -space), including the boundary conditions in the domain of the transition operator (which in general is a differential operator), and hence necessarily interpreting the corresponding processes as transition.

Here we extend these methods by allowing for complete flexibility in the definition of the birth/infection and transition processes. To do this, we build our approach on the extended space framework by [83, 88]. We define a suitable integral mapping from the extended space to the space of absolutely continuous functions. This permits us to see processes described by boundary conditions as perturbations of an operator with trivial domain condition and, on the other hand, it allows us to work with polynomial interpolation, since point evaluation is well-defined [7, 26, 121, 122]. Then, as in [25, 29, 31, 72, 102], we identify birth(/infection) and transition operators, and for any given splitting we discretize them via pseudospectral collocation.

The convergence of the method is proved using the well-established spectral approximation theory of [45]. To prove the norm convergence of the discretized operators in AC , we take advantage of the injection of AC into L^1 , which is compact by the Rellich–Kondrach Theorem [40, p. 285, Theorem 9.16], and of interpolation error bounds in the L^1 -norm [114, Theorem 1].

We prove that the convergence order of the approximating reproduction numbers is driven by the interpolation error on the relevant eigenspaces, which in turn depends on the regularity of the model coefficients.

The content of the chapter is organized as follows. In Section 2.1, we introduce a prototype,

linear, multi-group, age-structured model with finite age-span and, with reference to it, we illustrate the theoretical framework, the reformulation via integration of the state in the age variable, and prove the compactness of the continuous operators. In Section 2.2, we present the numerical method and we prove the well-posedness of the discretized operator. The convergence proof is developed in Section 2.3. In Section 2.4, we give details about the implementation of the method, while Section 2.5 contains numerical results and applications to epidemiological models. Finally, in Section 2.6 we discuss how the discretization presented in this chapter can be adapted to also compute the dominant part of the spectrum relevant to the prototype model of Section 2.1.

2.1 Prototype model and theoretical framework

In this section, we introduce a general, linear, multi-group, age-structured, population model with finite age span, which encompasses many models of the literature obtained from the linearization of a nonlinear model around an equilibrium. With reference to this prototype model and following [83, 86, 88, 128], we recall the definition of the reproduction numbers within the extended space framework. Then, we introduce an integral mapping to the space of absolutely continuous functions and provide the equivalent definitions within the AC-framework, which is more advantageous for the development of the discretization technique presented in Section 2.2.

Let $a^+ \in (0, +\infty)$ denote the maximum age. For $x(t, \cdot) \in L^1([0, a^+], \mathbb{R}^d)$, $t \geq 0$ and d a positive integer, the model reads

$$\begin{cases} \mathcal{D}x(t, a) = \int_0^{a^+} \beta(a, \alpha)x(t, \alpha) d\alpha + \delta(a)x(t, a), & t \geq 0, \quad a \in [0, a^+], \\ x(t, 0) = \int_0^{a^+} b(a)x(t, a) da, & t \geq 0, \end{cases} \quad (2.1.1)$$

where $\mathcal{D}$ is defined as in (1.2.6). In the context of infectious disease modeling, (2.1.1) enables one to describe several types of transmission routes and biological processes: the boundary term can account for either natural infection (when a represents infection age) or vertical transmission (when a represents demographic age), while the right-hand side of the first equation includes horizontal transmission terms, as well as the removal of individuals via death or recovery.

To allow for flexibility in the definition of reproduction numbers associated to different ways of inflow into the infected compartments, in the following we assume that

$$\beta = \beta^+ + \beta^-, \quad b = b^+ + b^-,$$

where $\beta^+, \beta^-, b^+, b^-$ are chosen to conveniently split the inflow processes into two parts where β^+, b^+ collect the birth processes and β^-, b^- collect the transition processes,¹

The following requirements are necessary to proceed with the analysis [88, p. 77].

Assumption 2.1.

- (i) $\beta^+, \beta^- \in L^\infty([0, a^+]^2, \mathbb{R}^{d \times d})$ are nonnegative,
- (ii) $b^+, b^- \in L^\infty([0, a^+], \mathbb{R}^{d \times d})$ are nonnegative,
- (iii) $\delta \in L^\infty([0, a^+], \mathbb{R}^{d \times d})$ is essentially nonnegative² with non-positive diagonal elements.³

Since we are interested in the spectral theory, we enlarge our attention to complex-valued functions. We consider the Banach space $X := L^1([0, a^+], \mathbb{C}^d)$ and we work in the extended state

¹The $+/-$ notation was inspired by [90].

²i.e., all off-diagonal elements are nonnegative

³Assumption 2.1 (iii) ensures that the fundamental solution matrix associated to δ is non-negative and non-singular [88, p. 77].

space of the density function and its boundary value $Z := \mathbb{C}^d \times X$, equipped with the following norm:

$$\|(\eta; \phi)\|_Z := |\eta| + \|\phi\|_X,$$

where $\|\cdot\|_X$ is the standard L^1 -norm, see [83] and [88, Chapter 6.4.2]. Furthermore, we introduce the subspace

$$Z_0 = \{0\} \times X \subset Z,$$

which is isomorphic to X .

We define the baseline transition operator $\mathcal{M}^Z: D(\mathcal{M}^Z) \subset Z_0 \rightarrow Z$ as follows

$$\mathcal{M}^Z(0; \phi)(a) := (\phi(0); \phi'(a) - \delta(a)\phi(a)), \quad a \in [0, a^\dagger],$$

where

$$D(\mathcal{M}^Z) := \{(0; \phi) \in Z_0 \mid \phi \in \text{AC}([0, a^\dagger], \mathbb{C}^d)\},$$

and the bounded linear birth operators $\mathcal{B}_\pm^Z: Z_0 \rightarrow Z$

$$\mathcal{B}_\pm^Z(0; \phi)(a) := \left(\int_0^{a^\dagger} b^\pm(\alpha)\phi(\alpha) d\alpha; \int_0^{a^\dagger} \beta^\pm(a, \alpha)\phi(\alpha) d\alpha \right), \quad a \in [0, a^\dagger].$$

From the assumption on δ , it follows that $\mathcal{M}^Z$ is invertible with bounded inverse. Thus, we can define the following:

$$\mathcal{K}_\pm^Z := \mathcal{B}_\pm^Z(\mathcal{M}^Z)^{-1}.$$

To compute the reproduction number for the birth process described by $\mathcal{B}_+^Z$, we define the transition operator $\mathcal{M}_-^Z := \mathcal{M}^Z - \mathcal{B}_-^Z$, whose domain coincides with $D(\mathcal{M}^Z)$, and we note that $\mathcal{M}_-^Z = (\mathcal{I}_Z - \mathcal{K}_-^Z)\mathcal{M}^Z$. Then we make the following assumption.

Assumption 2.2. The operator $\mathcal{K}_-^Z$ satisfies $\rho(\mathcal{K}_-^Z) < 1$

Under Assumption 2.2, we have the following result [86, Section 4].

Proposition 2.1.1. *Let Assumption 2.2 hold. Then, the operator $\mathcal{M}_-^Z$ is invertible with bounded inverse.*

In the following, we assume that Assumption 2.2 holds. Hence, we can define the positive operator

$$\mathcal{H}^Z := \mathcal{B}_+^Z(\mathcal{M}_-^Z)^{-1} = \mathcal{K}_+^Z(\mathcal{I}_Z - \mathcal{K}_-^Z)^{-1}. \quad (2.1.2)$$

and characterize the *reproduction number* R for the birth process $\mathcal{B}_+^Z$ and the transition operator $\mathcal{M}_-^Z$ as its spectral radius [58], i.e.,

$$R := \rho(\mathcal{H}^Z). \quad (2.1.3)$$

In Section 2.1.1, we prove that the operator in (2.1.2) is compact. Hence, if $R > 0$, then it is a dominant real eigenvalue, with an associated non-negative eigenfunction [99].

We generically refer to “reproduction number” to include several different interpretations as specific cases, including the basic and type reproduction numbers, as well as more general definitions [62, 76, 88].

- If $\mathcal{B}_+^Z$ contains all processes leading to new infections, then $\mathcal{H}^Z$ is the standard NGO and R is precisely R_0 ;
- If $\mathcal{B}_+^Z$ only contains a subset of the new infections (e.g., horizontal vs vertical, vector vs host) and $\mathcal{B}_-^Z$ contains all other processes, then $\mathcal{H}^Z$ is the *type reproduction operator*⁴ and R is the type reproduction number, and $\mathcal{K}_+^Z$ and $\mathcal{K}_-^Z$ are the *type-specific NGOs* [88, pag. 477];

⁴Indeed, note that in line with the interpretation, the operator $(\mathcal{I}_Z - \mathcal{K}_-^Z)^{-1} = \sum_{i=0}^{\infty} (\mathcal{K}_-^Z)^i$ captures the chains of transmission through any sequence of any other type not included in $\mathcal{B}_+^Z$.

- If $\mathcal{B}_+^Z$ contains the inflow in a generic compartment (possibly not a state-at-infection), then R is the *state reproduction number* according to the terminology in [90].

Moreover, depending on the assumptions on population immunity and interventions, (2.1.3) can capture the concepts of *effective* and *control* reproduction numbers. Additionally, (2.1.3) provides a unifying abstract framework to introduce the numerical method in Section 2.2.

Now, let us consider the Banach space $Y := \text{AC}([0, a^\dagger], \mathbb{C}^d)$ equipped with the norm

$$\|\psi\|_Y := |\psi(0)| + \|\psi'\|_X,$$

and its closed subspace $Y_0 = \{\psi \in Y \mid \psi(0) = 0\}$. The integral operator $\mathcal{V}: Z \rightarrow Y$ given by

$$\mathcal{V}(\eta; \phi) := \eta + \int_0^a \phi(\alpha) d\alpha, \quad a \in [0, a^\dagger],$$

defines an isomorphism between Z and Y and between Z_0 and Y_0 .

By defining $y(t, \cdot) := \mathcal{V}(0; x(t, \cdot))$, $t \geq 0$, the model (2.1.1) for $x(t, \cdot) \in X$ is equivalent to the following model⁵

$$\begin{cases} \mathcal{D}y(t, a) = \int_0^{a^\dagger} b(\alpha) y(t, d\alpha) \\ \quad + \int_0^a \int_0^{a^\dagger} \beta(\zeta, \alpha) y(t, d\alpha) d\zeta \\ \quad + \int_0^a \delta(\alpha) y(t, d\alpha), & t \geq 0, \quad a \in [0, a^\dagger], \\ y(t, 0) = 0, & t \geq 0. \end{cases} \quad (2.1.4)$$

for $y(t, \cdot) \in Y_0$. Now, we introduce the birth operators $\mathcal{B}_\pm^Y: Y_0 \rightarrow Y$

$$\mathcal{B}_\pm^Y := \mathcal{V} \mathcal{B}_\pm^Z \mathcal{V}^{-1},$$

and the transition operators $\mathcal{M}^Y, \mathcal{M}_-^Y: D(\mathcal{M}^Y) \subset Y_0 \rightarrow Y$

$$\mathcal{M}^Y := \mathcal{V} \mathcal{M}^Z \mathcal{V}^{-1}, \quad \mathcal{M}_-^Y := \mathcal{V} \mathcal{M}_-^Z \mathcal{V}^{-1},$$

where $D(\mathcal{M}^Y) := \mathcal{V}(D(\mathcal{M}^Z))$. Explicitly, they read

$$(\mathcal{B}_\pm^Y \psi)(a) := \int_0^a \int_0^{a^\dagger} \beta^\pm(\zeta, \alpha) \psi'(\alpha) d\alpha d\zeta + \int_0^{a^\dagger} b^\pm(\alpha) \psi'(\alpha) d\alpha, \quad a \in [0, a^\dagger],$$

for $\psi \in Y_0$,

$$(\mathcal{M}^Y \psi)(a) := \psi' - \int_0^a \delta(\alpha) \psi'(\alpha) d\alpha, \quad a \in [0, a^\dagger],$$

for $\psi \in D(\mathcal{M}^Y)$, where

$$D(\mathcal{M}^Y) := \{\psi \in Y_0 \mid \psi' \in Y\},$$

and

$$\mathcal{M}_-^Y = \mathcal{M}^Y - \mathcal{B}_-^Y.$$

It is clear that the spectral radius of

$$\mathcal{H}^Y := \mathcal{V} \mathcal{H}^Z \mathcal{V}^{-1} = \mathcal{B}_+^Y (\mathcal{M}_-^Y)^{-1} \quad (2.1.5)$$

coincides with R . In fact, the relations $\sigma(\mathcal{H}^Z) = \sigma(\mathcal{H}^Y)$ [67, Section 2.1] and $\sigma_p(\mathcal{H}^Z) = \sigma_p(\mathcal{H}^Y)$ (see Proposition 1.3.1) hold, and there is a one-to-one correspondence of the eigenfunctions via the operator $\mathcal{V}$.

⁵Note that, in (2.1.4), we consider an absolutely continuous function as a measure.

2.1.1 Compactness of $\mathcal{H}^Y$ and $\mathcal{H}^Z$

To conclude this section, we prove that the operator $\mathcal{H}^Y$ in (2.1.5) is compact in Y , which implies that the operator $\mathcal{H}^Z$ in (2.1.2) is compact in Z through the relation in (2.1.5). For simplicity, in the following we identify Z_0 with X , so that for a linear operator $\mathcal{Q}_0: Z_0 \rightarrow Y$ we write $\mathcal{Q}_0\phi$ for $\mathcal{Q}_0(0; \phi)$.

We consider the bounded operator $\mathcal{W}: X \rightarrow Y \subset X$ defined as

$$(\mathcal{W}\phi)(a) := \int_0^a \delta(\alpha)\phi(\alpha) d\alpha + \int_0^a \int_0^{a^\dagger} \beta^-(\zeta, \alpha)\phi(\alpha) d\alpha d\zeta + \int_0^{a^\dagger} b^-(\alpha)\phi(\alpha) d\alpha, \quad a \in [0, a^\dagger],$$

and the natural immersion of Y into X , $\mathcal{J}: Y \rightarrow X$, which is compact due to the Rellich–Kondrach embedding Theorem [40, p. 285, Theorem 9.16]. Note that, thanks to this, the restriction to Y of a linear and bounded operator from X to Y is compact. In the following, to simplify the notation, we omit to write $\mathcal{J}$ when the domain of application is clear from the context.

Now, let us observe that, for $\psi \in D(\mathcal{M}_-^Y)$, we have

$$\mathcal{M}_-^Y \psi = \mathcal{M}_-^Y \mathcal{V}\psi' = (\mathcal{I}_Y - \mathcal{W})\psi', \quad \psi' \in Y. \quad (2.1.6)$$

Hence, it is easy to see that $\mathcal{M}_-^Y$ is invertible with bounded inverse if and only if the operator $\mathcal{I}_Y - \mathcal{W}: Y \rightarrow Y$ is invertible with bounded inverse. Moreover, we can prove the following result that will be widely used in the proof of convergence.

Lemma 2.1.2. *The operator*

$$\mathcal{I}_X - \mathcal{W}: X \rightarrow X$$

is invertible with bounded inverse. Moreover, we have

$$(\mathcal{M}_-^Y)^{-1} = \mathcal{V}(\mathcal{I}_X - \mathcal{W})^{-1}\mathcal{J}, \quad (2.1.7)$$

and the following inequality holds

$$\|(\mathcal{M}_-^Y)^{-1}\|_{Y_0 \leftarrow Y} \leq a^\dagger \cdot \|(\mathcal{I}_X - \mathcal{W})^{-1}\|_{X \leftarrow X}. \quad (2.1.8)$$

Proof. Observe that $\mathcal{W}$ is compact in X . Thus, we only need to show that there exists no $\phi \in X \setminus \{0\}$ such that $\phi = \mathcal{W}\phi$. Suppose in fact that $\phi \in X$ solves $\phi = \mathcal{W}\phi$. Then, $\phi \in Y$ and the invertibility of $\mathcal{I}_Y - \mathcal{W}$ in Y implies that $\phi = 0$.

Now, let us note that given $\xi \in Y$, solving $\mathcal{M}_-^Y \psi = \xi$ in Y for $\psi = \mathcal{V}\psi'$ is equivalent to solve

$$\psi' - \mathcal{W}\psi' = \mathcal{J}\xi$$

in X for $\psi' \in Y$, hence (2.1.7) holds. Finally, the bound (2.1.8) follows from (2.1.7) by observing that $\|\mathcal{V}\|_{Y_0 \leftarrow X} = 1$ and that

$$\|\mathcal{J}\xi\|_X \leq a^\dagger \|\xi\|_Y, \quad \xi \in Y. \quad (2.1.9)$$

□

From Theorem 2.1.2, we have that the following diagram commutes

$$\begin{array}{ccc} Y & \xrightarrow{(\mathcal{M}_-^Y)^{-1}} & Y_0 \\ \mathcal{J} \downarrow & & \uparrow \mathcal{V} \\ X & \xrightarrow{(\mathcal{I}_X - \mathcal{W})^{-1}} & X \end{array}$$

and, from the compactness of $\mathcal{J}$, we immediately get the following results.

Corollary 2.1.3. *The operator $(\mathcal{M}_-^Y)^{-1}$ is compact in Y .*

Proof. The thesis follows by combining (2.1.7) with the compactness of $\mathcal{J}$. $\square$

Corollary 2.1.4. *The operator $\mathcal{H}^Y$ in (2.1.5) is compact.*

Proof. Since $\mathcal{B}_+^Y$ is bounded, the compactness of $\mathcal{H}^Y$ follows from Theorem 2.1.3. $\square$

Corollary 2.1.5. *The operator $\mathcal{H}^Z$ in (2.1.2) is compact, $0 \in \sigma(\mathcal{H}^Z)$ and $\sigma(\mathcal{H}^Z) \setminus \{0\}$ consists of eigenvalues only which are at most countable and are either isolated or accumulate at 0. In addition, if R in (2.1.3) is positive, then it is a dominant real eigenvalue (in the sense of largest in magnitude) with associated a real nonnegative eigenfunction.*

Proof. Since $\mathcal{H}^Z = \mathcal{V}^{-1}\mathcal{H}^Y\mathcal{V}$, the compactness of $\mathcal{H}^Z$ follows from Theorem 2.1.4 and from the boundedness of $\mathcal{V}, \mathcal{V}^{-1}$. As a result, the assertion on $\sigma(\mathcal{H}^Z)$ follows from [40, Theorem 6.8]. Finally, the last part of the thesis follows from the positivity of $\mathcal{H}^Z$ and the Krein–Rutmann Theorem [99]. $\square$

Corollary 2.1.6. *The operator $\mathcal{H}^Y$ in (2.1.5) is such that $0 \in \sigma(\mathcal{H}^Y)$ and $\sigma(\mathcal{H}^Y) \setminus \{0\}$ consists of eigenvalues only which are at most countable and are either isolated or accumulate at 0. In addition, if R in (2.1.3) is positive, then it is a dominant real eigenvalue of $\mathcal{H}^Y$ with associated a real nondecreasing eigenfunction.*

2.2 The numerical approach

In this section, we illustrate how to approximate the reproduction number of a class of models that can be recast in the framework of Section 2.1. To obtain an approximation R_N of R , we derive a finite-dimensional approximation $\mathcal{H}_N$ of $\mathcal{H}^Y$, and we approximate the eigenvalues of the latter through those of the former. This is achieved by separately discretizing the operators $\mathcal{B}_+^Y$ and $\mathcal{M}_-^Y$ in Section 2.1 via pseudospectral collocation.

In the following, we only work in the space Y and, to simplify the notation, we drop the superscript Y from the operators acting on Y .

2.2.1 Discretization of $\mathcal{B}_+$ and $\mathcal{M}_-$

Given a positive integer N , we consider the space $Y_N \subset Y$ of algebraic polynomials on $[0, a^\dagger]$ of degree at most N and taking values in $\mathbb{C}^d$, together with

$$Y_{0,N} := \{\psi_N \in Y_N \mid \psi_N(0) = 0\} \subset Y_0.$$

Let $\Theta_N := \{a_1 < \dots < a_N\}$ denote a mesh of N points in $(0, a^\dagger)$ and $\Theta_{0,N} := \{0\} \cup \Theta_N$. We define restriction and prolongation operators respectively as

$$\mathcal{R}_N: Y \rightarrow \mathbb{C}^{dN}, \quad \mathcal{R}_N\psi := (\psi(a_1); \dots; \psi(a_N)),$$

and

$$\mathcal{P}_{0,N}: \mathbb{C}^{dN} \rightarrow Y_{0,N}, \quad \mathcal{P}_{0,N}\Psi := \sum_{i=1}^N \ell_{0,i} \Psi_i,$$

where $\Psi := (\Psi_1; \dots; \Psi_N)$, for $\Psi_i \in \mathbb{C}^d$, $i = 1, \dots, N$, and $\{\ell_{0,i}\}_{i=0}^N$ is the Lagrange algebraic polynomial basis relevant to $\Theta_{0,N}$. Observe that

$$\mathcal{R}_N \mathcal{P}_{0,N} = \mathcal{I}_{\mathbb{C}^{dN}}, \quad \mathcal{P}_{0,N} \mathcal{R}_N = \mathcal{L}_{0,N},$$

where $\mathcal{L}_{0,N}: Y_0 \rightarrow Y_{0,N}$ is the Lagrange interpolation operator relevant to $\Theta_{0,N}$.

Then, we derive the finite-dimensional approximations $\mathcal{B}_N, \mathcal{M}_N: \mathbb{C}^{dN} \rightarrow \mathbb{C}^{dN}$ of $\mathcal{B}_+$ and $\mathcal{M}_-$, respectively, as

$$\mathcal{B}_N := \mathcal{R}_N \mathcal{B}_+ \mathcal{P}_{0,N}, \quad \mathcal{M}_N := \mathcal{R}_N \mathcal{M}_- \mathcal{P}_{0,N}. \quad (2.2.1)$$

In order to derive a finite-dimensional approximation $\mathcal{H}_N$ of $\mathcal{H}$, in Section 2.2.2 we show that there exists a positive integer $\bar{N}$ such that $\mathcal{M}_N$ is invertible for every integer $N \geq \bar{N}$ under the following assumption.

Assumption 2.3. Θ_N is the mesh of Chebyshev zeros in $[0, a^+]$.

Subsequently, the finite-dimensional approximation $\mathcal{H}_N: \mathbb{C}^{dN} \rightarrow \mathbb{C}^{dN}$ of $\mathcal{H}$ is obtained as

$$\mathcal{H}_N := \mathcal{B}_N \mathcal{M}_N^{-1}, \quad N \geq \bar{N}.$$

The discrete eigenvalue problem can be solved either by using the standard MATLAB function `eig` or by solving the generalized eigenvalue problem $\mathcal{B}_N \Psi = \lambda \mathcal{M}_N \Psi$ [29]. Note that the eigenvectors of $\mathcal{H}_N$ give an approximation of the values of the eigenfunctions of $\mathcal{H}$ at the Chebyshev zeros. Thus, an approximation of the eigenfunctions of $\mathcal{H}$ can be obtained by interpolating the eigenvectors of $\mathcal{H}_N$ at the nodes in Θ_N and, subsequently, an approximation of the eigenfunctions of $\mathcal{H}^Z$ can be obtained by applying $\mathcal{V}^{-1}$ to those polynomials.

2.2.2 Invertibility of $\mathcal{M}_N$

In this section we prove that, for N sufficiently large, the matrix $\mathcal{M}_N$ is invertible. To do so, we consider the Lagrange polynomial basis relevant to Θ_N , $\{\ell_i\}_{i=1}^N$, and define the prolongation operator

$$\mathcal{P}_{N-1}: \mathbb{C}^{dN} \rightarrow Y_{N-1} \subset Y, \quad \mathcal{P}_{N-1} \Psi := \sum_{i=1}^N \ell_i \Psi_i.$$

Note that

$$\mathcal{R}_N \mathcal{P}_{N-1} = \mathcal{I}_{\mathbb{C}^{dN}}, \quad \mathcal{P}_{N-1} \mathcal{R}_N = \mathcal{L}_{N-1},$$

where $\mathcal{L}_{N-1}: Y \rightarrow Y_{N-1}$ is the Lagrange interpolation operator relevant to Θ_N .

Then, we observe that $\mathcal{M}_N$ is invertible if and only if, for every $\Xi \in \mathbb{C}^{dN}$, there exists a unique $\Psi \in \mathbb{C}^{dN}$ such that

$$\mathcal{M}_N \Psi = \Xi. \quad (2.2.2)$$

In this case, let $\psi_N := \mathcal{P}_{0,N} \Psi$. From $\psi_N = \mathcal{V}_0 \psi'_N$, (2.1.6) and (2.2.2), we get

$$\mathcal{R}_N \mathcal{M}_- \mathcal{P}_{0,N} \Psi = \mathcal{R}_N (\mathcal{I}_Y - \mathcal{W}) \psi'_N = \Xi,$$

and by applying $\mathcal{P}_{N-1}$, since $\psi'_N = \mathcal{L}_{N-1} \psi'_N$, we obtain

$$(\mathcal{I}_Y - \mathcal{L}_{N-1} \mathcal{W}) \psi'_N = \mathcal{P}_{N-1} \Xi. \quad (2.2.3)$$

Now, we prove that $\mathcal{M}_N$ is invertible by showing that (2.2.3) has a unique polynomial solution ψ'_N in X .

Lemma 2.2.1. *Let Assumption 2.3 hold. Then there exists a positive integer $\bar{N}$ such that $\mathcal{I}_X - \mathcal{L}_{N-1} \mathcal{W}$ is invertible and*

$$\left\| (\mathcal{I}_X - \mathcal{L}_{N-1} \mathcal{W})^{-1} \right\|_{X \leftarrow X} \leq 2 \left\| (\mathcal{I}_X - \mathcal{W})^{-1} \right\|_{X \leftarrow X}, \quad (2.2.4)$$

for every integer $N \geq \bar{N}$. Moreover, $\mathcal{M}_N: \mathbb{C}^{dN} \rightarrow \mathbb{C}^{dN}$ is invertible for every integer $N \geq \bar{N}$ with inverse

$$\mathcal{M}_N^{-1} := \mathcal{R}_N \mathcal{V}_0 (\mathcal{I}_X - \mathcal{L}_{N-1} \mathcal{W})^{-1} \mathcal{P}_{N-1}. \quad (2.2.5)$$

Proof. We use a proof technique similar to [39, Chapter 5]. Let us observe that

$$\mathcal{I}_X - \mathcal{L}_{N-1}\mathcal{W} = (\mathcal{I}_X - \mathcal{W}) + (\mathcal{I}_X - \mathcal{L}_{N-1})\mathcal{W}.$$

Then, since $\text{Range}(\mathcal{W}) \subset Y$ and $\mathcal{W}: X \rightarrow Y$ is bounded, we have

$$\|(\mathcal{I}_X - \mathcal{L}_{N-1})\mathcal{W}\|_{X \leftarrow X} \leq C \cdot \|\mathcal{J}(\mathcal{I}_Y - \mathcal{L}_{N-1})\|_{X \leftarrow Y} \|\mathcal{W}\|_{Y \leftarrow X}.$$

Moreover, Assumption 2.3 and Corollary 1.1.15 guarantee that there exists a positive constant C independent of N such that

$$\|\mathcal{J}(\mathcal{I}_Y - \mathcal{L}_{N-1})\|_{X \leftarrow Y} \leq C \cdot \frac{\log N}{N}, \quad (2.2.6)$$

from which we get

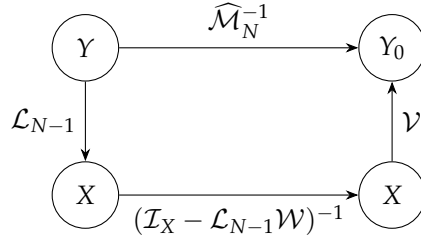
$$\|(\mathcal{I}_X - \mathcal{L}_{N-1})\mathcal{W}\|_{X \leftarrow X} \leq C \cdot \frac{\log N}{N} \cdot \|\mathcal{W}\|_{Y \leftarrow X} \rightarrow 0, \quad N \rightarrow \infty. \quad (2.2.7)$$

Hence, the Banach perturbation Lemma [100, Theorem 10.1] ensures that there exists a positive integer $\bar{N}$ such that $\mathcal{I}_X - \mathcal{L}_{N-1}\mathcal{W}$ is invertible in X and (2.2.4) holds for every integer $N \geq \bar{N}$. Finally, (2.2.5) follows from (2.2.2) and (2.2.3). $\square$

Note that, if $\Xi = \mathcal{R}_N \xi$, for $\xi \in Y$, then the unique polynomial solution ψ'_N of (2.2.3) is given by $\psi'_N = (\mathcal{I}_X - \mathcal{L}_{N-1}\mathcal{W})^{-1} \mathcal{L}_{N-1} \xi$. Hence, by introducing the operator $\widehat{\mathcal{M}}_N^{-1}: Y \rightarrow Y_{0,N}$ defined as⁶

$$\widehat{\mathcal{M}}_N^{-1} := \mathcal{V}(\mathcal{I}_X - \mathcal{L}_{N-1}\mathcal{W})^{-1} \mathcal{L}_{N-1}, \quad (2.2.8)$$

we have that $\psi_N = \widehat{\mathcal{M}}_N^{-1} \xi$, and the following diagram commutes



Remark 2.2.2. Note that in (2.2.8), $\mathcal{L}_{N-1}$ is seen as an operator from Y to X . This is very advantageous since in (2.2.6) and Section 2.3 we are able to estimate the interpolation error on absolutely continuous functions using the X -norm. Then, the problem is mapped back again to Y via the isomorphism $\mathcal{V}$. We like to refer to this approach as the “upside down” method.

2.3 Convergence analysis

In this section, we investigate the convergence of the eigenvalues (and the corresponding eigenvectors) of $\mathcal{H}_N$ to those of $\mathcal{H}$ via the spectral approximation theory of [45]. To this aim, let us define the operator

$$\widehat{\mathcal{H}}_N := \mathcal{P}_{N-1} \mathcal{H}_N \mathcal{R}_N: Y \rightarrow Y,$$

which has the same nonzero eigenvalues with the same geometric and partial multiplicities of $\mathcal{H}_N$, see Proposition 1.3.1. Then, since $\widehat{\mathcal{H}}_N - \mathcal{H}$ is compact for every $N \geq \bar{N}$ thanks to Theorem 2.1.4, it is sufficient to show that [45, p. 498]

$$\|\widehat{\mathcal{H}}_N - \mathcal{H}\|_{Y \leftarrow Y} \rightarrow 0, \quad N \rightarrow \infty. \quad (2.3.1)$$

⁶For the sake of readability, in (2.2.5) and (2.2.8) we omit to explicitly write $\mathcal{J}$.

From (2.2.8), we have that $\mathcal{L}_{0,N}\widehat{\mathcal{M}}_N^{-1} = \widehat{\mathcal{M}}_N^{-1}$, hence we can write

$$\widehat{\mathcal{H}}_N = \mathcal{L}_{N-1}\mathcal{B}_+\widehat{\mathcal{M}}_N^{-1},$$

and

$$\widehat{\mathcal{H}}_N - \mathcal{H} = (\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{B}_+(\widehat{\mathcal{M}}_N^{-1} - \mathcal{M}_-^{-1}) + (\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{B}_+\mathcal{M}_-^{-1} + \mathcal{B}_+(\widehat{\mathcal{M}}_N^{-1} - \mathcal{M}_-^{-1}).$$

Thus, in order to prove the convergence of $\widehat{\mathcal{H}}_N$ to $\mathcal{H}$, we need to investigate the behavior of $(\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{B}_+$ and $\widehat{\mathcal{M}}_N^{-1} - \mathcal{M}_-^{-1}$ as $N \rightarrow \infty$.

2.3.1 Norm convergence of $\widehat{\mathcal{H}}_N$ to $\mathcal{H}$

Lemma 2.3.1. *Let Assumption 2.3 hold. Then*

$$\left\| \widehat{\mathcal{M}}_N^{-1} - \mathcal{M}_-^{-1} \right\|_{Y_0 \leftarrow Y} \rightarrow 0, \quad N \rightarrow \infty.$$

Proof. Observe that, from (2.1.7) and (2.2.8), we can write $\widehat{\mathcal{M}}_N^{-1} - \mathcal{M}_-^{-1}$ as

$$\widehat{\mathcal{M}}_N^{-1} - \mathcal{M}_-^{-1} = \mathcal{V}_0 \left[(\mathcal{I}_X - \mathcal{L}_{N-1}\mathcal{W})^{-1} \mathcal{J}(\mathcal{L}_{N-1} - \mathcal{I}_Y) \right. \quad (2.3.2)$$

$$\left. + \left((\mathcal{I}_X - \mathcal{L}_{N-1}\mathcal{W})^{-1} - (\mathcal{I}_X - \mathcal{W})^{-1} \right) \mathcal{J} \right]. \quad (2.3.3)$$

Simple computations show that

$$(\mathcal{I}_X - \mathcal{L}_{N-1}\mathcal{W})^{-1} - (\mathcal{I}_X - \mathcal{W})^{-1} = (\mathcal{I}_X - \mathcal{L}_{N-1}\mathcal{W})^{-1}(\mathcal{L}_{N-1} - \mathcal{I}_X)\mathcal{W}(\mathcal{I}_X - \mathcal{W})^{-1}. \quad (2.3.4)$$

Hence, from (2.1.9) and (2.2.4), we get

$$\left\| \widehat{\mathcal{M}}_N^{-1} - \mathcal{M}_-^{-1} \right\|_{Y_0 \leftarrow Y} \leq C_1 \left\| \mathcal{J}(\mathcal{L}_{N-1} - \mathcal{I}_Y) \right\|_{X \leftarrow Y}, \quad (2.3.5)$$

where

$$C_1 := 2 \left\| (\mathcal{I}_X - \mathcal{W})^{-1} \right\|_{X \leftarrow X} \left(1 + 2a^\dagger \left\| (\mathcal{I}_X - \mathcal{W})^{-1} \right\|_{X \leftarrow X} \left\| \mathcal{W} \right\|_{X \leftarrow X} \right),$$

The term on the right hand-side of (2.3.5) tends to zero as $N \rightarrow \infty$ thanks to (2.2.6). The thesis follows. $\square$

Now, in order to prove (2.3.1), we make the following assumption.

Assumption 2.4. $\beta^+(\cdot, \alpha) \in C([0, a^\dagger], \mathbb{R}^{d \times d})$ for almost all $\alpha \in [0, a^\dagger]$.

Theorem 2.3.2. *Let Assumption 2.3 and Assumption 2.4 hold. Then $\left\| \widehat{\mathcal{H}}_N - \mathcal{H} \right\|_{Y \leftarrow Y} \rightarrow 0$ as $N \rightarrow \infty$.*

Proof. Let us observe that

$$\left\| \widehat{\mathcal{H}}_N - \mathcal{H} \right\|_{Y \leftarrow Y} \leq \left\| (\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{B}_+ \right\|_{Y \leftarrow Y_0} \cdot \left\| \widehat{\mathcal{M}}_N^{-1} - \mathcal{M}_-^{-1} \right\|_{Y_0 \leftarrow Y} \quad (2.3.6)$$

$$+ \left\| (\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{B}_+\mathcal{M}_-^{-1} \right\|_{Y \leftarrow Y} \quad (2.3.7)$$

$$+ \left\| \mathcal{B}_+ \right\|_{Y \leftarrow Y_0} \cdot \left\| \widehat{\mathcal{M}}_N^{-1} - \mathcal{M}_-^{-1} \right\|_{Y_0 \leftarrow Y}. \quad (2.3.8)$$

The term in (2.3.8) tends to zero as $N \rightarrow \infty$ thanks to Equation (6.4.1). As for (2.3.6) and (2.3.7), let us recall that for every $\psi \in Y_0$ we have

$$\left\| (\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{B}_+\psi \right\|_Y = \left| \left\| (\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{B}_+\psi \right\|_{a=0} \right| + \left\| ((\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{B}_+\psi)' \right\|_X. \quad (2.3.9)$$

The first term on the right-hand side of (2.3.9) tends to zero as $N \rightarrow \infty$ since $\mathcal{B}_+ Y_0 \subseteq Y$ ensures the convergence of the Lagrange interpolation at the Chebyshev zeros in the infinite-norm [101, Theorem 1]. As for the second term, Assumption 2.4 guarantees that $(\mathcal{B}_+ \psi)' \in C([0, a^+], \mathbb{C}^d)$, from which it follows that [125, Theorem 1]

$$\|(\mathcal{L}_{N-1} \mathcal{B}_+ \psi)' - (\mathcal{B}_+ \psi)'\|_X \rightarrow 0, \quad N \rightarrow \infty. \quad (2.3.10)$$

Since $\mathcal{M}_-^{-1}$ is compact thanks to Corollary 2.1.3, [100, Theorem 10.6] ensures that (2.3.7) tends to zero as $N \rightarrow \infty$. Finally, from the uniform boundedness principle [40, Theorem 2.2], we get

$$\sup_{\substack{N \in \mathbb{N} \\ N \geq 1}} \|(\mathcal{L}_{N-1} - \mathcal{I}_Y) \mathcal{B}_+\|_{Y \leftarrow Y_0} < \infty. \quad (2.3.11)$$

Hence, (2.3.6) tends to zero as $N \rightarrow \infty$ thanks to Equation (6.4.1). $\square$

2.3.2 Convergence of eigenvalues and eigenspaces

Theorem 2.3.3. *Let Assumption 2.3 and Assumption 2.4 hold. Let $\lambda \in \mathbb{C}$ be an isolated nonzero eigenvalue of $\mathcal{H}$ with finite algebraic multiplicity s and ascent l and let Δ be a neighborhood of λ such that λ is the sole eigenvalue of $\mathcal{H}$ in Δ . Then there exists $\bar{N}$ such that, for $N \geq \bar{N}$, $\hat{\mathcal{H}}_N$ has in Δ exactly m eigenvalues $\lambda_{N,i}$, $i = 1, \dots, s$, counting their multiplicities. Moreover,*

$$\max_{i=1, \dots, m} |\lambda_{N,i} - \lambda| = O(\varepsilon_N^{1/l})$$

where

$$\varepsilon_N := \|\hat{\mathcal{H}}_N - \mathcal{H}\|_{Y \leftarrow E_\lambda} \quad (2.3.12)$$

and E_λ is the generalized eigenspace of λ . Finally, for any $i = 1, \dots, s$ and for any eigenfunction $\psi_{N,i}$ of $\hat{\mathcal{H}}_N$ relevant to $\lambda_{N,i}$ such that $\|\psi_{N,i}\|_Y = 1$, we have

$$\text{dist}(\psi_{N,i}, \ker(\lambda \mathcal{I}_Y - \mathcal{H})) = O(\varepsilon_N^{1/l}),$$

where dist is the distance in the space Y between an element and a subspace.

Proof. The thesis follows from [45, Proposition 2.3 and Proposition 4.1]. $\square$

Now, we complete the analysis with error bounds under each of the following regularity conditions.

Assumption 2.5.

- (i) $\beta^+, \beta^- \in \text{Lip}^s([0, a^+]^2, \mathbb{R}^{d \times d})$ and $\delta \in \text{Lip}^s([0, a^+], \mathbb{R}^{d \times d})$ for some integer $s \geq 0$,
- (ii) $\beta^+, \beta^- \in C^\infty([0, a^+]^2, \mathbb{R}^{d \times d})$ and $\delta \in C^\infty([0, a^+], \mathbb{R}^{d \times d})$,
- (iii) β^+, β^-, δ are real analytic.

Corollary 2.3.4. *Let Assumption 2.3 and Assumption 2.5 hold. Let $\lambda, \lambda_{N,i}, i = 1, \dots, s, E_\lambda$ and ε_N be as in Theorem 2.3.3. Then*

$$\varepsilon_N = O(\rho_N),$$

where

$$\rho_N := \begin{cases} N^{-(s+1)} \log N & \text{under Assumption 2.5 (i),} \\ N^{-r} \log N & \text{for every integer } r \geq 1 \text{ under Assumption 2.5 (ii),} \\ p^{-N} \log N & \text{for some constant } p > 1 \text{ under Assumption 2.5 (iii).} \end{cases}$$

Proof. The Riesz theory for compact operators [100, section 3.1] ensures that the generalized eigenspaces of $\mathcal{H}$ have finite dimension. Hence, given a basis of E_λ , $\{\psi_{\lambda,i}\}_{i=1}^k$, where $k := \dim E_\lambda$, it is enough to show that

$$\max_{i=1,\dots,k} \|(\hat{\mathcal{H}}_N - \mathcal{H})\psi_{\lambda,i}\|_Y = O(\rho_N). \quad (2.3.13)$$

Then, the thesis will follow from Theorem 1.3.3. We start by observing that, from (2.2.4), (2.3.2)-(2.3.4), (2.3.6)-(2.3.8) and (2.3.11), we have

$$\|(\hat{\mathcal{H}}_N - \mathcal{H})\psi_{\lambda,i}\|_Y \leq C(\|\mathcal{J}(\mathcal{L}_{N-1} - \mathcal{I}_Y)\psi_{\lambda,i}\|_X \quad (2.3.14)$$

$$+ \|(\mathcal{L}_{N-1} - \mathcal{I}_X)\mathcal{W}(\mathcal{I}_X - \mathcal{W})^{-1}\psi_{\lambda,i}\|_X) \quad (2.3.15)$$

$$+ \|(\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{H}\psi_{\lambda,i}\|_Y, \quad (2.3.16)$$

for every $i = 1, \dots, k$, where

$$C := 2\|(\mathcal{I}_X - \mathcal{W})^{-1}\|_{X \leftarrow X} \left(\sup_{\substack{N \in \mathbb{N} \\ N \geq 1}} \|(\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{B}_+\|_{Y \leftarrow Y_0} + \|\mathcal{B}_+\|_{Y \leftarrow Y_0} \right).$$

Moreover, for $\mathcal{T} \in \{\mathcal{I}_Y, \mathcal{H}, \mathcal{W}(\mathcal{I}_X - \mathcal{W})^{-1}\mathcal{J}\}$, we have

(i) $\mathcal{T}\psi_{\lambda,i} \in \text{Lip}^{m+1,p}([0, a^\dagger], \mathbb{C}^{d \times d})$ under Assumption 2.5 (i),

(ii) $\mathcal{T}\psi_{\lambda,i} \in C^\infty([0, a^\dagger], \mathbb{C}^{d \times d})$ under Assumption 2.5 (ii),

(iii) $\mathcal{T}\psi_{\lambda,i}$ is analytic under Assumption 2.5 (iii).

Hence, we can bound the term on the right-hand side of (2.3.14) as follows

$$\|\mathcal{J}(\mathcal{L}_{N-1} - \mathcal{I}_Y)\psi_{\lambda,i}\|_X \leq a^\dagger \|(\mathcal{L}_{N-1} - \mathcal{I}_Y)\psi_{\lambda,i}\|_\infty,$$

and, from Theorem 1.1.6, Theorem 1.1.7 and Theorem 1.1.10 we get

$$\|(\mathcal{L}_{N-1} - \mathcal{I}_Y)\psi_{\lambda,i}\|_\infty \leq O((1 + \Lambda_{N-1})\mathcal{E}_{N-1}(\psi_{\lambda,i})) = O(\rho_N),$$

where Λ_{N-1} is the Lebesgue constant relevant to Θ_N , that under Assumption 2.3 is $O(\log N)$ [108, Theorem 4.2.1], and $\mathcal{E}_{N-1}(\cdot)$ is defined as in (1.1.1). The term in (2.3.15) can be bounded as

$$\|(\mathcal{L}_{N-1} - \mathcal{I}_X)\mathcal{W}(\mathcal{I}_X - \mathcal{W})^{-1}\psi_{\lambda,i}\|_X \leq a^\dagger \|(\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{W}(\mathcal{I}_X - \mathcal{W})^{-1}\psi_{\lambda,i}\|_\infty,$$

which, in turn, can be bounded as

$$\|(\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{W}(\mathcal{I}_X - \mathcal{W})^{-1}\psi_{\lambda,i}\|_\infty \leq O\left((1 + \Lambda_{N-1})\mathcal{E}_{N-1}(\mathcal{W}(\mathcal{I}_X - \mathcal{W})^{-1}\psi_{\lambda,i})\right) = O(\rho_N).$$

Finally, the term in (2.3.16) can be bounded as

$$\|(\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{H}\psi_{\lambda,i}\|_Y \leq \|(\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{H}\psi_{\lambda,i}\|_\infty + a^\dagger \|((\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{H}\psi_{\lambda,i})'\|_\infty.$$

For these, from Theorem 1.1.6, Theorem 1.1.7 and Theorem 1.1.10 we get

$$\|(\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{H}\psi_{\lambda,i}\|_\infty = O((1 + \Lambda_{N-1})\mathcal{E}_{N-1}(\mathcal{H}\psi_{\lambda,i})) = O(\rho_N),$$

and, from [108, Theorem 4.2.11] we get

$$\|((\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{H}\psi_{\lambda,i})'\|_\infty = O((1 + \Lambda_{N-1})\mathcal{E}_{N-2}((\mathcal{H}\psi_{\lambda,i})')) = O(\rho_N).$$

□

Remark 2.3.5. Under Assumption 2.5 (i), one can show that the convergence of $R_N = \rho(\mathcal{H}_N)$ to R gains one order compared to ρ_N , i.e., it has order $O((N^{-(s+2)} \log N)^{1/l})$. In fact, one can consider the compact operator

$$\mathcal{M}_-^{-1} \mathcal{B}_+ : Y \rightarrow D(\mathcal{M}_-),$$

for which the relation $\sigma_p(\mathcal{M}_-^{-1} \mathcal{B}_+) = \sigma(\mathcal{H})$ holds. Indeed, $\varphi_\lambda \in D(\mathcal{M}_-)$ is an eigenfunction of $\mathcal{M}_-^{-1} \mathcal{B}_+$ with relevant eigenvalue λ if and only if there exists an eigenfunction of $\mathcal{H}$ relevant to λ , $\psi_\lambda \in Y$, such that $\varphi_\lambda = \mathcal{M}_-^{-1} \psi_\lambda$. Consequently, we have $R = \rho(\mathcal{M}_-^{-1} \mathcal{B}_+)$.

Correspondingly, the matrices $\mathcal{M}_N^{-1} \mathcal{B}_N$ and $\mathcal{B}_N \mathcal{M}_N^{-1}$ are similar for $N \geq \bar{N}$, hence they have the same eigenvalues for every $N \geq \bar{N}$.

Thus one can investigate the convergence of the eigenvalues of $\mathcal{H}_N$ to those of $\mathcal{H}$ by investigating the convergence of the eigenvalues of $\mathcal{M}_N^{-1} \mathcal{B}_N$ to those of $\mathcal{M}_-^{-1} \mathcal{B}_+$. This can be done by proceeding as before. The operator $\mathcal{P}_{N,0} \mathcal{M}_N^{-1} \mathcal{B}_N \mathcal{R}_N : Y \rightarrow Y_{0,N}$ has the same nonzero eigenvalues with the same geometric and partial multiplicities of $\mathcal{M}_N^{-1} \mathcal{B}_N$ (see Proposition 1.3.1), and from (2.2.8) it can be expressed as $\widehat{\mathcal{M}}_N^{-1} \mathcal{B} \mathcal{L}_{N,0}$. Moreover, since

$$\text{Range}(\widehat{\mathcal{M}}_N^{-1}) \subset Y_{0,N},$$

Proposition 1.3.2 ensures that $\widehat{\mathcal{M}}_N^{-1} \mathcal{B} \mathcal{L}_{N,0}$ has the same nonzero eigenvalues with the same geometric and partial multiplicities, and the same eigenfunctions as the operator $\widehat{\mathcal{M}}_N^{-1} \mathcal{B}_+$. The norm convergence of $\widehat{\mathcal{M}}_N^{-1} \mathcal{B}$ to $\mathcal{M}_-^{-1} \mathcal{B}_+$ easily follows from Equation (6.4.1), and an analogous of Theorem 2.3.3 can be derived. The main difference is that, since the convergence order of the approximation error on the eigenvalue λ is driven by the interpolation error on $\mathcal{M}_-^{-1} \mathcal{B}_+ \varphi_\lambda$, which under Assumption 2.5 (i) has one more degree of smoothness compared to $\mathcal{H} \psi_\lambda$, we get that

$$|R_N - R| = O((N^{-(s+2)} \log N)^{1/l}).$$

Figure 2.5.1 (lower row) in Section 2.5 illustrates this behavior.

2.4 Implementation issues

Here we give an explicit description of the entries of the matrices $\mathcal{B}_N$ and $\mathcal{M}_N$. For the sake of simplicity, we restrict to the case $d = 1$. Thanks to the cardinal property of the Lagrange polynomials in (1.1.3), it is easy to see that the entries of the matrices are explicitly given by

$$\begin{aligned} [\mathcal{B}_N]_{ij} &= \int_0^{a_i} \int_0^{a^\dagger} \beta^+(\zeta, \alpha) \ell'_{0,j}(\alpha) \, d\alpha \, d\zeta \\ &\quad + \int_0^{a^\dagger} b^+(\alpha) \ell'_{0,j}(\alpha) \, d\alpha, \end{aligned} \quad i, j = 1, \dots, N, \quad (2.4.1)$$

and

$$\begin{aligned} [\mathcal{M}_N]_{ij} &= \ell'_{0,j}(a_i) - \int_0^{a_i} \delta(\alpha) \ell'_{0,j}(\alpha) \, d\alpha \\ &\quad - \int_0^{a_i} \int_0^{a^\dagger} \beta^-(\zeta, \alpha) \ell'_{0,j}(\alpha) \, d\alpha \, d\zeta \\ &\quad + \int_0^{a^\dagger} b^-(\alpha) \ell'_{0,j}(\alpha) \, d\alpha, \end{aligned} \quad i, j = 1, \dots, N. \quad (2.4.2)$$

When the integrals in (2.4.1) and (2.4.2) cannot be computed analytically, we approximate them via a quadrature formula. For the integrals in $[0, a^\dagger]$, we use the Fejer's first rule quadrature with

N nodes [139], and for the integrals in $[0, a_i]$, $i = 1, \dots, N$, we use the quadrature weights given by the i -th row of the inverse of the differentiation matrix [60]

$$[\mathcal{D}_N]_{ij} := \ell'_{0,j}(a_i), \quad i, j = 1, \dots, N.$$

In this case, the bounds in Theorem 2.3.4 are preserved under the following regularity conditions (see [53, p. 85] and [131]).

Assumption 2.6.

- (i) $b^+, b^- \in \text{Lip}^s([0, a^\dagger], \mathbb{R}^{d \times d})$ for some integer $s \geq 0$,
- (ii) $b^+, b^- \in C^\infty([0, a^\dagger], \mathbb{R}^{d \times d})$,
- (iii) b^+, b^- are real analytic.

Here we used a unique polynomial all over the age interval $[0, a^\dagger]$ as approximating function. Yet, in the presence of discontinuities in the model coefficients or in their derivatives, one can resort to a *piecewise* approach, i.e., using as approximation continuous functions which, restricted to subintervals of $[0, a^\dagger]$, are algebraic polynomials. The MATLAB codes available at <http://cdlab.uniud.it/software> used to make all the tests in Section 2.5 implement this piecewise alternative.

2.5 Numerical results

In this section, we experimentally validate the theoretical results in Section 2.3 and we illustrate some possible applications of the method. We apply the numerical method to some examples of linear age-structured models in the context of infectious disease dynamics, which are obtained from the linearization of a nonlinear model around an equilibrium, and that can be recast as in (2.1.1). The examples are chosen to cover a range of cases.

The first example is scalar, and is constructed to have explicit expressions for R and the associated eigenfunctions. For this model, we numerically illustrate the relation between the convergence order of the numerical approximation R_N of R , and the approximation error on the relevant eigenspaces, which in turn depends on the regularity of the (generalized) eigenfunctions through the smoothness of the model parameters, see Theorem 2.3.3, Corollary 2.3.4 and Remark 2.3.5.

The second example is two-dimensional, structured by infection/disease age, where the infection process is described by a boundary condition. We use it to analyze the effect of quadrature error, and to reflect on the interpretation of the birth processes.

The last example is again two-dimensional, but it is structured by demographic age, with horizontal and vertical transmission, and with piecewise C^∞ coefficients estimated from real data.

In the last two examples, analytic expressions for R are not available. Hence, the errors are computed with respect to reference values (obtained with $N = 150$).

The modeling details and the linearization around the equilibria are described in Appendix A.

Example 1 We consider the SIR model structured by demographic age, without vertical transmission, in (I.2.18). The linearization around the DFE of the equation for the infected individuals can be recast as in (2.1.1) by taking $d = 1$, and parameters

$$\beta(a, \alpha) = k(a, \alpha)w_0, \quad b(a) \equiv 0, \quad \delta(a) = -\gamma(a).$$

In particular, we take

$$k(a, \alpha) = \frac{1}{c}q(a), \quad w_0 = \frac{(a^\dagger - \alpha)}{a^\dagger}, \quad \gamma(a) \equiv \gamma,$$

where $a^\dagger, \gamma > 0$, q is a given function and, for any choice of q ,

$$c := \int_0^{a^\dagger} w_0(a) \int_0^a e^{-\gamma(a-\alpha)} q(\alpha) d\alpha da.$$

With this choice of the parameters, the basic reproduction number is exactly $R_0 = 1$, and is obtained in our framework by taking $\beta^+ = \beta$, $\beta^- \equiv 0$ and $b^+ = b^- \equiv 0$. Note that, in this case, $\mathcal{H}$ is a rank-one operator and the eigenfunction relevant to $R = R_0$ is explicitly known:

$$\psi(a) = \int_0^a q(s) ds, \quad a \in [0, a^\dagger].$$

Moreover,

$$\varphi(a) := \mathcal{M}_-^{-1} \psi(a) = \int_0^a e^{-\gamma(a-\alpha)} \psi(\alpha) d\alpha, \quad a \in [0, a^\dagger].$$

Figure 2.5.1 shows, for increasing N , the error $|R_N - R|$ and the error

$$\varepsilon_{\infty, N}(\psi) := |(\widehat{\mathcal{H}}_N - \mathcal{H})\psi|_{a=0}| + \|((\widehat{\mathcal{H}}_N - \mathcal{H})\psi)'\|_\infty,$$

which gives a bound on ε_N in (2.3.12), with $a^\dagger = \gamma = 1$, and for three different choices of q , namely $q(a) = e^{-2a}$ (analytic, upper row, left), $q(a) = e^{-(x-0.5)^{-2}}(x-0.5)^{-2}\chi_{[0.5, a^\dagger]}(a)$ (C^∞ , upper row, right) and $q(a) = (0.5 - a)^2|0.5 - a|$ (Lip^2 , lower row). The infinite norm is estimated by computing the maximum absolute value over a mesh of 1000 equidistant points in $[0, a^\dagger]$.

In Figure 2.5.1, upper row, we observe infinite convergence order, being the relevant eigenfunction ψ either analytic or C^∞ , which confirms the validity of Corollary 2.3.4 under Assumption 2.5 (ii) and (iii), respectively.

The lower row of Figure 2.5.1 shows order 4 for the approximation error on R (left and right), order 3 for $\varepsilon_{\infty, N}(\psi)$ (left), and order 4 for the error $\|((\widehat{\mathcal{M}}_N^{-1} - \mathcal{M}_-^{-1})\mathcal{B}\varphi)'\|_\infty$ (right), in accordance with Remark 2.3.5.

Remark 2.5.1. In real-world applications, both $a^\dagger$ and γ may be large. For instance: in a model for human populations structured by demographic age, one may have $a^\dagger = 75$ (yr) (or larger), while in epidemiology one may have $\gamma = 30$ (yr^{-1}) for diseases that last less than 10 days on average. In this case, the magnitude of the recovery rate γ and the length of the age interval $a^\dagger$, may affect the approximation error on R . Indeed, from the proof in Section 2.3, it is clear that the error on R is related to the interpolation error on the exponential function $e^{-\gamma a}$ in the operator $\mathcal{M}_-^{-1}$, which depends on the derivative of the function (whose norm increases with γ) and on the length of the interval. See for instance Example 3.

Example 2 We consider an SAIR model inspired by [90], see also [22, Section 9.5.3]. We assume that, upon infection, the individuals enter an asymptomatic phase, which is characterized by the infection age $a_1 \in [0, a_1^\dagger]$. Then, they can either recover without developing symptoms with rate $\gamma_I(a_1)$, or they can develop symptoms with rate $\sigma(a_1)$. The symptomatic phase is characterized by the disease age, $a_2 \in [0, a_2^\dagger]$, i.e., by the time since the onset of symptoms. Then, the symptomatic individuals recover with rate $\gamma_I(a_2)$. In the following we assume for simplicity that $a_1^\dagger = a_2^\dagger$. Hence, with abuse of notation, we denote both a_1 and a_2 by a .

Let $A(t, a)$ denote the density of asymptomatic individuals at time $t \geq 0$ and infection age $a \in [0, a^\dagger]$, and let $I(t, a)$ denote the density of symptomatic individuals at time $t \geq 0$ and disease age $a \in [0, a^\dagger]$. The linearization around the DFE reads (see Appendix A.1)

$$\begin{cases} \mathcal{D}A(t, \tau) = -(\sigma(a) + \gamma_A(a))A(t, a), \\ \mathcal{D}I(t, \tau) = -\gamma_I(a)I(t, a), \\ A(t, 0) = \int_0^{a^\dagger} (b_A(a)A(t, a) + b_I I(t, a)) da, \\ I(t, 0) = \int_0^{a^\dagger} \sigma(a)A(t, a) da, \end{cases} \quad (2.5.1)$$

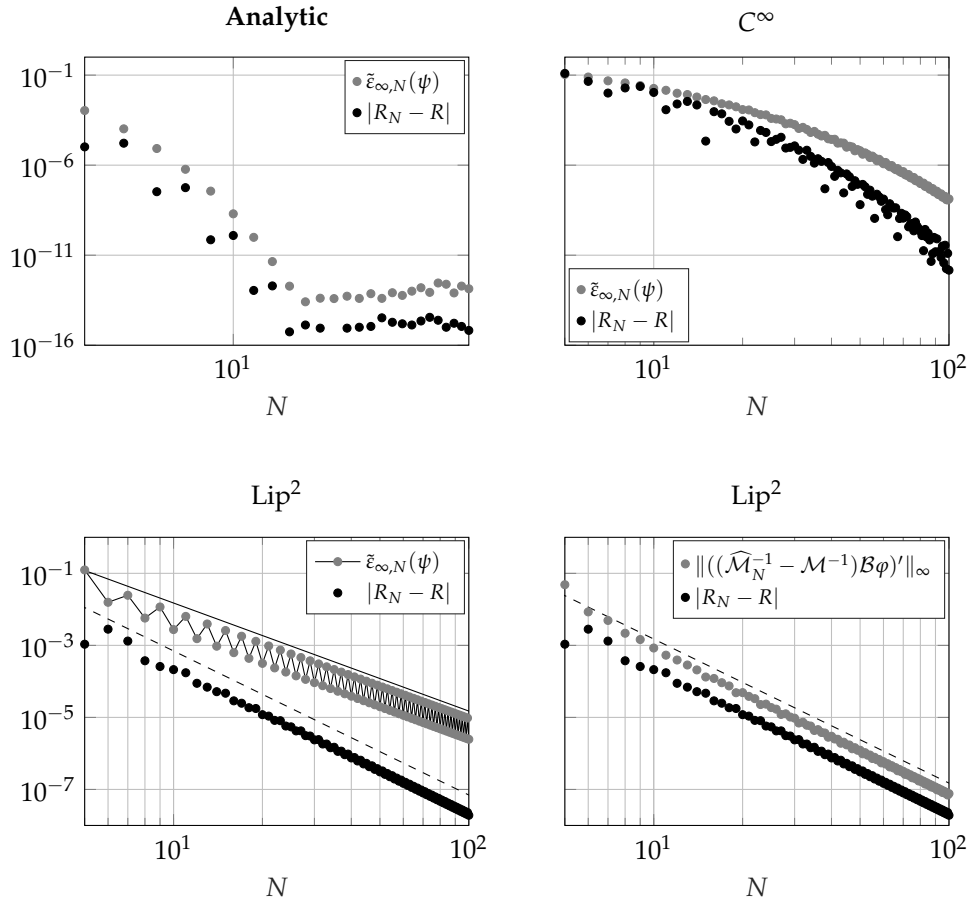


Figure 2.5.1: Upper row: Example 1 with $q(a) = e^{-2a}$ (analytic, left) and $q(a) = e^{-(x-0.5)^{-2}}(x - 0.5)^{-2}\chi_{[0.5, a^+]}(a)$ (C^∞ , right), with $a^+ = \gamma = 1$. Log-log plot for increasing N of the approximation error on R (black) and the error $\tilde{\epsilon}_{\infty,N}(\psi)$ (gray). Infinite order of convergence is observed in both panels, in agreement with Corollary 2.3.4. Lower row: Example 1 with $q(a) = (0.5 - a)^2|0.5 - a|$ (Lip^2) and $a^+ = \gamma = 1$. Left: log-log plot for increasing N of the approximation error on R (black) computed as $\rho(\mathcal{H}_N)$, and the error $\tilde{\epsilon}_{\infty,N}(\psi)$ (gray). Convergence of order 4 and order 3 is observed for $|R_N - R|$ and $\tilde{\epsilon}_{\infty,N}(\psi)$, respectively. Right: log-log plot for increasing N of the approximation error on R (black) computed as $\rho(\mathcal{M}_N^{-1}\mathcal{B}_N)$, and the error $\|((\widehat{\mathcal{M}}_N^{-1} - \mathcal{M}_N^{-1})\mathcal{B}\phi)'\|_\infty$ (gray). Convergence of order 4 is observed for all the errors, in agreement with Remark 2.3.5. The dashed lines have slope -4 , while the solid line has slope -3 . Original figure from [55].

where $b_I(a)$ is the per capita infection rate at infection age a in the asymptomatic phase, and $b_I(A)$ is the infection rate at disease age a in the symptomatic phase.

(2.5.1) can be recast in (2.1.1) by taking $d = 2$ and

$$\beta(a, \alpha) \equiv 0_{\mathbb{R}^{2 \times 2}}, \quad b(a) = \begin{pmatrix} b_A(a) & b_I(a) \\ \sigma(a) & 0 \end{pmatrix}, \quad \delta(a) = \begin{pmatrix} -(\sigma(a) + \gamma_A(a)) & 0 \\ 0 & -\gamma_I(a) \end{pmatrix}.$$

We take $a^\dagger = 14$ (days), $\gamma_A \equiv 0$ in $[0, \tau_1^\dagger]$ (days⁻¹), $\gamma_I \equiv 0.45$ in $[0, \tau_2^\dagger]$ (days⁻¹), $\sigma \equiv 0.676$ (days⁻¹), and we vary b_A and b_I .

Note that, for this model, we can compute two different reproduction numbers corresponding to different interpretations of “birth” [50, 90]. For the choice

$$b^+ = \begin{pmatrix} b_A & b_I \\ 0 & 0 \end{pmatrix}, \quad b^- = \begin{pmatrix} 0 & 0 \\ \sigma & 0 \end{pmatrix},$$

R is interpreted as R_0 , as we consider all new infections coming from asymptomatic and symptomatic individuals as birth processes, and consider the development of symptoms as transition process. On the other hand, since asymptomatic individuals are invisible from the point of view of the public health system (in the absence of other interventions like test-and-trace and asymptomatic testing), we may be interested in studying the effectiveness of control measures to the class of symptomatic individuals only (e.g., isolation upon symptoms) [90]. In this case, we interpret the entrance in the class of symptomatic individuals as birth, while the asymptomatic phase is interpreted as transition [17]. This leads to the choice

$$b^+ = \begin{pmatrix} 0 & 0 \\ \sigma & 0 \end{pmatrix}, \quad b^- = \begin{pmatrix} b_A & b_I \\ 0 & 0 \end{pmatrix},$$

for which R correspond to the state reproduction number of symptomatic individuals, T_S [90]

We use this model to investigate the effect of quadrature in the convergence order of the approximation R_N of R and the relation between R_0 and T_S . Note that, for both choices of b^+ and b^- , the eigenfunction relevant to R is constant. Figure 2.5.2 shows the behavior of the approximation error on $R = R_0$ and $R = T_S$ for $b_A \equiv 0.665$ and $b_I(a) \equiv b_0$ (left) and $b_I(a) = b_0 \sqrt{a} e^{-a}$ (right), with $b_0 = 0.7$. Infinite order of convergence is observed in the right panel, being b_I constant (and hence, analytic). As for the right panel, finite order of convergence is observed, consistently with the fact that b_I' is unbounded at $a = 0$.

Figure 2.5.3 is obtained by fixing $b_I \equiv 0.7$ (yr⁻¹), and varying b_A/σ . As expected, R_0 and T_S have different values in general, but the same threshold at 1. Additionally, Figure 2.5.3 illustrates another important theoretical property: the state reproduction number T_S is finite (and well defined) only when the spectral radius of the NGO relevant to asymptomatic transmission is smaller than one. When the latter becomes larger than one, then asymptomatic individuals alone can sustain the epidemic, hence interventions that are targeted to only symptomatic individuals are not sufficient to control its spread. This feature is reflected in the behavior of T_S , which tends to infinity and becomes not well defined.

Example 3 We consider a demographic age-structured model inspired by [2] for the spread of congenital rubella syndrome in the United Kingdom.⁷ The model definition and the derivation of the DFE and the corresponding linearization are described in detail in Appendix A.2.

Note that, although in the literature, the term control reproduction number is typically used in the presence of interventions, here, for simplicity, we refer to R_0 (or to T when denoting the type reproduction number) even in the presence of vaccinations.

⁷Rubella is also known as three-day measles, and is an acute and contagious viral infection that can be vertically transmitted [61]. It is not particularly severe in children and adults, but infection during pregnancy can result in the congenital rubella syndrome (CRS), which can lead, among others, to fetal death [136]. The probability of passing the virus to the fetus in the first trimester of pregnancy is estimated to be 90% [136]. As, in general, there are no treatment for Rubella, vaccination policies plays a fundamental role in controlling the spread of the disease [2, 3, 4].

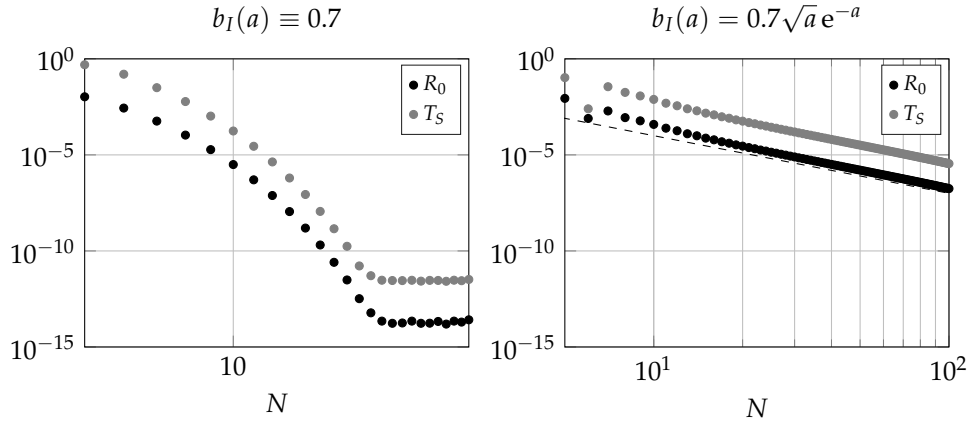


Figure 2.5.2: Example 2 with $b_A = 0.665$, $b_I(a) \equiv b_0$ (left) and $b_I(a) = b_0\sqrt{a}e^{-a}$ (right), with $b_0 = 0.7$. Log-log plot for increasing N of the approximation error on $R = R_0$ (black) and $R = T_S$ (gray). Left: infinite convergence order is observed. The reference values are $R_0 \approx 0.985453121496726$ and $T_S \approx 0.709490732440074$. Right: finite convergence order occurs. The reference values are $R_0 \approx 1.105184144018464$ and $T_S \approx 3.100985953765218$. The slope of the dashed line is -3 .

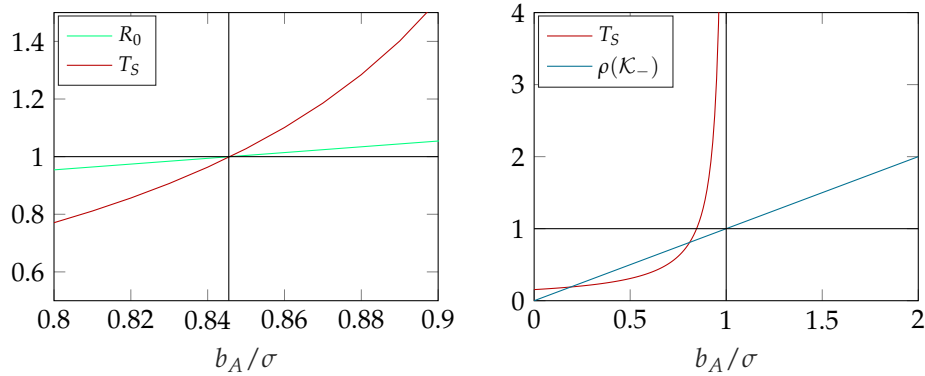


Figure 2.5.3: Example 2. Left: R_0 and T_S as functions of b_A/σ . Right: T_S and the spectral radius of the NGO relevant to the asymptomatic individuals as functions of b_A/σ . Both figures are obtained with $b_I = 0.7$ and $N = 50$. Original figure from [54].

Let $e(t, a)$ and $i(t, a)$ denote the density (divide by the age-density of the host population) of exposed (not infectious) and infectious individuals, respectively, at time $t \geq 0$ and demographic age $a \in [0, a^+]$, and let $s^*(a)$ denote the density of susceptible individuals at equilibrium, which is determined by the rate of loss of protection provided by maternal antibodies η and the vaccination rate ν (see Appendix A.2 for more details). The linearization around the DFE reads as follows:

$$\begin{cases} \mathcal{D}e(t, a) = s^*(a) \int_0^{a^+} \Pi(\alpha) k(a, \alpha) i(t, \alpha) d\alpha - \sigma e(t, a), \\ \mathcal{D}i(t, a) = \sigma e(t, a) - \gamma i(t, a), \\ e(t, 0) = q \int_0^{a^+} f(a) \Pi(a) i(t, a) da, \\ i(t, 0) = 0, \end{cases} \quad (2.5.2)$$

for $t \geq 0$ and $a \in [0, a^+]$, where σ is the rate of acquisition of infectiousness, γ is the recovery rate

from the infectious period, $k(a, \alpha)$ is the transmission rate between infectious individuals of age α and susceptible individuals aged a , $\Pi(a)$ is the survival probability in $[0, a^\dagger]$, $f(a)$ is the per capita birth rate, and q is the proportion of vertically infected newborns.

(2.5.2) can be recast in (2.1.1) by taking $d = 2$ and

$$\beta(a, \alpha) = \begin{pmatrix} 0 & s^*(a)\Pi(\alpha)k(a, \alpha) \\ 0 & 0 \end{pmatrix}, \quad b(a) = \begin{pmatrix} 0 & \theta f(a)\Pi(a) \\ 0 & 0 \end{pmatrix}, \quad \delta(a) = \begin{pmatrix} -\sigma & 0 \\ \sigma & -\gamma \end{pmatrix}.$$

Note that, for this model we can compute three reproduction numbers: the basic reproduction number R_0 for $\beta^+ = \beta$, $\beta^- \equiv 0$, $b^+ = b$, $b^- \equiv 0$; the type reproduction number for horizontal transmission T_H for $\beta^+ = \beta$, $\beta^- \equiv 0$, $b^+ \equiv 0$, $b^- = b$; and the type reproduction number for vertical transmission T_V for $\beta^+ \equiv 0$, $\beta^- = \beta$, $b^+ = b$, $b^- \equiv 0$.

In the following we assume $a^\dagger = 75$ (yr), $\eta = 4$ (yr⁻¹), $\sigma = 34.76$ (yr⁻¹), $\gamma = 31.74$ (yr⁻¹), $\Pi(a) \equiv 1$, $f(a) \equiv 1/a^\dagger$ (yr⁻¹), $q = 0.9$, and we vary $\nu \geq 0$. As for k , following [2], we assume that the transmission rate k is piecewise constant among six age groups,⁸ i.e., given $0 = \bar{a}_0 < \bar{a}_1 < \dots \bar{a}_6 = a^\dagger$,

$$k(a, \alpha) \equiv k_{ij} \quad \text{for} \quad (a, \alpha) \in [\bar{a}_{i-1}, \bar{a}_i) \times [\bar{a}_{j-1}, \bar{a}_j), \quad i, j = 1, \dots, 6, \quad (2.5.3)$$

so that we can estimate it from existing data using the well-known procedure of [4, Appendix A] (we recall i in Appendix A.2 for the reader's convenience). To do so, we consider force of infection data from two different datasets: one for the South East of England in 1980 (case a) and one for Leeds in 1978 (case b), as summarized in Table A.2.1. In particular, the datasets fix the age division as follow: $\bar{a}_1 = 5$, $\bar{a}_2 = 10$, $\bar{a}_3 = 15$, $\bar{a}_4 = 20$, and $\bar{a}_5 = 30$ (yr).

The piecewise form in (2.5.3) gives us a *Who Acquires Infection From Whom* (WAIFW) matrix $(k_{ij})_{i,j=1,\dots,6}$, which collects the contact rates between different age groups. We consider the followig form of the WAIFW, and we refer to [2, 4] for other possible choices

WAIFW

Age class	1	2	3	4	5	6
1	k_1	k_1	k_3	k_4	k_5	k_6
2	k_1	k_2	k_3	k_4	k_5	k_6
3	k_3	k_3	k_3	k_4	k_5	k_6
4	k_4	k_4	k_4	k_4	k_5	k_6
5	k_5	k_5	k_5	k_5	k_5	k_6
6	k_6	k_6	k_6	k_6	k_6	k_6

The estimated values of k_{ij} are illustrated in Figure 2.5.4 and reported in Table A.2.1. See Appendix A.2 for more details on the parameters and data used for the estimation. To conveniently deal with the lack of regularity given by the piecewise constant choice of the parameters, in this section we resort to the piecewise version of the method along different age subintervals. Yet, note that the length of the interval $[\bar{a}_5, \bar{a}_6] = [30, 75]$ may affect the convergence order of our method. Hence, in the following we split also this interval by fixing the division at $a = 40$, $a = 50$ and $a = 60$. Figure 2.5.5 shows the comparison between the errors of approximation on $R = R_0$ for the nonpiecewise and the piecewise version of the method on the interval $[30, 75]$. Infinite order of convergence is observed for the piecewise approach. On the other hand, larger values of N are required in the nonpiecewise approach to obtain errors lower than 10^{-6} , which is in accordance with Remark 2.5.1. Now, we compute the basic reproduction number, R_0 , and the type reproduction number for horizontal transmission, T_H , for different choices of the vaccination rate ν . The results are collected in Table 2.5, rounded to four decimal digits. The computed values of R_0 and T_H are never substantially different (we can appreciate some differences only at the third decimal digit), which suggests that, for these data-informed parameter values, vertical transmission has a smaller effect on the epidemic spread compared to horizontal transmission. As in Example 2, the

⁸Here we use the IPDE form of (2.5.2) to illustrate the use of the piecewise version of the numerical method. Yet, we mention that, under the assumption that all the coefficients of the model are piecewise constant among different age-groups, one can “reduce” an age-structured model like (2.5.2) to a large system of ODEs by integrating the age-state over different age-intervals [5, 79]. Note that this does not hold in general for other choices of the parameters.

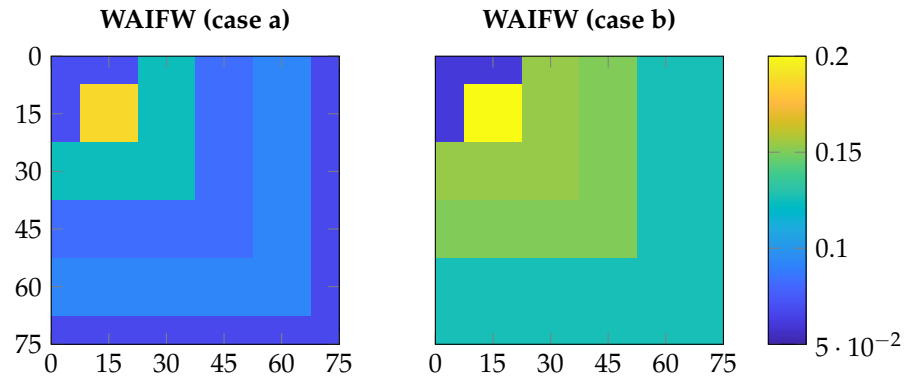


Figure 2.5.4: Example 3. Estimated WAIFW matrices (k_{ij}) for case a (upper row) and case b (lower row). Numerical values reported in Table A.2.1. Original figure from [54].

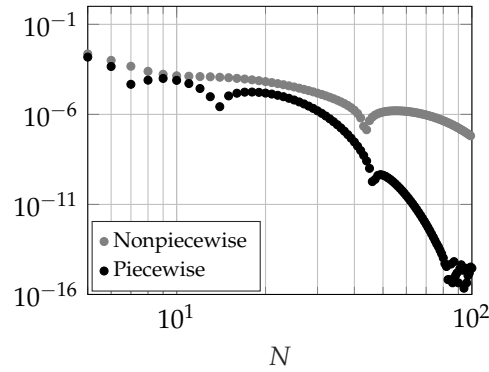


Figure 2.5.5: Example 3. Log-log plot of the approximation error for increasing N on $R = R_0$ using a unique polynomial over the age subinterval $[30, 75]$ (gray) and using a piecewise approach over the age subinterval (black) for case a with $\nu = 0.08$ (yr^{-1}). The reference value $R_0 \approx 1.176079226989241$ is obtained with the piecewise approach with $N = 150$.

v	case a		case b	
	R_0	T_H	R_0	T_H
0	5.4206	5.4223	9.5110	9.5110
0.05	1.7240	1.7242	2.5013	2.5018
0.09	1.0580	1.0580	1.3776	1.3777
0.10	0.9588	0.9588	1.2236	1.2237
0.15	0.6317	0.6316	0.7449	0.7448

Table 2.5.1: Example 3. R_0 and T_H for different values of the vaccination rate v for case a (left column) and case b (right column).

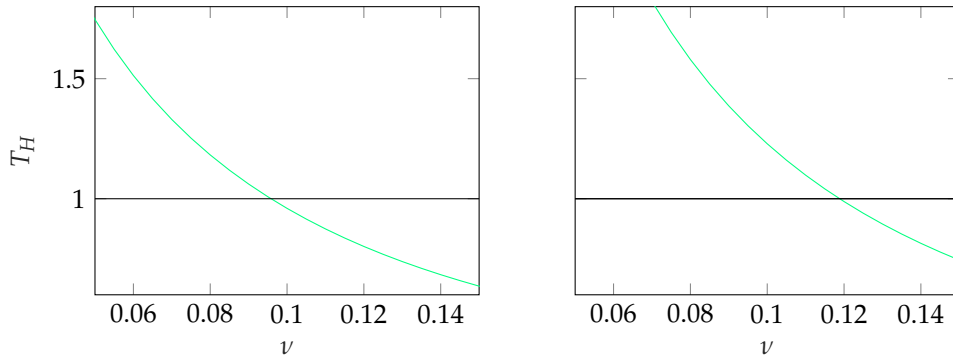


Figure 2.5.6: Example 3. T_H as a function of v for different choices of the WAIFW-matrix, case a (left) and case b (right) according to Table A.2.1. Original figure from [54].

values in Table 2.5, also numerically illustrate the known relations between T_H and R_0 , namely $0 < T_H < R_0 < 1$ and $1 < R_0 < T_H$ [86]. Both R_0 and T_H decrease for increasing v , which is in accordance with the fact that a larger vaccination rate reduces the density of the susceptible population at equilibrium, see Figure 2.5.6

Finally, Figure 2.5.7 shows how the type reproduction number for vertical transmission T_V depends on v (left) and q (right) for case b. T_V is a decreasing function of v and linearly increases with q (the ad hoc values of v are chosen for illustrating purposes).

2.6 Reproduction numbers vs spectral bound

In the previous sections, we focused on the numerical computation of the reproduction numbers relevant to (2.1.1). Yet, in view of investigating stability of equilibria, one may also consider the computation of the dominant part of the spectrum of the infinitesimal generator relevant to (2.1.1), $\mathcal{A}^X: D(\mathcal{A}^X) \subseteq X \rightarrow X$, which is defined as

$$\mathcal{A}^X \phi(a) := -\phi'(a) + \int_0^{a^+} \beta(a, \alpha) \phi(\alpha) d\alpha + \delta(a) \phi(a), \quad a \in [0, a^+],$$

where

$$D(\mathcal{A}^X) := \left\{ \phi \in Y \mid \phi(0) = \int_0^{a^+} b(a) \phi(a) da \right\}. \quad (2.6.1)$$

In fact, the well known relation $\text{sign}(s(\mathcal{A}^X)) = \text{sign}(R - 1)$, for R a reproduction number of (2.1.1), ensures that the two approaches are equally informative on the stability of the null equilibrium. The problem of computing the spectrum of $\mathcal{A}^X$ is again infinite-dimensional, hence numerical methods are typically required in practical computations [34, 35, 38].

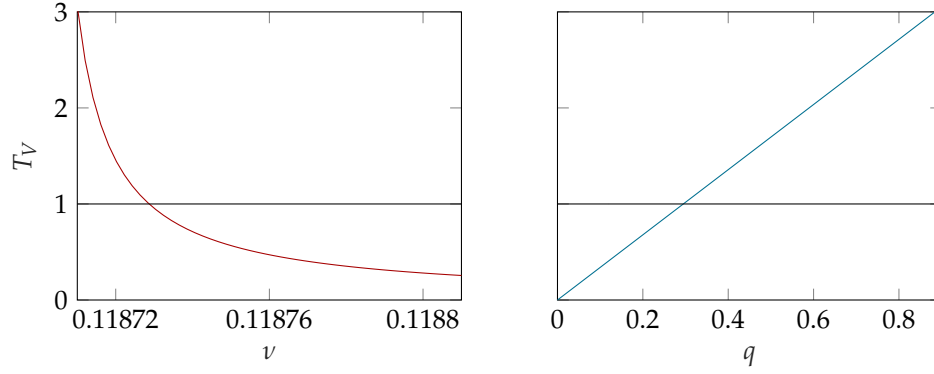


Figure 2.5.7: Example 3. T_V as a function of v (left) and q (right) for case b with WAIFW1. When not varied, the parameters are $v = 0.11871$ and $q = 0.9$. Original figure from [54].

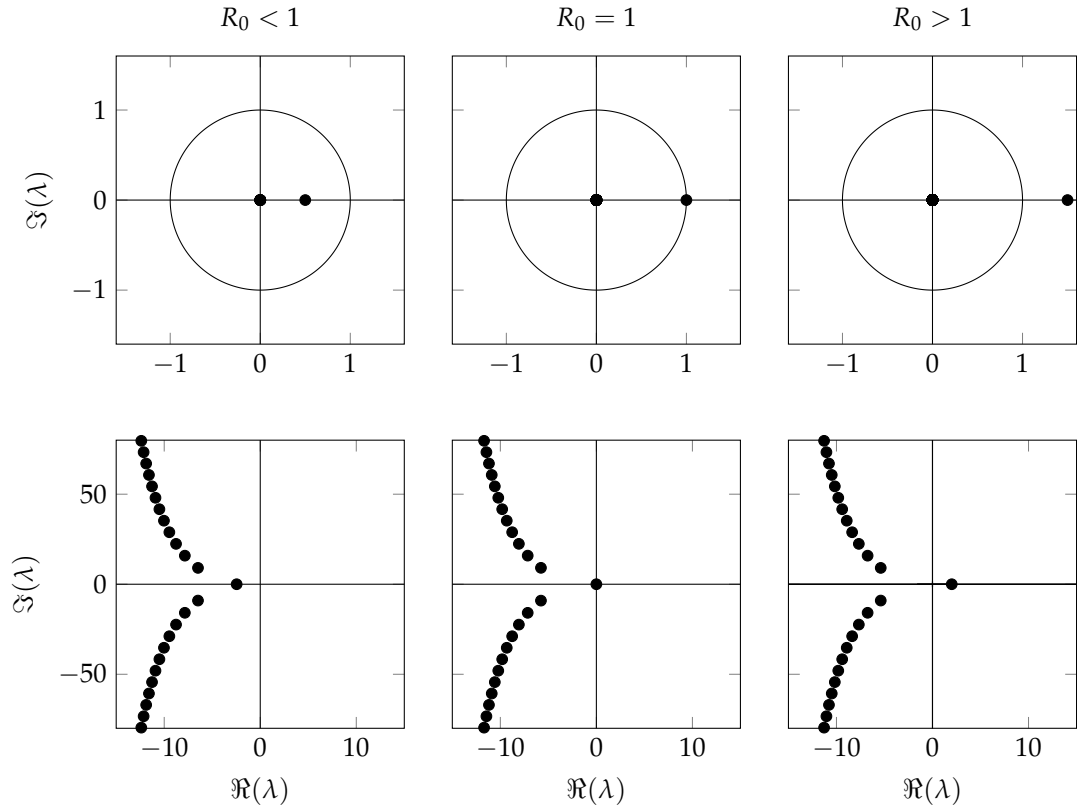


Figure 2.6.1: Example 1 with $k(a, \alpha) = \frac{R_0}{c} e^{-2a}$. Computed spectra in the complex plane of $\mathcal{H}$ (upper row) and $\mathcal{A}^Y$ (lower row) for $R_0 < 1$, $R_0 = 1$ and $R_0 > 1$ with $N = 100$.

Aim of this section, is to show that the method presented in Section 2.2 can be adapted to numerically approximate $\sigma(\mathcal{A}^X)$. Indeed, let us note that $\mathcal{A}^X$ has the same spectrum as the operator $\mathcal{A}^Z := \mathcal{B}_+^Z - \mathcal{M}_-^Z$ [107, Section 4.5], which in turn has the same spectrum of $\mathcal{A}^Y := \mathcal{B}_+^Y - \mathcal{M}_-^Y$. Then, the spectrum of the latter can be approximated through the spectrum of the matrix $\mathcal{A}_N := \mathcal{B}_N - \mathcal{M}_N$, where $\mathcal{B}_N, \mathcal{M}_N$ are defined as in (2.2.1). Hence, by recombining the same discretization in a different way, we can obtain a method to approximate also the spectrum of $\mathcal{A}^X$. This makes the approach presented in this chapter more flexible with respect to previous methods [23, 30, 38]. Deriving a convergence proof for this method is not easy, if not under special assumptions like the separable mixing (i.e., $\beta(a, \alpha) = \beta_1(a)\beta_2(\alpha)$), as in general one cannot derive a characteristic equation as in [23, 30, 38] (in the latter in fact, the authors consider the separable mixing assumption). We believe that a proof of convergence may be derived by suitably adapting the arguments used in Section 2.2.2 and Section 2.3. To conclude, we show an application of the method presented in this section. We consider (2.1.1) with the same parameters used in Example 1, but for k that we assume to be $k(a, \alpha) = \frac{R_0}{c} e^{-2a}$. The numerical results are shown in Figure 2.6.1, which illustrate the already mentioned relation between R_0 and $s(\mathcal{A}^X)$.

3

Time-periodic models: a hidden structure

The aim of this chapter is to introduce a general and efficient numerical method to approximate R_0 in time periodic epidemic (and, more in general, population) models formulated as ODEs. The content of this chapter is mainly taken from the work in preparation by the author, D. Breda and J. Ripoll [24].

Many diseases show seasonal fluctuations. For example, in vector transmitted diseases, fluctuations in the vector population may be due to changes in the temperature and humidity, or for viral infectious diseases like measles, the seasonality in the contact rates may be due to changes in the school system [57, Section 7.9, 98, Chapter 5].

The generalization of the definition of R_0 (and other reproduction numbers) to periodic models is not immediate, as in the generational interpretation of the infection process (or of population growth in general) considered in the definition of [58], it does not matter when individuals are generated. However, in periodic systems the moment in which an individual has been generated actually matters [57, Section 7.9].

There have been many attempts to generalize the definition of R_0 to models including seasonality, see for example [74, 75, 85] and references therein. Probably, the most recognized extension of R_0 to the time-periodic case is that of [12], which was derived starting from the theory of periodic renewal equations [126].

In this definition, the individuals are explicitly structured by the instant in the time period interval at which they are generated. This corresponds to declare, in the general definition of Section I.3.1, that the instant of birth/infection is part of the h -state. As a result, the NGO becomes an infinite-dimensional operator acting on a space of periodic functions, even though the state space of the system is finite-dimensional [57, Section 7.9].

Consequently, the analytical computation of R_0 in the periodic case is typically not achievable in practice, if not under some appropriate conditions [132], and numerical approximations are again necessary.

Numerical methods to compute R_0 in this framework have been proposed in [9, 111, 113, 132]. These methods are based either on the discretization of the NGO or on the solution of an associated nonlinear equation, see [57, Section 7.9].

In this chapter, we propose an alternative and general method to approximate R_0 in this framework. We take advantage of the characterization of the NGO via its connection with the theory of evolution semigroups [48, 89, 128]. Thanks to this, inspired by Chapter 2, we identify birth and transition operators, and we discretized them via pseudospectral collocation. We propose two approaches: one based on Fourier collocation, which uses trigonometric polynomials as approximating functions, and one based on Chebyshev collocation, which uses algebraic polynomials instead.

The two approaches require different proofs of convergence. For the Fourier method, the convergence is investigated using the well-established spectral approximation theory of [45], and to prove the norm convergence of the discretized operators, we use interpolation error bounds in

the L^1 -norm [108, p. 221, Theorem 3.2.9]. For the Chebyshev method, the convergence is proved by adapting the results of [31] and by using interpolation error bounds in weighted spaces [108, p. 271, eq. 4.33 and p. 274, Theorem 4.3.2].

For both methods, we prove that the convergence order of the approximating reproduction number depends on the regularity of the model coefficients.

The content of the chapter is organized as follows. In Section 3.1, we introduce a prototype linear model of ODEs with time-periodic coefficients. With reference to this model, we illustrate the definition of R_0 in the periodic case and its connection with the theory of evolution semigroups. The section is concluded by the proof of compactness of the NGO. In Section 3.2, we present the numerical methods. The convergence proofs are presented in Section 2.3. In Section 3.4, we give details about the implementation of the method. Finally, in Section 2.5 we present numerical results and we discuss the extension of the method to the computation of the type reproduction number.

3.1 The definition of R_0

In this section, we consider a prototype linear system of ODEs describing the dynamics of a vector population evolving in a periodic environment according to linear birth/infection and transition processes (death, recovery, change of status). With reference to this prototype model and following [12, 85, 86, 89, 128, 132] and [57, Section 7.9], we recall the definition of the basic reproduction number and other relevant reproduction numbers in the time-periodic setting.

Let $\tau > 0$ denote the time-period. For $u(t) \in \mathbb{R}^d$, $t \geq 0$ and d a positive integer, consider the model

$$\begin{cases} u'(t) = B(t)u(t) - M(t)u(t), & t \geq s, \\ u(s) = u_0 \in \mathbb{R}^d, & s \in \mathbb{R}, \end{cases} \quad (3.1.1)$$

where $B, M: \mathbb{R} \rightarrow \mathbb{R}^{d \times d}$ are τ -periodic functions accounting for birth/infection and transition, respectively, and satisfy the following requirements.

Assumption 3.1.

- (i) $B \in L^\infty_\tau(\mathbb{R}, \mathbb{R}^{d \times d})$ is nonnegative,
- (ii) $M \in L^\infty_\tau(\mathbb{R}, \mathbb{R}^{d \times d})$, and $-M$ generates a family of evolution linear operators $\{V(t, s)\}_{t, s \in \mathbb{R}}$, where $V(t, s): \mathbb{R}^d \rightarrow \mathbb{R}^d$ satisfies [128]
 - $V(s, s) = \mathcal{I}_{\mathbb{R}^d}$ for every $s \in \mathbb{R}$,
 - $V(t, r)V(r, s) = V(t, s)$ for every $t \geq r \geq s$,
 - for all $x \in \mathbb{R}^d$, $V(t, s)x$ is a continuous function of (t, s) , $t \geq s$,
 - $V(t, s)$ is nonnegative for every $t \geq s$,
 - $\omega(V) < 0$, where¹

$$\omega(V) := \inf \{ \tilde{\omega} \geq 1 \mid \exists C \geq 1 \text{ such that } \|V(t + s, s)\|_{\mathbb{R}^d \leftarrow \mathbb{R}^d} \leq C e^{\tilde{\omega} t}, \forall s \in \mathbb{R}, t \geq 0 \}.$$

Since we are interested in the spectral theory, we extend our attention to complex vectors. With reference to [57, Section 7.9], we derive an expression for the NGO starting from the general definition in (I.3.1). To do so, let us recall that in this framework, the individuals are characterized by the instant in the time-period interval $[0, \tau]$ at which they are generated. Hence, the NGO in (I.3.1) becomes

$$(\mathcal{K}\phi)(t) := \int_0^\tau k(t, s)\psi(s) ds, \quad t \in [0, \tau], \quad (3.1.2)$$

¹Note that, from the τ -periodicity of M , we have $V(t + \tau, s + \tau) = V(t, s)$ for all $t \geq s$. Hence, the condition $\omega(V) < 0$ is equivalent to $\rho(V(t + \tau, t)) < 1$ for every $t \in \mathbb{R}$ [128].

where ψ is an $\mathbb{R}^d$ -valued periodic function that represents the density of the distribution with respect to the time at birth of individuals. To determine the kernel $k(t, s)$, we recall that

$$k(t, s) = \int_0^\infty \mathfrak{A}(t, s, a) da, \quad (3.1.3)$$

where $\mathfrak{A}(t, s, a)$ denotes the rate at which an individual that was generated at time s in the cycle produces, a units of time after its generation, secondary cases with state-at-birth t . From this definition, one immediately obtains that

$$\mathfrak{A}(t, s, a) \neq 0 \iff t = s + a \pmod{\tau}.$$

Hence, we must have

$$\mathfrak{A}(t, s, a) = B(s + a)V(s + a, s)\delta_0(t - [s + a]), \quad (3.1.4)$$

where $[s + a] = s + a \pmod{\tau}$, and δ_0 denote the Dirac delta measure concentrated at 0. Note in fact that $V(s + a, s)$ gives the probability that an individual is still fertile/infectious at time $s + a$ knowing that it was fertile/infectious at time s . Inserting (3.1.4) in (3.1.3), we get

$$k(t, s) = \int_0^\infty \mathfrak{A}(t, s, a) da = B(t) \begin{cases} \sum_{j=0}^\infty V(t, s - jp), & t > s, \\ \sum_{j=1}^\infty V(t, s - jp), & t < s. \end{cases}$$

Eventually, substituting $k(t, s)$ in (4.3.1), one obtains²

$$(\mathcal{K}\psi)(t) = B(t) \int_0^\infty V(t, t - s)\psi(t - s) ds, \quad t \in [0, \tau], \quad (3.1.5)$$

which is a positive operator acting on the space $X := L_\tau^1(\mathbb{R}, \mathbb{C}^d)$ equipped with the norm³

$$\|\psi\|_X = \int_0^\tau |\psi(t)| dt.$$

The basic reproduction number is then characterized as the spectral radius of (3.1.5), i.e.,

$$R_0 := \rho(\mathcal{K}). \quad (3.1.6)$$

In Section 2.1.1, we prove that under Assumption 3.1 the operator in (3.1.5) is compact. Hence, if $R > 0$, then it is a dominant real eigenvalue, with an associated nonnegative eigenfunction [99].

Remark 3.1.1. From (3.1.5)-(3.1.6), one can also characterize R_0 as the unique solution of the nonlinear equation

$$\rho\left(U^{(\lambda)}(\tau, 0)\right) = 1, \quad \lambda > 0, \quad (3.1.7)$$

where $U^{(\lambda)} : \mathbb{R} \times \mathbb{R} \rightarrow \mathbb{C}^{d \times d}$ is the principal matrix solution (PMS) of the linear ODE

$$v'(t) = \left(\frac{1}{\lambda}B(t) - M(t)\right)v(t),$$

i.e., $U^{(\lambda)}(\cdot, s)$ satisfies for all $s \in \mathbb{R}$,

$$\begin{cases} \partial_t U^{(\lambda)}(t, s) = \left(\frac{1}{\lambda}B(t) - M(t)\right)U^{(\lambda)}(t, s), & t \geq s, \\ U^{(\lambda)}(s, s) = \mathcal{I}_{\mathbb{C}^d}. \end{cases} \quad (3.1.8)$$

We refer to [9, 57, Section 8, 132] and [13, Section 7.2, Proposition 7.9] for further details.

²We omit the computations for the sake of readability. The reader may refer to [57, p. 179] for further the details.

³Alternatively, one can work in the space $C_\tau(\mathbb{R}; \mathbb{C}^d)$ equipped with the norm $\|\psi\|_\infty = \max_{t \in [0, \tau]} |\psi(t)|_{\mathbb{C}^d}$ [85, 128, 132].

Remark 3.1.2. Observe that, in the periodic case the computation of R_0 leads to deal with either the solution of the infinite-dimensional eigenvalue problem

$$\mathcal{K}\psi = \lambda\psi, \quad (\lambda, \psi) \in \mathbb{C} \times X \quad (3.1.9)$$

for positive λ and nontrivial ψ , or with the solution of the nonlinear equation (3.1.7) which, in general, cannot be analytically solved. Methods based on the discretization of (3.1.9) have been proposed in [9, 113], while methods based on the numerical solution of (3.1.7) by combining ODE solvers with dichotomy methods have been proposed in [9, 132]. See [111] for a review of all these approaches. As for the methods based on the discretization of (3.1.9), one of the main drawback is that one explicitly needs derive the NGO (which in general cannot be done analytically), and to approximate the integral over the halfline. Methods based on the numerical solution of (3.1.7) are typically more flexible, as they do not require to explicitly derive the NGO. Yet, they require to numerically compute from scratch at each iteration an approximation of the monodromy operator in (3.1.7), and then to solve a nonlinear equation, which in turn requires to choose an appropriate starting point for the iteration.

3.1.1 Reproduction numbers and evolution semigroups

In this section, following [85, 86, 89, 128], we illustrate the connection of the theory presented in Section 3.1 with the theory of evolution semigroups [48].

We consider the space $Y := AC_\tau(\mathbb{R}, \mathbb{C}^d)$ equipped with the norm $\|\phi\|_Y := \|\phi\|_X + \|\phi'\|_X$, and we introduce the operators $\mathcal{B}: X \rightarrow X$ and $\mathcal{M}: Y \rightarrow X$ respectively defined as

$$(\mathcal{B}\phi)(t) := B(t)\phi(t), \quad t \in \mathbb{R}, \quad \phi \in X, \quad (3.1.10)$$

and

$$(\mathcal{M}\phi)(t) := \phi'(t) + M(t)\phi(t), \quad t \in \mathbb{R}, \quad \phi \in Y. \quad (3.1.11)$$

One can show that $-\mathcal{M}$ is the infinitesimal generator of the strongly continuous evolution semigroup $\{T(s)\}_{s \geq 0}$ on X defined as [48, Section 2.2.1, 85, 128]

$$(T(s)\psi)(t) := V(t, t-s)\psi(t-s), \quad t \geq s > -\infty.$$

Moreover, Assumption 3.1 (ii) ensures that $\mathcal{M}$ is invertible with bounded inverse [128, Section 5]. Consequently, from standard results in semigroups theory [67, Theorem 1.10], we get

$$(\mathcal{M}^{-1}\psi)(t) = \int_0^\infty (T(s)\psi)(t) ds = \int_0^\infty V(t, t-s)\psi(t-s) ds, \quad \psi \in X.$$

Hence, the NGO in (3.1.5) can be obtained as [85, 89, 128]

$$(\mathcal{K}\psi)(t) := (\mathcal{B}\mathcal{M}^{-1}\psi)(t), \quad t \in \mathbb{R}, \quad \psi \in X. \quad (3.1.12)$$

From (3.1.12), we immediately obtain the following result.

Theorem 3.1.3. *The NGO $\mathcal{K}$ in (3.1.5) is compact, $0 \in \sigma(\mathcal{K})$ and $\sigma(\mathcal{K}) \setminus \{0\}$ consists of eigenvalues only which are at most countable and are either isolated or accumulate at 0. In addition, if R in (3.1.6) is positive, then it is a dominant real eigenvalue (in the sense of largest in magnitude) with associated a real nonnegative eigenfunction.*

Proof. Since the operator $\mathcal{B}$ in (3.1.10) is bounded, it is enough to show that $\mathcal{M}^{-1}$ is compact. To do so, let us note that $\text{Range}(\mathcal{M}^{-1}) = Y$ and that $\mathcal{M}: X \rightarrow Y$ is bounded. Indeed, under Assumption 3.1 we have

$$\|\mathcal{M}^{-1}\|_{Y \leftarrow X} = \sup_{\substack{\psi \in X, \\ \|\psi\|_X = 1}} \left(\|\mathcal{M}^{-1}\psi\|_X + \|(\mathcal{M}^{-1}\psi)'\|_X \right)$$

$$\begin{aligned}
&\leq \sup_{\substack{\psi \in X, \\ \|\psi\|_X=1}} \left(\|\mathcal{M}^{-1}\|_{X \leftarrow X} \|\psi\|_X + \|\psi - M\mathcal{M}^{-1}\psi\|_X \right) \\
&\leq \sup_{\substack{\psi \in X, \\ \|\psi\|_X=1}} \left(\|\mathcal{M}^{-1}\|_{X \leftarrow X} \|\psi\|_X + \|\psi\|_X + \|M\|_{L^\infty_\tau(\mathbb{R}, \mathbb{C}^{d \times d})} \|\mathcal{M}^{-1}\|_{X \leftarrow X} \|\psi\|_X \right) \\
&= 1 + \left(1 + \|M\|_{L^\infty_\tau(\mathbb{R}, \mathbb{C}^{d \times d})} \right) \|\mathcal{M}^{-1}\|_{X \leftarrow X}.
\end{aligned}$$

Then, the thesis follows from the compactness of the natural immersion of Y into X , from [40, Theorem 6.8], and from the Krein–Rutmann Theorem [99]. $\square$

Let us note that, in light of (3.1.12), R_0 can be equivalently computed by solving either the eigenvalue problem

$$\mathcal{B}\mathcal{M}^{-1}\psi = \lambda\psi, \quad (\lambda, \psi) \in \mathbb{C} \times X,$$

for positive λ and nontrivial ψ , or by solving the generalized eigenvalue problem

$$\mathcal{B}\phi = \lambda\mathcal{M}\phi, \quad (\lambda, \phi) \in \mathbb{C} \times Y, \quad (3.1.13)$$

for $\phi = \mathcal{M}^{-1}\psi$. This characterization of $\mathcal{K}$ is particularly convenient for investigating numerical approximations of R_0 . In fact, following the idea of Chapter 2, we can exploit the discretization of the operators $\mathcal{B}$ and $\mathcal{M}$ to derive a finite dimensional version of the NGO. In this way, we do not need to explicitly compute the operator $\mathcal{K}$ in (3.1.5) (avoiding also the computation/approximation of the integral on $[0, +\infty)$ in (3.1.12)) or to solve the nonlinear equation (3.1.7).

3.2 The numerical approach

Following the idea of Chapter 2, in order to obtain an approximation R_N of R , we construct finite-dimensional approximations of the operators $\mathcal{B}$ and $\mathcal{M}$ defined in (3.1.10) and (3.1.11), respectively. This is achieved by pseudospectral collocation.

Of course, collocation is meaningless in the whole space X , but the method is restricted to the eigenfunctions of $\mathcal{K}$, which in general are smooth enough.

We propose two alternative methods. The first method is based on Fourier collocation, i.e., we use trigonometric polynomials as approximating functions. This choice is motivated by the fact that trigonometric polynomials are periodic, hence one does not need to enforce a periodicity condition. On the other hand, in the presence of discontinuities in the model coefficients or in their derivatives, extending the Fourier collocation method to a piecewise approach is not an easy task in general. In this case, we can resort to an algebraic collocation method, where we use algebraic (piecewise continuous) polynomials to locally approximate functions in Y on $[0, \tau]$. Yet, note that algebraic polynomials are not periodic functions. Hence, in this approach we need to enforce the periodicity at the boundary of the period interval. As in this case we use the Chebyshev extrema in $[0, \tau]$ as discretization points, in the following we refer to this approach as the Chebyshev collocation method [21, 70, 130].

To rigorously introduce the numerical methods, we make the following assumption.

Assumption 3.2. $B, M \in C_\tau(\mathbb{R}, \mathbb{R}^{d \times d})$.

3.2.1 Discretization via Fourier collocation

Given an even positive integer N , we consider the space $Y_{f,N} \subset Y$ of trigonometric polynomials on $\mathbb{R}$ of degree at most $N/2$ and taking values in $\mathbb{C}^d$. Let $\Theta_{f,N} := \{t_{f,0} < \dots < t_{f,N}\}$ denote a mesh of $N+1$ points in $[0, \tau)$. We define restriction and prolongation operators respectively as⁴

$$\mathcal{R}_N: C_\tau(\mathbb{R}, \mathbb{C}^d) \rightarrow \mathbb{C}^{d(N+1)}, \quad \mathcal{R}_N\psi := (\psi(t_{f,0}); \dots; \psi(t_{f,N})),$$

⁴Observe that the restriction operator is defined on the space of periodic continuous functions, so that pointwise evaluation is well-defined.

and

$$\mathcal{P}_N: \mathbb{C}^{d(N+1)} \rightarrow Y_{f,N}, \quad \mathcal{P}_N \Psi := \sum_{i=0}^N \ell_{f,i} \Psi_i,$$

where $\Psi := (\Psi_0; \dots; \Psi_N)$, for $\Psi_i \in \mathbb{C}^d$, $i = 0, \dots, N$, and $\{\ell_{f,i}\}_{i=0}^N$ is the Lagrange trigonometric polynomial basis relevant to $\Theta_{f,N}$, see (1.2.5). Observe that

$$\mathcal{R}_N \mathcal{P}_N = \mathcal{I}_{\mathbb{C}^{d(N+1)}}, \quad \mathcal{P}_N \mathcal{R}_N = \mathcal{L}_{f,N},$$

where $\mathcal{L}_{f,N}: Y_0 \rightarrow Y_{f,N}$ is the Lagrange trigonometric interpolation operator relevant to $\Theta_{f,N}$.

Then, we derive the finite-dimensional approximations $\mathcal{B}_{f,N}, \mathcal{M}_{f,N}: \mathbb{C}^{d(N+1)} \rightarrow \mathbb{C}^{d(N+1)}$ of $\mathcal{B}$ and $\mathcal{M}$, respectively, as⁵

$$\mathcal{B}_{f,N} := \mathcal{R}_N \mathcal{B} \mathcal{P}_N, \quad \mathcal{M}_{f,N} := \mathcal{R}_N \mathcal{M} \mathcal{P}_N.$$

To derive a finite-dimensional approximation $\mathcal{K}_N$ of $\mathcal{K}$, in Section 2.2.2 we show that there exists a positive integer $\bar{N}$ such that $\mathcal{M}_{f,N}$ is invertible for every integer $N \geq \bar{N}$ under the following assumption.

Assumption 3.3. $\Theta_{f,N}$ is the mesh of equidistant nodes

$$t_{f,i} := i \frac{\tau}{N+1}, \quad i = 0, \dots, N.$$

Consequently, the finite-dimensional approximation $\mathcal{K}_{f,N}: \mathbb{C}^{d(N+1)} \rightarrow \mathbb{C}^{d(N+1)}$ of $\mathcal{K}$ is obtained as

$$\mathcal{K}_{f,N} := \mathcal{B}_{f,N} \mathcal{M}_{f,N}^{-1}, \quad N \geq \bar{N}. \quad (3.2.1)$$

The associated discrete eigenvalue problem can be solved either by using the standard MATLAB function `eig` or by solving the generalized eigenvalue problem $\mathcal{B}_{f,N} \Phi = \lambda \mathcal{M}_{f,N} \Phi$. Note that the eigenvectors of $\mathcal{K}_{f,N}$ give an approximation of the values of the eigenfunctions of $\mathcal{K}$ at the equidistant nodes in $[0, \tau)$. Thus, an approximation of the eigenfunctions of $\mathcal{K}$ can be obtained by interpolating the eigenvectors of $\mathcal{K}_{f,N}$ at the nodes in $\Theta_{f,N}$.

3.2.2 Discretization via Chebyshev collocation

As already observed, algebraic polynomials are not periodic functions in general. Consequently, we can not proceed as in Section 3.2.1 to present the Chebyshev method. Nevertheless, inspired by [29, 31], we can proceed in a slightly different way by collocating the generalized eigenvalue problem (3.1.13) over the time-period interval $[0, \tau]$. For the sake of simplicity, in this section we restrict ourselves to presenting the method in the nonpiecewise case, that is, we consider a unique collocating polynomial over $[0, \tau]$. The generalization to the piecewise case is straightforward, yet technical.

Given a positive integer N , let $\Theta_{c,N} := \{0 = t_{c,0} < t_{c,1} < \dots < t_{c,N} = \tau\}$ denote a mesh of $N+1$ points in $[0, \tau]$. The underlying idea is that of locally approximating a function $\phi \in Y$ through a vector $\Phi \in \mathbb{C}^{dN}$ according to

$$\phi(t_{c,i}) \approx \Phi_i \in \mathbb{C}^d, \quad i = 1, \dots, N.$$

The collocation approach reduces (3.1.13) to the discrete generalized eigenvalue problem

$$\mathcal{B}_{c,N} \Phi = \lambda_N \mathcal{M}_{c,N} \Phi, \quad (\lambda_N, \Phi) \in \mathbb{C} \times \mathbb{C}^{dN}, \quad (3.2.2)$$

⁵Note that $\mathcal{B}_{f,N}, \mathcal{M}_{f,N}$ are well-defined as Assumption 3.2 ensures that $\mathcal{B} \mathcal{P}_N \phi_{f,N}$ and $\mathcal{M} \mathcal{P}_N \phi_{f,N}$ are continuous for every $\phi_{f,N} \in Y_{f,N}$.

and R_0 is approximated through

$$R_{0,N} := \max \left\{ |\lambda| \mid \lambda \in \mathbb{C} \text{ and } B_{c,N}\Phi = \lambda M_{c,N}\Phi \text{ for some } \Phi \in \mathbb{C}^{dN} \setminus \{0\} \right\}.$$

We derive (3.2.2) as follows. Let $Y_{c,N}$ denote the space of $\mathbb{C}^d$ -valued algebraic polynomials on $[0, \tau]$ of degree at most N . Let $\phi_{c,N} \in Y_{c,N}$ collocate (3.1.13) as

$$\phi_{c,N}(0) = \phi_{c,N}(\tau), \quad (3.2.3)$$

$$B(t_{c,i})\phi_{c,N}(t_{c,i}) = \lambda(\phi'_{c,N}(t_{c,i}) + M(t_{c,i})\phi_{c,N}(t_{c,i})), \quad i = 1, \dots, N, \quad \lambda \in \mathbb{C}. \quad (3.2.4)$$

We rewrite $\phi_{c,N}$ in its Lagrange representation

$$\phi_{c,N}(t) := \Phi_N(\ell_{c,0}(t) + \ell_{c,N}(t)) + \sum_{i=1}^{N-1} \ell_{c,i}(t)\Phi_i, \quad t \in [0, \tau],$$

where $\{\ell_{c,i}\}_{i=0,\dots,N}$ is the Lagrange algebraic polynomial basis relevant to $\Omega_{c,N}$, see (1.1.3). Then, the finite-dimensional approximations $\mathcal{B}_N, \mathcal{M}_N: \mathbb{C}^{dN} \rightarrow \mathbb{C}^{dN}$ of $\mathcal{B}$ and $\mathcal{M}$ are obtained as

$$[\mathcal{B}_{c,N}\Phi]_i := B(t_{c,i})\phi_{c,N}(t_{c,i}), \quad [\mathcal{M}_{c,N}\Phi]_i := \phi'_{c,N}(t_{c,i}) + M(t_{c,i})\phi_{c,N}(t_{c,i}), \quad i = 1, \dots, N.$$

Note that $[\mathcal{B}_{c,N}\Phi]_i, [\mathcal{M}_{c,N}\Phi]_i \in \mathbb{C}^d, i = 1, \dots, N$. As before, the generalized eigenvalue problem (3.2.2) is solved by using the standard MATLAB function `eig`.

We conclude this section with the following assumption.

Assumption 3.4. $\Theta_{c,N}$ is the mesh of $N + 1$ Chebyshev extremal nodes in $[0, \tau]$.

Remark 3.2.1. Here we presented the collocation method using as approximating function a unique polynomial all over the time-period interval $[0, \tau]$. Anyway, as already mentioned, for the Chebyshev method, in the presence of discontinuities in the model coefficients or in their derivatives, one can resort to a piecewise approach, i.e., using piecewise continuous polynomials as approximating functions. The MATLAB codes available at <http://cdlab.uniud.it/software> used to make all the tests in Section 3.5 implement this piecewise alternative.

3.3 Convergence analysis

In this section, we investigate the convergence of the methods presented in Section 3.2. For the Fourier method, we prove that under Assumption 3.3 there exists a positive integer $\bar{N}$ such that $\mathcal{M}_{f,N}$ is invertible for every integer $N \geq \bar{N}$. We do this by explicitly making use of the inclusion $Y_{f,N} \subset Y$. This allows us to define the operator $\mathcal{K}_{f,N}$ in (3.2.1) and to investigate the convergence of its eigenvalues to those of $\mathcal{K}$ via the spectral approximation theory of [45], adapting the proof of Section 2.3.

The same analysis cannot be carried out for the Chebyshev method, as algebraic polynomials (and their extension to the real line via periodicity) are not contained in Y , in general. Nevertheless, we can still prove the convergence for the Chebyshev method by adapting the arguments of [31, Section 4]. More in details, we derive characteristic equations for both (3.1.13) and (3.2.2). Then, we prove the well-posedness of the collocation problem underlying (3.2.2), and we investigate the convergence of the eigenvalues by confronting the characteristic equations via the Rouché Theorem [31, Section 4].

The analysis for both the Fourier and the Chebyshev method is completed with error bounds under each of the following requirements.

Assumption 3.5.

- (i) $B, M \in \text{Lip}_\tau^s(\mathbb{R}, \mathbb{R}^{d \times d})$ for some integer $s \geq 0$,
- (ii) $B, M \in C_\tau^\infty(\mathbb{R}, \mathbb{R}^{d \times d})$,
- (iii) B, M are real analytic.

3.3.1 Fourier collocation method

In this section, we prove the convergence of the Fourier collocation method. To do so, we adapt the convergence proof of Chapter 2 and we make use of the spectral approximation theory in [45].

Invertibility of $\mathcal{M}_{f,N}$

The following requirement is necessary to proceed with the analysis.

Assumption 3.6. $B, M \in \text{AC}_\tau(\mathbb{R}, \mathbb{R}^{d \times d})$.

In this section we prove that, for N sufficiently large, the matrix $\mathcal{M}_{f,N}$ is invertible. To do so, we observe that $\mathcal{M}_{f,N}$ is invertible if and only if, for every $\Xi \in \mathbb{C}^{d(N+1)}$, there exists a unique $\Phi \in \mathbb{C}^{d(N+1)}$ such that

$$\mathcal{M}_{f,N}\Phi = \Xi. \quad (3.3.1)$$

By letting $\phi_N := \mathcal{P}_N\Phi$, it is easy to see that, since $\mathcal{M}\mathcal{P}_N\Phi \in C_\tau(\mathbb{R}, \mathbb{C}^d)$, then $\mathcal{R}_N\mathcal{M}\mathcal{P}_N\Phi$ is well defined, and

$$\mathcal{M}_{f,N}\Phi = \mathcal{R}_N\mathcal{M}\mathcal{P}_N\Phi = \mathcal{R}_N\mathcal{M}\phi_N = \Xi. \quad (3.3.2)$$

Thus, applying $\mathcal{P}_N$ to both sides of (3.3.2), we get

$$\mathcal{L}_{f,N}\mathcal{M}\phi_N = \mathcal{P}_N\Xi. \quad (3.3.3)$$

Since $\mathcal{L}_{f,N}\phi'_N = \phi'_N$, we have $\mathcal{L}_{f,N}\mathcal{M}\phi_N = \phi'_N + \mathcal{L}_{f,N}(M\phi_N)$. Hence, (3.3.3) can be equivalently rewritten as

$$\phi'_N = \mathcal{P}_N\Xi - \mathcal{L}_{f,N}(M\phi_N), \quad (3.3.4)$$

and, by adding $M\phi_N$ to both sides of (3.3.4), we get⁶

$$\mathcal{M}\phi_N = \mathcal{P}_N\Xi + (\mathcal{I}_X - \mathcal{L}_{f,N})(M\phi_N). \quad (3.3.5)$$

Now, let us observe that, since $\phi_N \in Y$ and $\mathcal{M}$ is invertible,⁷ there exists unique $\psi \in X$ such that $\phi_N = \mathcal{M}^{-1}\psi$. Then, it is easy to see that solving (3.3.5) for ϕ_N is equivalent to solve

$$\psi = \mathcal{P}_N\Xi + (\mathcal{I}_X - \mathcal{L}_{f,N})M \left(\mathcal{M}^{-1}\psi \right),$$

for ψ , which can be equivalently rewritten as

$$\left[\mathcal{I}_X + (\mathcal{L}_{f,N} - \mathcal{I}_X)MM^{-1} \right] \psi = \mathcal{P}_N\Xi. \quad (3.3.6)$$

Now, we prove that $\mathcal{M}_{f,N}$ is invertible by showing that (3.3.6) admits a unique solution.

Lemma 3.3.1. *Let Assumption 3.3 and Assumption 3.6 hold. Then, there exists a positive integer $\bar{N}$ such that*

$$\left\| \left(\mathcal{I}_X + (\mathcal{L}_{f,N} - \mathcal{I}_X)MM^{-1} \right)^{-1} \right\|_{X \leftarrow X} \leq 2 \quad (3.3.7)$$

for every integer $N \geq \bar{N}$. Moreover, $\mathcal{M}_{f,N}$ is invertible for every integer $N \geq \bar{N}$ with inverse

$$\mathcal{M}_{f,N}^{-1} = \mathcal{R}_N\mathcal{M}^{-1} \left(\mathcal{I}_X + (\mathcal{L}_{f,N} - \mathcal{I}_X)MM^{-1} \right)^{-1} \mathcal{P}_N.$$

⁶Note that here we see $\mathcal{L}_{f,N}$ as an operator from Y to X .

⁷Note that this is true only for the case of a trigonometric polynomial. In fact, in general, an algebraic polynomial is not a function of X .

Proof. Let us observe that $M\mathcal{M}^{-1}: X \rightarrow Y$ is bounded (see the proof of Theorem 3.1.3). Moreover, [108, p. 221, Theorem 3.2.9] ensures that there exists a constant $C > 0$ independent of N such that

$$\|(\mathcal{L}_{f,N} - \mathcal{I}_X)\phi\|_X \leq C \frac{\log N}{N} \|\phi'\|_X \leq C \frac{\log N}{N} \|\phi\|_Y \quad (3.3.8)$$

for every $\phi \in Y$. Thus

$$\left\| (\mathcal{L}_{f,N} - \mathcal{I}_X)M\mathcal{M}^{-1} \right\|_{X \leftarrow X} \rightarrow 0, \quad N \rightarrow \infty, \quad (3.3.9)$$

and [100, Theorem 10.1] ensures that there exists a positive integer $\bar{N}$ such that the operator $\mathcal{I}_X + (\mathcal{L}_{f,N} - \mathcal{I}_X)M\mathcal{M}^{-1}$ is invertible and (3.3.7) holds for every integer $N \geq \bar{N}$. The thesis follows. $\square$

Let us observe that, if $\Xi := \mathcal{R}_N \xi$, for $\xi \in C_\tau(\mathbb{R}, \mathbb{C}^d)$, then the unique solution ϕ_N of (3.3.5) is a (trigonometric) polynomial, and is given by $\phi_N = \mathcal{M}^{-1} \left(\mathcal{I}_X + (\mathcal{L}_{f,N} - \mathcal{I}_X)M\mathcal{M}^{-1} \right)^{-1} \mathcal{L}_{f,N} \xi$. Hence, by introducing the operator $\widehat{\mathcal{M}}_N^{-1}: C_\tau(\mathbb{R}, \mathbb{C}^d) \rightarrow Y$ defined as

$$\widehat{\mathcal{M}}_N^{-1} := \mathcal{M}^{-1} \left(\mathcal{I}_X + (\mathcal{L}_{f,N} - \mathcal{I}_X)M\mathcal{M}^{-1} \right)^{-1} \mathcal{L}_{f,N}, \quad (3.3.10)$$

we have $\phi_N := \widehat{\mathcal{M}}_N^{-1} \xi$.

Remark 3.3.2. Note that, in the proof of Theorem 3.3.1, we resort again to the upside-down method discussed in Theorem 2.2.2. This is made possible by the regularizing effect of the operator $\mathcal{M}^{-1}$, which allows us to evaluate the interpolation error of a function of Y with the X -norm, and then map the problem back again to the space Y via $\mathcal{M}^{-1}$.

Convergence analysis

In this section, we prove that the eigenvalues of $\mathcal{K}_{f,N}$ converge to those of $\mathcal{K}$ via the spectral approximation theory of [45].

To do this, we observe that, differently from Chapter 2, here the operator $\mathcal{B}$ is a multiplication operator, hence it has no regularizing effect on X and Y . This brings in some difficulties in directly comparing $\mathcal{K}$ and $\mathcal{K}_{f,N}$. Nevertheless, we can proceed in a slightly different way by observing that for the compact operator $\mathcal{Q} := \mathcal{M}^{-1}\mathcal{B}$ and the matrix $\mathcal{Q}_N := \mathcal{M}_{f,N}^{-1}\mathcal{B}_{f,N}$, the following relations hold⁸ (see also Theorem 2.3.5)

$$\sigma(\mathcal{Q}) = \sigma(\mathcal{K}), \quad \sigma(\mathcal{Q}_{f,N}) = \sigma(\mathcal{K}_{f,N}).$$

Hence, in order to investigate the convergence of the eigenvalues of $\mathcal{K}_{f,N}$ to those of $\mathcal{K}$, we can investigate the convergence of the eigenvalues of $\mathcal{Q}_{f,N}$ to those of $\mathcal{Q}$. Furthermore, let us note that $\text{Range}(\mathcal{Q}) = Y$. Hence, in the following we can restrict to Y .

We start by considering the operator $\mathcal{P}_N \mathcal{Q}_{f,N} \mathcal{R}_N: Y \rightarrow Y$, which has the same nonzero eigenvalues with the same algebraic and partial multiplicities of $\mathcal{Q}_{f,N}$, see Proposition 1.3.1. Then, we note that $\mathcal{P}_N \mathcal{Q}_{f,N} \mathcal{R}_N = \widehat{\mathcal{M}}_N^{-1} \mathcal{B}_{f,N}$. Since $\text{Range}(\mathcal{P}_N) \subset Y_{f,N}$, Proposition 1.3.2 ensures that $\mathcal{P}_N \mathcal{Q}_{f,N} \mathcal{R}_N$ has the same nonzero eigenvalues with the same geometric and partial multiplicities, and the same eigenfunctions of the operator

$$\widehat{\mathcal{Q}}_{f,N} := \widehat{\mathcal{M}}_N^{-1} \mathcal{B}: Y \rightarrow Y_{f,N}.$$

⁸We remark that the operator $\mathcal{Q}$ is actually the one considered in [132] for the computation of R_0 . See also [128].

Hence, to apply the spectral approximation theory, since $\widehat{\mathcal{Q}}_{f,N} - \mathcal{Q}$ is compact⁹ from Y into itself for every $N \geq 0$, it is enough to show that [45, pag. 498]

$$\|\widehat{\mathcal{Q}}_{f,N} - \mathcal{Q}\|_{Y \leftarrow Y} \rightarrow 0, \quad N \rightarrow \infty.$$

To do so, we observe that

$$\widehat{\mathcal{Q}}_{f,N} - \mathcal{Q} = (\widehat{\mathcal{M}}_N^{-1} - \mathcal{M}^{-1})\mathcal{B}.$$

Thus, in order to prove the norm convergence of $\widehat{\mathcal{Q}}_{f,N} - \mathcal{Q}$ to 0, we just need to investigate the behavior of $\widehat{\mathcal{M}}_{f,N}^{-1} - \mathcal{M}^{-1}$ as $N \rightarrow \infty$.

Lemma 3.3.3. *Let Assumption 3.3 and Assumption 3.6 hold. Then*

$$\|\widehat{\mathcal{M}}_{f,N}^{-1} - \mathcal{M}^{-1}\|_{Y \leftarrow Y} \rightarrow 0, \quad N \rightarrow \infty.$$

Proof. Observe that, from (3.3.10), we have

$$\widehat{\mathcal{M}}_N^{-1} - \mathcal{M}^{-1} = \mathcal{M}^{-1} \left(\mathcal{I}_X + (\mathcal{L}_{f,N} - \mathcal{I}_X) \mathcal{M} \mathcal{M}^{-1} \right)^{-1} (\mathcal{L}_{f,N} - \mathcal{I}_X) \quad (3.3.11)$$

$$+ \mathcal{M}^{-1} \left((\mathcal{I}_X + (\mathcal{L}_{f,N} - \mathcal{I}_X) \mathcal{M} \mathcal{M}^{-1})^{-1} - \mathcal{I}_X \right). \quad (3.3.12)$$

Simple computations show that

$$(\mathcal{I}_X + (\mathcal{L}_{f,N} - \mathcal{I}_X) \mathcal{M} \mathcal{M}^{-1})^{-1} - \mathcal{I}_X = (\mathcal{I}_X + (\mathcal{L}_{f,N} - \mathcal{I}_X) \mathcal{M} \mathcal{M}^{-1})^{-1} (\mathcal{L}_{f,N} - \mathcal{I}_X) \mathcal{M} \mathcal{M}^{-1}.$$

Hence, from (3.3.11) and (3.3.12), we get

$$\|\widehat{\mathcal{M}}_{f,N}^{-1} - \mathcal{M}^{-1}\|_{Y \leftarrow Y} \leq C \left(\|(\mathcal{L}_{f,N} - \mathcal{I}_X)\|_{X \leftarrow Y} + \|(\mathcal{L}_{f,N} - \mathcal{I}_X) \mathcal{M} \mathcal{M}^{-1}\|_{X \leftarrow Y} \right), \quad (3.3.13)$$

where $C := 2\|\mathcal{M}^{-1}\|_{Y \leftarrow X}$. Then, the first term on the right hand-side of (3.3.13) tends to zero thanks to (3.3.8), while the second term tends to zero thanks to (3.3.9). The thesis follows. $\square$

Theorem 3.3.4. *Let Assumption 3.3 and Assumption 3.6 hold. Then, $\|\widehat{\mathcal{Q}}_{f,N} - \mathcal{Q}\|_{Y \leftarrow Y} \rightarrow 0$ as $N \rightarrow \infty$.*

Proof. Note that, under Assumption 3.6, the operator $\mathcal{B}$ is bounded from Y into itself. Hence, the thesis follows from Theorem 3.3.3 by observing that

$$\|\widehat{\mathcal{Q}}_{f,N} - \mathcal{Q}\|_{Y \leftarrow Y} \leq \|\widehat{\mathcal{M}}_N^{-1} - \mathcal{M}^{-1}\|_{Y \leftarrow Y} \|\mathcal{B}\|_{Y \leftarrow Y}.$$

$\square$

Convergence of eigenvalues and eigenspaces

Theorem 3.3.5. *Let Assumption 3.3 and Assumption 3.6 hold. Let $\lambda \in \mathbb{C}$ be an isolated nonzero eigenvalue of $\mathcal{Q}$ with finite algebraic multiplicity m and ascent l and let Δ be a neighborhood of λ such that λ is the sole eigenvalue of $\mathcal{Q}$ in Δ . Then there exists $\bar{N}$ such that, for $N \geq \bar{N}$, $\widehat{\mathcal{Q}}_N$ has in Δ exactly m eigenvalues $\lambda_{N,i}$, $i = 1, \dots, m$, counting their multiplicities. Moreover,*

$$\max_{i=1, \dots, m} |\lambda_{N,i} - \lambda| = O(\varepsilon_N^{1/l}),$$

⁹In fact, the compactness of the natural immersion of Y into X ensures that the restriction to Y of a bounded operator from X to Y is compact.

where

$$\varepsilon_N := \|\widehat{\mathcal{Q}}_N - \mathcal{Q}\|_{Y \leftarrow E_\lambda} \quad (3.3.14)$$

and E_λ is the generalized eigenspace of λ . Finally, for any $i = 1, \dots, m$ and for any eigenfunction $\psi_{N,i}$ of $\widehat{\mathcal{Q}}_N$ relevant to $\lambda_{N,i}$ such that $\|\psi_{N,i}\|_Y = 1$, we have

$$\text{dist}(\psi_{N,i}, \ker(\lambda \mathcal{I}_Y - \mathcal{Q})) = O(\varepsilon_N^{1/l}),$$

where dist is the distance in the space Y between an element and a subspace.

Proof. See the proof of Theorem 2.3.3. $\square$

Now, we complete the analysis with error bounds under each of the regularity conditions in Assumption 3.5.

Corollary 3.3.6. *Let Assumption 3.3 and Assumption 3.5 hold. Let $\lambda, \lambda_{N,i}, i = 1, \dots, m, E_\lambda$ and ε_N be as in Theorem 3.3.5. Then*

$$\varepsilon_N = O(f_{N/2}),$$

where

$$f_N := \begin{cases} N^{-(s+1)} \log N & \text{under Assumption 3.5 (i),} \\ N^{-r} & \text{for every integer } r \geq 1 \text{ under Assumption 3.5 (ii),} \\ p^{-N} & \text{for some constant } p > 1 \text{ under Assumption 3.5 (iii).} \end{cases}$$

Proof. As in the proof of Theorem 2.3.4, the Riesz theory for compact operators [100, section 3.1] ensures that the generalized eigenspaces of $\mathcal{Q}$ have finite dimension. Hence, given a basis for E_λ , $\{\psi_{\lambda,i}\}_{i=1}^k$, where $k = \dim E_\lambda$, it is enough to show that

$$\max_{i=1,\dots,k} \|(\widehat{\mathcal{Q}}_N - \mathcal{Q})\psi_{\lambda,i}\|_Y = O(\varepsilon_N). \quad (3.3.15)$$

Then, the thesis will follow from Theorem 1.3.3. In this regard, let us observe that from , we have

$$\|(\widehat{\mathcal{Q}}_N - \mathcal{Q})\psi_{\lambda,i}\|_Y \leq C \left(\|(\mathcal{L}_{f,N} - \mathcal{I}_X)B\psi_{\lambda,i}\|_X + \|(\mathcal{L}_{f,N} - \mathcal{I}_X)MM^{-1}B\psi_{\lambda,i}\|_X \right). \quad (3.3.16)$$

where $C := 2\|\mathcal{M}^{-1}\|_{Y \leftarrow X}$, and that

- (i) $B\psi_{\lambda,i}, MM^{-1}B\psi_{\lambda,i} \in \text{Lip}_\tau^p(\mathbb{R}, \mathbb{C}^d)$ under Assumption 3.5 (i),
- (ii) $B\psi_{\lambda,i}, MM^{-1}B\psi_{\lambda,i} \in C_\tau^\infty(\mathbb{R}, \mathbb{C}^d)$ under Assumption 3.5 (ii),
- (iii) $B\psi_{\lambda,i}, MM^{-1}B\psi_{\lambda,i}$ are analytic under Assumption 3.5 (iii).

Moreover, we have

$$\|(\mathcal{L}_{f,N} - \mathcal{I}_X)B\psi_{\lambda,i}\|_X \leq \tau \|(\mathcal{L}_{f,N} - \mathcal{I}_Y)B\psi_{\lambda,i}\|_\infty, \quad (3.3.17)$$

and

$$\|(\mathcal{L}_{f,N} - \mathcal{I}_Y)MM^{-1}B\psi_{\lambda,i}\|_X \leq \tau \|(\mathcal{L}_{f,N} - \mathcal{I}_Y)MM^{-1}B\psi_{\lambda,i}\|_\infty. \quad (3.3.18)$$

Then, under Assumption 3.5 (i), Theorem 1.2.9 and Theorem 1.2.6 ensure that

$$\|(\mathcal{L}_{f,N} - \mathcal{I}_Y)B\psi_{\lambda,i}\|_\infty \leq (1 + \Lambda_{f,N})\mathcal{E}_{f,N}(B\psi_{\lambda,i}) = O(f_{N/2}),$$

and

$$\|(\mathcal{L}_{f,N} - \mathcal{I}_Y)MM^{-1}B\psi_{\lambda,i}\|_\infty \leq (1 + \Lambda_{f,N})\mathcal{E}_{f,N}(MM^{-1}B\psi_{\lambda,i}) = O(f_{N/2}),$$

where $\Lambda_{f,N}$ is the (trigonometric) Lebesgue constant relevant to $\Theta_{f,N}$ which, under Assumption 3.3, is $O(\log N/2)$ [108, Theorem 3.2.4], and $\mathcal{E}_{f,N}(\cdot)$ is defined as in (1.2.1). The bounds under Assumption 3.5 (ii) and (iii) follow from (3.3.17), (3.3.18), [138, Theorem 4.2] and Theorem 1.2.7. Hence, (3.3.15) holds, and the thesis follows from Theorem 1.3.3. $\square$

3.3.2 Chebyshev collocation method

In this section, we prove the convergence of the Chebyshev collocation method. To do so, we adapt the convergence proof of [31, Section 4].

Characteristic equations

To investigate the convergence of the approximated eigenvalues, we derive a characteristic equation for the generalized eigenvalue problem (3.1.13). Since we are interested in the (positive) spectral radius of $\mathcal{K}$, we assume that $\lambda \neq 0$, so that (3.1.13) can be rewritten as

$$\frac{1}{\lambda} \mathcal{B}\phi = \mathcal{M}\phi. \quad (3.3.19)$$

We set $A^{(\lambda)} := \frac{1}{\lambda} \mathcal{B} - \mathcal{M}$ for brevity. Then, we observe that $(\lambda, \phi) \in \mathbb{C} \times Y \setminus \{(0, 0)\}$ is a solution of (3.3.19) if and only if ϕ solves the PBVP

$$\begin{cases} \phi'(t) = A^{(\lambda)} \phi(t), & t \in [0, T], \\ \phi(0) = \phi(\tau). \end{cases} \quad (3.3.20)$$

Now, let us consider the family of IVPs for $\alpha \in \mathbb{C}^d$

$$\begin{cases} \phi'(t) = A^{(\lambda)}(t) \phi(t), & t \in [0, \tau], \\ \phi(0) = \alpha, \end{cases} \quad (3.3.21)$$

which admits a unique solution for every $\alpha \in \mathbb{C}^d$. Then, every solution $\phi(t; \lambda, \alpha)$ of (3.3.21) can be expressed as

$$\phi(t; \lambda, \alpha) = U^{(\lambda)}(t, 0) \alpha, \quad t \in [0, T],$$

where $U^{(\lambda)}$ is the PMS of (3.3.21) defined in (3.1.8). For brevity, with abuse of notation, we write $U^{(\lambda)}(t) = U^{(\lambda)}(t, 0)$, $t \in \mathbb{R}$. Now, let us observe that a solution of (3.3.21) is solution of (3.3.20) if and only if

$$\phi(0; \lambda, \alpha) = U^{(\lambda)}(\tau) \alpha \iff (\mathcal{I}_{\mathbb{C}^d} - U^{(\lambda)}(\tau)) \alpha = 0.$$

Hence, we arrive at the characteristic equation

$$c(\lambda) = 0, \quad (3.3.22)$$

for the characteristic function

$$c(\lambda) := \det(\mathcal{I}_{\mathbb{C}^d} - U^{(\lambda)}(\tau)).$$

Now, we derive the discrete counterpart of (3.3.22). Let us observe that $(\lambda, \Psi) \in \mathbb{C} \times \mathbb{C}^{dN} \setminus \{(0, 0)\}$ satisfies

$$\frac{1}{\lambda} \mathcal{B}_{c,N} \Psi = \mathcal{M}_{c,N} \Psi \quad (3.3.23)$$

if and only if the polynomial ϕ_N interpolating Ψ at the Chebyshev nodes satisfies

$$\begin{cases} \phi'_N(t_{c,i}) = A^{(\lambda)}(t_{c,i}) \phi_N(t_{c,i}), & i = 1, \dots, N, \\ \phi_N(0) = \phi_N(\tau). \end{cases} \quad (3.3.24)$$

Let us consider the auxiliary collocation problem for (3.3.21) at the Chebyshev nodes

$$\begin{cases} p'_N(t_{c,i}) = A^{(\lambda)}(t_{c,i}) p_N(t_{c,i}), & i = 1, \dots, N, \\ p_N(0) = \alpha. \end{cases} \quad (3.3.25)$$

In the following section, we prove that (3.3.25) has a unique solution for every $\alpha \in \mathbb{C}^d$. Hence, we can define $U_N^{(\lambda)}: [0, \tau] \rightarrow \mathbb{C}^{d \times d}$ such that

$$p_N(t; \lambda, \alpha) = U_N^{(\lambda)}(t)\alpha, \quad t \in [0, \tau],$$

i.e., $U_N^{(\lambda)}$ is the PMS for (3.3.25). Now, it is easy to see that a solution $p_N(t; \lambda, \alpha)$ of (3.3.25) is solution of (3.3.24) if and only if

$$p_N(0; \lambda, \alpha) = U_N^{(\lambda)}(\tau)\alpha \iff (\mathcal{I}_{\mathbb{C}^d} - U_N^{(\lambda)}(\tau))\alpha = 0.$$

Hence, we arrive at the characteristic equation

$$c_N(\lambda) = 0, \tag{3.3.26}$$

for the characteristic function

$$c_N(\lambda) := \det(\mathcal{I}_{\mathbb{C}^d} - U_N^{(\lambda)}(\tau)).$$

Then, the convergence of the eigenvalues is investigated by studying the error

$$|c_N(\lambda) - c(\lambda)|$$

in a neighborhood of a spectral value of $\mathcal{K}$.

Let $B(\lambda, z)$ denote the closed ball in $\mathbb{C}$ of center λ and radius $z > 0$. From (3.3.21) and (3.3.25) we define the collocation error

$$e_N(\cdot; \lambda, \alpha) := p_N(\cdot; \lambda, \alpha) - \phi(\cdot; \lambda, \alpha).$$

Then, we note that, since $\det(A)$ is a locally Lipschitz function with respect to $A \in \mathbb{C}^{d \times d}$, for every $\lambda^* \in \mathbb{C}$ and $z > 0$, there exists $C_1 = C_1(\lambda^*, z) > 0$ such that

$$|c_N(\lambda) - c(\lambda)| \leq C_1 \left\| U_N^{(\lambda)}(\tau) - U^{(\lambda)}(\tau) \right\|_{\mathbb{C}^d \leftarrow \mathbb{C}^d} = C_1 \sup_{\substack{\alpha \in \mathbb{C}^d \\ |\alpha|_{\mathbb{C}^d} = 1}} |e_N(\tau; \lambda, \alpha)|_{\mathbb{C}^d}. \tag{3.3.27}$$

From this, we see that to investigate the behavior of $|c_N(\lambda) - c(\lambda)|$ in a neighborhood of $\lambda \in \mathbb{C}$, we need to give a bound to $|e_N(\tau; \lambda, \alpha)|_{\mathbb{C}^d}$.

Collocation error

In the following we assume that Assumption 3.5 holds. From this, we have that the solutions of (3.3.21) are continuously differentiable, which in turn implies that e_N is continuously differentiable. Hence, in the following we can restrict our attention to the space $C([0, \tau], \mathbb{C}^d)$. For the sake of readability, hereafter we avoid to explicitly write the dependence of ϕ , p_N and e_N on λ, α , if not necessary.

Let $\tilde{\mathcal{L}}_{N-1}: C([0, \tau], \mathbb{C}^d) \rightarrow C([0, \tau], \mathbb{C}^d)$ denote the Lagrange algebraic interpolation operator relevant to $\Theta_{c,N} \setminus \{0\}$. Then, since $\tilde{\mathcal{L}}_{N-1}p'_N = p'_N$, it is easy to see from (3.3.21) and (3.3.25) that e_N satisfies the functional equation

$$e_N := \mathcal{V}\tilde{\mathcal{L}}_{N-1}A^{(\lambda)}e_N + \mathcal{V}r_N, \tag{3.3.28}$$

where $\mathcal{V}: C([0, \tau], \mathbb{C}^d) \rightarrow C([0, \tau], \mathbb{C}^d)$ is the Volterra operator

$$\mathcal{V}\eta(t) = \int_0^t \eta(\xi) d\xi, \quad t \in [0, \tau],$$

and

$$r_N := (\tilde{\mathcal{L}}_{N-1} - \mathcal{I}_{C([0,\tau],\mathbb{C}^d)})A^{(\lambda)}\phi.$$

Now, we show that the collocation equation (3.3.28) has a unique solution, and we derive a bound to $|e_N(\tau)|$ in terms of the interpolation error r_N . To do this, we need to work under the hypothesis that the Lebesgue constant relevant to $\Theta_{c,N} \setminus \{0\}$, $\tilde{\Lambda}_{N-1}$, satisfies

$$\lim_{N \rightarrow \infty} \frac{\tilde{\Lambda}_{N-1}}{N} = 0. \quad (3.3.29)$$

Unfortunately, this is not ensured under Assumption 3.4 when working in the space $C([0, \tau], \mathbb{C}^d)$ endowed with the infinite norm. Indeed, in this case the limit in (3.3.29) is only known to be bounded [108, Section 4.2].

To overcome this problem, the well-posedness of (3.3.28) is investigated using the (weaker) weighted uniform norm $\|\eta\|_{w,\infty} := \|\eta \cdot w\|_\infty$, where $w(t) := \sqrt{(\tau - t)t}$, $t \in [0, \tau]$. This ensures that the Lebesgue constant relevant to $\Theta_{c,N} \setminus \{0\}$ is $O(\log N)$ [108, p. 274, Theorem 4.3.2]. For brevity, we denote by C_w the space $C([0, \tau], \mathbb{C}^d)$ when endowed with the norm $\|\cdot\|_{w,\infty}$. Additionally, we also consider the space Lip_w , which is the space $\text{Lip}^0([0, \tau], \mathbb{C}^d)$ endowed with the w -weighted norm $\|g\|_{\text{Lip}_w^0} := \|gw\|_\infty + L_w(g)$, where $L_w(g)$ denotes the Lipschitz constant of g with respect to the norm $\|\cdot\|_{w,\infty}$.

Proposition 3.3.7. *Let Assumption 3.4 and Assumption 3.5 hold. Then, there exists a positive integer $\bar{N}$ such that, for every integer $N \geq \bar{N}$, (3.3.28) has a unique solution e_N in C_w and*

$$|e_N(\tau)| \leq 2\pi \left\| \left(\mathcal{I}_X - A^{(\lambda)}\mathcal{V} \right)^{-1} \right\|_{C_w \leftarrow C_w} \|r_N\|_{w,\infty}. \quad (3.3.30)$$

Proof. The proof is adapted from [31, Proposition 3]. Let us consider the auxiliary problem

$$\tilde{e}_N = \tilde{\mathcal{L}}_{N-1}A^{(\lambda)}\mathcal{V}\tilde{e}_N + r_N, \quad (3.3.31)$$

whose solutions are in one-to-one correspondence with those of (3.3.28) through $e_{N,\alpha} = \mathcal{V}\tilde{e}_{N,\alpha}$. We prove that there exists a positive integer $\bar{N}$ such that (3.3.31) admits a unique solution for every integer $N \geq \bar{N}$. To do so, we rewrite (3.3.31) as

$$(\mathcal{I}_{C_w} - \tilde{\mathcal{L}}_{N-1}A^{(\lambda)}\mathcal{V})\tilde{e}_{N,\alpha} = r_N.$$

and we observe that

$$(\mathcal{I}_{C_w} - \tilde{\mathcal{L}}_{N-1}A^{(\lambda)}\mathcal{V}) = (\mathcal{I}_{C_w} - A^{(\lambda)}\mathcal{V}) + (\mathcal{I}_{C_w} - \tilde{\mathcal{L}}_{N-1})A^{(\lambda)}\mathcal{V}.$$

It is easy to see that $\mathcal{I}_{C_w} - A^{(\lambda)}\mathcal{V}$ is invertible with bounded inverse in C_w . Furthermore, since $\text{Range}(A^{(\lambda)}\mathcal{V}) \subset \text{Lip}_w$ and $A^{(\lambda)}\mathcal{V}: C_w \rightarrow \text{Lip}_w$ is bounded, Assumption 3.4 and Theorem 1.1.6 guarantee that there exists a positive constant C independent of N such that [108, p. 271, eq. 4.33 and p. 274, Theorem 4.3.2]

$$\left\| (\mathcal{I}_{C_w} - \tilde{\mathcal{L}}_{N-1})A^{(\lambda)}\mathcal{V} \right\|_{C_w \leftarrow C_w} \leq C \cdot \|A^{(\lambda)}\mathcal{V}\|_{\text{Lip}_w \leftarrow C_w} \cdot \frac{\log N}{N} \rightarrow 0, \quad N \rightarrow \infty. \quad (3.3.32)$$

Hence, the Banach perturbation Lemma [100, Theorem 10.1] ensures that there exists a positive integer $\bar{N}$ such that $\mathcal{I}_{C_w} - \tilde{\mathcal{L}}_{N-1}A^{(\lambda)}\mathcal{V}$ is invertible in C_w and

$$\|\tilde{e}_{N,\alpha}\|_{w,\infty} \leq 2 \left\| \left(\mathcal{I}_{C_w} - A^{(\lambda)}\mathcal{V} \right)^{-1} \right\|_{C_w \leftarrow C_w} \|r_N\|_{w,\infty}$$

holds for every integer $N \geq \bar{N}$. Finally, (3.3.30) follows from

$$|e_N(\tau)|_{\mathbb{C}^d} \leq \|\tilde{e}_N\|_{L^1([0,\tau],\mathbb{C}^d)} \leq \|w^{-1}\|_{L^1([0,\tau],\mathbb{C})} \|\tilde{e}_N\|_{w,\infty} = \pi \|\tilde{e}_N\|_{w,\infty}.$$

□

Proposition 3.3.8. *Let Assumption 3.4 and Assumption 3.5 hold. Then, there exists a positive integer $\bar{N}$ such that, for all the integers $N \geq \bar{N}$,*

$$\|r_N\|_{w,\infty} = O(\rho_N),$$

where

$$\rho_N := \begin{cases} N^{-(s+1)} \log N, & \text{under Assumption 3.5 (i),} \\ N^{-r} \log N, & \text{for every integer } r \geq 1 \text{ under Assumption 3.5 (ii),} \\ p^{-N} \log N, & \text{for some constant } k > 1 \text{ under Assumption 3.5 (iii).} \end{cases} \quad (3.3.33)$$

Proof.

$$\|r_N\|_{w,\infty} \leq (1 + \|\tilde{\mathcal{L}}_{N-1}\|_{C_w \leftarrow C_w}) \mathcal{E}_{N-1}(A^{(\lambda)} \phi_\alpha)$$

follows from [108, p. 271, eq. 4.33] and standard results in approximation theory, where $\mathcal{E}_{N-1}(\cdot)$ is defined as in (1.1.1). The final bound follows from Assumption 3.4, which guarantees that $\|\tilde{\mathcal{L}}_{N-1}\|_{C_w \leftarrow C_w} = O(\log N)$ [108, p. 274, Theorem 4.3.2], and estimates of $\mathcal{E}_{N-1}(A^{(\lambda)} \phi_\alpha)$ can be obtained from Theorem 1.1.6 and Theorem 1.1.7. $\square$

Convergence of eigenvalues

We conclude by stating the main results for the Chebyshev collocation method.

Theorem 3.3.9. *Let λ^* be a zero of c in (3.3.22) with algebraic multiplicity m and $z > 0$ be such that λ^* is the only zero of c in $B(\lambda^*, z)$. Then, there exists a positive integer $\bar{N}$ such that, for all the integers $N \geq \bar{N}$, c_N in (3.3.26) has exactly m zeros $\lambda_{N,1}, \dots, \lambda_{N,m}$ (counted with their multiplicities) in $B(\lambda^*, z)$ and*

$$\max_{i=1,\dots,m} |\lambda^* - \lambda_{N,i}| = O(\rho_N^{1/m}),$$

where ρ_N is defined as in (3.3.33).

Proof. The thesis follows from (3.3.27), Proposition 3.3.7 and Proposition 3.3.8 by eventually applying Rouché's theorem as in [31, Section 4]. $\square$

Remark 3.3.10. From Theorem 3.3.5, Corollary 3.3.6, Proposition 3.3.8 and Theorem 3.3.9, one may expect that for a given number of points N , the Chebyshev method performs (slightly) better than the Fourier method. However, in Section 3.5 we numerically observe that if the coefficients are real analytic or of class C^∞ , then the Fourier method performs better than the Chebyshev method. Yet, in the presence of jump-discontinuities in the derivatives of the coefficients, the Chebyshev method seems to perform better in terms of convergence order. See Section 3.5 and Figure 3.5.2 for further details.

3.4 Implementation

In this section we give additional details on the implementation of both the Fourier and the Chebyshev method.

3.4.1 Implementation for the Fourier collocation

Here we give an explicit description of the entries of the matrices $\mathcal{B}_{f,N}$ and $\mathcal{M}_{f,N}$. Let us introduce the Fourier differentiation matrix $\mathcal{D}_{f,N} := [\ell'_{f,j}(t_{f,i})]_{i,j=0,\dots,N}$, which under Assumption 3.3 can be explicitly expressed as [15, 70]

$$[\mathcal{D}_{f,N}]_{i,j} := \begin{cases} \frac{\pi}{\tau} (-1)^{i+j} \csc \left(\frac{\pi(t_{f,i} - t_{f,j})}{\tau} \right), & i \neq j, \\ 0 & i = j. \end{cases}$$

Then, thanks to the cardinal property of the Lagrange trigonometric polynomials in (1.2.5), it is easy to see that $\mathcal{B}_{f,N}, \mathcal{M}_{f,N}: \mathbb{C}^{d(N+1)} \rightarrow \mathbb{C}^{d(N+1)}$ are explicitly given by

$$\mathcal{B}_{f,N} = \text{blkdiag}(B(t_{f,0}), \dots, B(t_{f,N})), \quad \mathcal{M}_{f,N} = (\mathcal{D}_{f,N} \otimes \mathcal{I}_{\mathbb{C}^d}) + \text{blkdiag}(M(t_{f,0}), \dots, M(t_{f,N})).$$

3.4.2 Implementation for the Chebyshev collocation

Here we give an explicit description of the entries of the matrices $\mathcal{B}_{c,N}$ and $\mathcal{M}_{c,N}$. Let us introduce the differentiation matrix $\mathcal{D}_{c,N} := [\ell'_{j,c}(t_{c,i})]_{i,j=0,\dots,N}$, which under Assumption 3.4 can be explicitly expressed as [70, 130]

$$[\mathcal{D}_{c,N}]_{i,j} := \frac{2}{\tau} \begin{cases} -\frac{2N^2+1}{6}, & i = h = 0, \\ \frac{c_i}{c_j} \frac{(-1)^{i+j+N}}{x_i - x_j}, & i \neq h, \\ -\frac{x_i}{2(1-x_i^2)}, & 0 < i = j < N, \\ \frac{2N^2+1}{6}, & i = j = N, \end{cases}$$

where $x_i = \cos(\pi(N-i)/N)$, $i = 0, \dots, N$, and $c_0 = c_N = 2$ and $c_i = 1$ for $i = 1, \dots, N-1$. Then, thanks to the cardinal property of the Lagrange polynomials in (1.1.3), it is easy to see that $\mathcal{B}_{c,N}, \mathcal{M}_{c,N}: \mathbb{R}^{dN} \rightarrow \mathbb{R}^{dN}$ are explicitly given by

$$\mathcal{B}_{c,N} = \text{blkdiag}(B(t_{f,1}), \dots, B(t_{f,N})), \quad \mathcal{M}_{c,N} = \widehat{\mathcal{D}_{c,N}} \otimes \mathcal{I}_{\mathbb{C}^d} + \text{blkdiag}(M(t_{f,N}), \dots, M(t_{f,N})),$$

where $\widehat{\mathcal{D}_{c,N}}$ is defined for $i, j = 0, \dots, N-1$ as

$$[\widehat{\mathcal{D}_{c,N}}]_{i,j} := \begin{cases} [\mathcal{D}_{c,N}]_{i+1,j+1} & \text{if } j \neq N-1, \\ [\mathcal{D}_{c,N}]_{i+1,1} + [\mathcal{D}_{c,N}]_{i+1,j+1} & \text{if } j = N-1. \end{cases}$$

3.5 Numerical results

In this section, we experimentally validate the theoretical results in Section 3.3 and we illustrate some possible applications of the method. We propose two test examples. The first one is obtained by the linearization of a d -dimensional SIR model around the DFE. We derive an explicit expression for R_0 , and we use it to numerically illustrate the convergence order of the numerical approximation R_N of R for both the Fourier and the Chebyshev method, which in turn depends on the regularity of the model parameters, see Theorem 3.3.5, Corollary 3.3.6 and Theorem 3.3.9.

The second example is two-dimensional, and represents the linearized equation around the disease-free periodic solution for a simplified vector-host model for dengue fever. In light of Chapter 2, we use this example to illustrate how the method can be easily adapted to compute also type reproduction numbers. In this case, analytic expressions for R are not available. Hence, the errors are computed with respect to reference values (obtained with $N = 150$).

The modeling details and the linearization around the equilibria are described in Appendix A.

Example 1 We consider the spread of an infectious disease in a population which is divided into $d \geq 1$ groups with time-periodic contact rates, see Appendix A.3.

The linearized equation for the infected individuals around the DFE reads

$$I'_j(t) = \sum_{k=1}^d \beta_{jk} I_k(t) - (\mu + \gamma) I_j(t), \quad (3.5.1)$$

where

$$\beta_{jk}(t) = b_0 f(t) \frac{\bar{c}_j \bar{c}_k}{\sum_{h=1}^d \bar{c}_h}, \quad j, k = 1, \dots, d.$$

for b_0 the infectiousness probability per contact, $\bar{c}_i$ the rate of contact of individuals of group i , μ is the mortality rate, γ is the recovery rate, and f is a nonnegative periodic function.

Model (3.5.1) can be recast in (3.1.1) by taking¹⁰ $B = [\beta_{jk}]_{j,k=1,\dots,d}$, and $M = (\mu + \gamma)\mathcal{I}_{\mathbb{R}^d}$. Here we assume parameters suitable for measles and taken from [82]. We take $\tau = 1$ (yr), $\mu = 1/82$ (yr⁻¹), $\gamma = 52$ (yr⁻¹) and $b_0 = 0.8$. As for $\bar{c}_i$, $i = 1, \dots, d$, we assume that they are generated from a normally distributed random variable with mean $10(\gamma + \mu)/b_0$, and variance equal to 5.¹¹ Finally, f satisfies one of the following assumptions:

- (F1) $f(t) = k^{\sin(\frac{2\pi}{\tau}t - \eta)} / (\tau I_0(\ln(k)))$, $k > 1$,
- (F2) $f(t) = 1 + \delta \sin(\frac{2\pi}{\tau}t - \eta)$, $\delta \in [0, 1)$,
- (F3) $f(t) = 1 + \delta \sin(\frac{2\pi}{\tau}t - \eta) \sin(\frac{10\pi}{\tau}t - \eta)$, $\delta \in [0, 1)$,
- (F4) $f(t) = 1 + \delta \sin(\frac{2\pi}{\tau}t - \eta) |\sin(\frac{2\pi}{\tau}t - \eta)|$, $\delta \in [0, 1)$,
- (F5) $f(t) = 0.65 + 0.5 \chi_{[0,0.4] \cup [0.7,1]}(\frac{t}{\tau} \bmod \tau)$,

where I_0 is the modified Bessel function of the second kind. The different choices of f are visualized in Figure 3.5.1. Note that, under (F1)-(F5), f has mean 1 over $[0, \tau]$, and is analytic under (F1)-(F3), Lip¹ under (F4), and piecewise constant under (F5). Let us observe that the matrix

$$\left[b_0 \frac{\bar{c}_j \bar{c}_k}{\sum_{h=1}^d \bar{c}_h} \right]_{j,k=1,\dots,d}$$

is symmetric, thus it is diagonalizable. Hence, since (3.5.1) is equivalent to a system with B and M diagonal, the basic reproduction number coincides with that of the averaged problem [111], i.e.,

$$R_0 = \rho \left(\langle B \rangle_\tau \langle M \rangle_\tau^{-1} \right) = \frac{b_0}{\mu + \gamma} \sum_{i=1}^d \frac{\bar{c}_i^2}{\sum_{s=1}^d \bar{c}_s},$$

where $\langle \cdot \rangle_\tau$ denotes the time average over the interval $[0, \tau]$. In particular, for $d = 1$ we have

$$R_0 = \frac{b_0 \bar{c}}{\mu + \gamma}, \quad (3.5.2)$$

We use the expression in (3.5.2) to investigate the convergence order of the numerical approximation R_N of R_0 under each of the hypotheses (F1)-(F5) on f . In light of what we have seen in Chapter 2 and Section 3.3, we expect the convergence order on R_0 to depend on the regularity of the model coefficients. Figure 2.5.1 and Figure 3.5.3 show, for increasing N , the error $|R_N - R|$ for $d = 1$, $k = 1.5$, $\delta = 0.6$, $\eta = 0.2$ and $c = 10(\gamma + \mu)/b_0$.

Figure 2.5.1 shows infinite convergence order for both the Fourier and the Chebyhsev method under (F1), (F2) and (F3) (with f analytic), confirming the validity of Corollary 3.3.6 and Theorem 3.3.9.

¹⁰Note that, since M is time independent, the associated evolution family $\{V(t, s)\}_{t \geq s}$ is explicitly given by

$$V(t, s) = e^{-M(t-s)}, \quad t \geq s.$$

Hence the next-generation operator $\mathcal{K}$ is explicitly given by

$$(\mathcal{K}\phi)(t) := B(t) \int_0^\infty e^{-M\tau} \phi(t - \tau) d\tau, \quad \phi \in X.$$

¹¹With this choice, in the case of time-independent parameters we have $R_0 \approx 10$, see [82, Section 8.8].

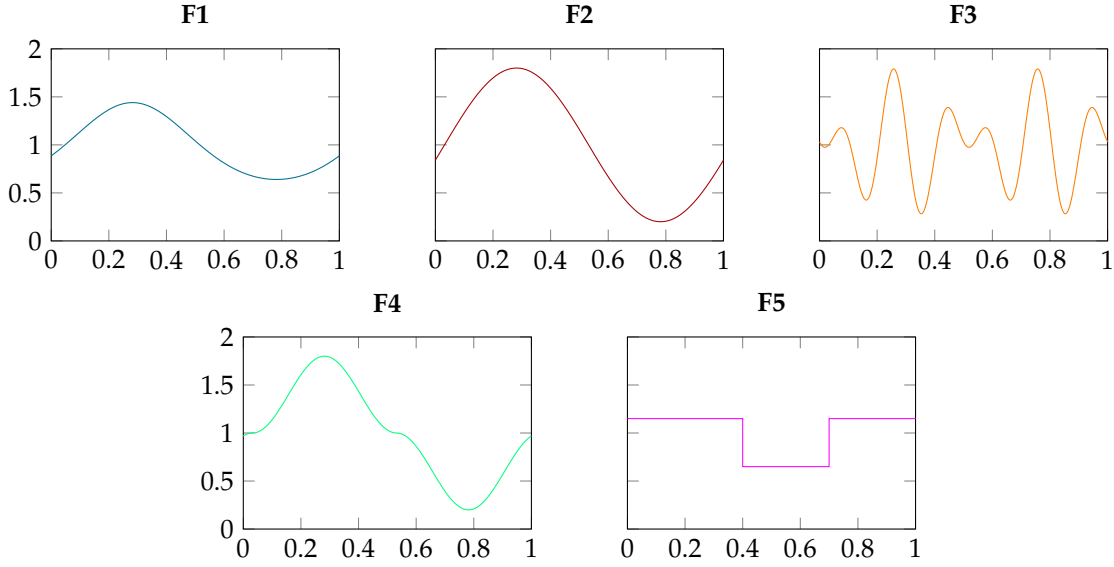


Figure 3.5.1: Example 1. The different choices for f with $k = 1.5$, $\delta = 0.8$ and $\eta = 0.2$. Original figure from [24].

Finite convergence order is observed under (F4) (below, right), seemingly of order 3 for the Fourier method and of order 4 for the Chebyshev method. Note that, as discussed in Remark 3.3.10, the Fourier method seems to perform better than the Chebyshev method when the model parameters are C^∞ . On the other hand, in the presence of jump-discontinuities in the derivatives of the model parameters, the (nonpiecewise version of the) Chebyshev method seems to perform better in terms of convergence order (this is observed also in other experiments conducted by the authors but not included here). Yet, the involved error constants seem to be smaller for the Fourier method.

Figure 3.5.3 shows infinite order of convergence for the piecewise version of the Chebyshev method under (F5).

Finally, Figure 3.5.4 shows the loglog plot for increasing values of N and different values of d of the computational times for the Fourier method when using the MATLAB built-in functions `eig` and `eigs`. The latter computes the dominant eigenvalue of $\mathcal{K}_{f,N}$ only.

Example 2 Inspired by [11, 132] and with reference to [1, 68, 75, 118], in this example we consider a simple vector-host model. Let $I_H(t)$ and $I_V(t)$ denote the number of infected humans and infected mosquitoes, respectively, at time $t \in \mathbb{R}$. We assume that the total human population P_H is constant, while the total mosquitoes population P_V periodically oscillates according to $P_V(t) = p_0 f(t)$, $p_0 > 0$ where

$$f(t) := e^{\delta \sin(2\pi t)}, \quad \delta \geq 0, \quad t \in \mathbb{R}.$$

By proceeding as in Appendix A.4, the linearized equations for the variables $i_H := I_H/P_H$ and $i_V := I_V/p_0$ read¹²

$$\begin{cases} i'_H(t) = \frac{\beta}{f(t)} i_V(t) - \gamma i_H(t), \\ i'_V(t) = \alpha f(t) i_H(t) - \mu i_V(t), \end{cases} \quad (3.5.3)$$

where β is the infection rate from vector to host, α is the infection rate from host to vector, γ is the recovery rate for hosts and μ is the mortality rate for vectors.

¹²Note that the reproduction numbers for model (A.4.2) and (3.5.3) coincide.

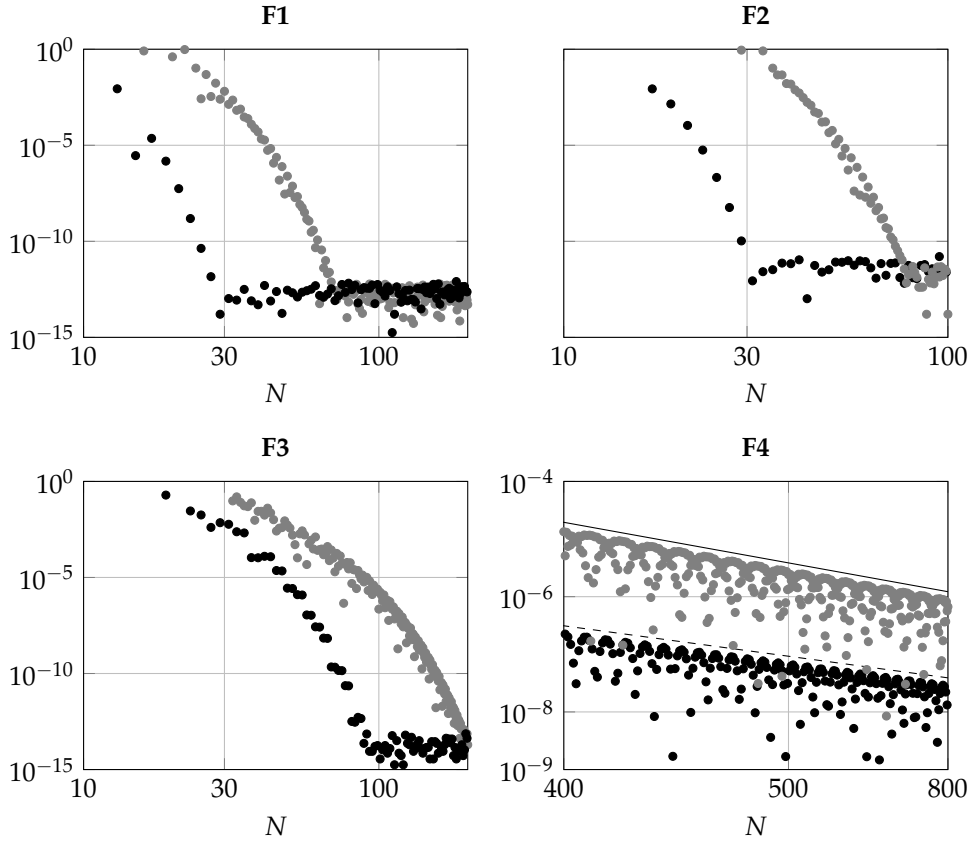


Figure 3.5.2: Example 1. Log-log plot for increasing N of the Fourier (black) and the Chebyshev (gray) approximation of R_0 under assumption (F1) (top, left), (F2) (top, right), (F3) (bottom, left) and (F4) (bottom, right), with $d = c_0 = 1$, $k = 1.5$ and $\delta = 0.6$. Infinite order of convergence is observed for (F1), (F2) and (F3) for both the methods, in agreement with Corollary 3.3.6 and Theorem 3.3.9. For the case (F4), finite convergence order occurs for both the Fourier and the Chebyshev method. The slope of the dashed line is -3 , while the slope of the black line is -4 . Original figure from [24].

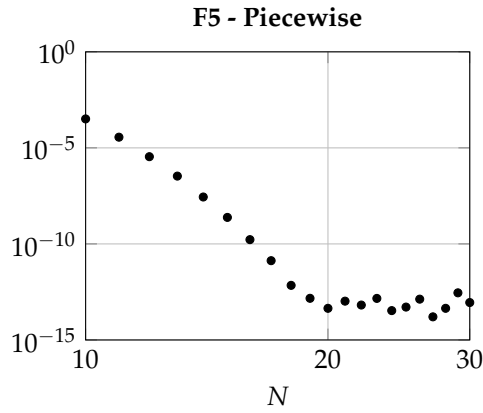


Figure 3.5.3: Example 1. Log-log plot for increasing N of the approximation error of the piecewise Chebyshev approximation of R_0 under (F5). Infinite order of convergence is observed. Original figure from [24].

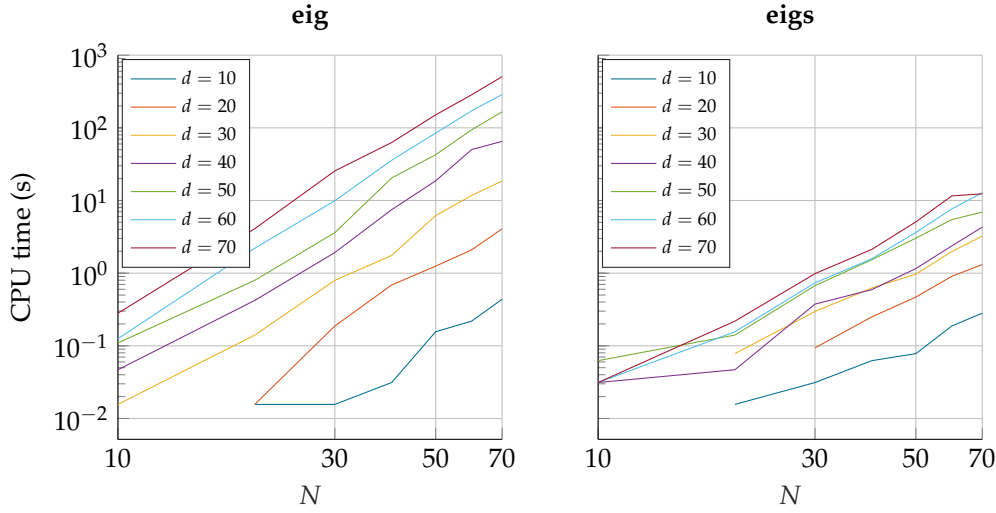


Figure 3.5.4: Example 1. Log-log plot for increasing N and different values of d of the computational times for the Fourier method when using the MATLAB built-in functions `eig` and `eigs`. Original figure from [24].

We assume that $\delta < 1$ [75], so that $P_V(t) \approx p_0 + p_0\delta \sin(2\pi t)$, and we take parameters inspired by dengue [1]. We take $\tau = 1$, $\mu = 1/7$ (day^{-1}), $\gamma = 1/7$ (day^{-1}), $\beta = 0.5$ (day^{-1}) and $\alpha = 0.75$ (day^{-1}), and we vary $\delta > 0$.

Now, let us define two T -periodic birth/infection matrices

$$B_1(t) = \begin{pmatrix} 0 & \beta/f(t) \\ 0 & 0 \end{pmatrix}, \quad B_2(t) = \begin{pmatrix} 0 & 0 \\ \alpha f(t) & 0 \end{pmatrix}, \quad t \in \mathbb{R},$$

and the baseline transition matrix

$$M_0 = \begin{pmatrix} \gamma & 0 \\ 0 & \mu \end{pmatrix}.$$

Then, it is easy to see that (3.5.3) can be recast as in (3.1.1) for each of the following choices:

- (i) $B := B_1 + B_2$ and $M := M_0$,
- (ii) $B := B_1$ and $M := M_0 - B_2$,
- (iii) $B := B_2$ and $M := M_0 - B_1$.

Note that (i) is the correct choice if the aim is to compute R_0 , as the matrix B contains all describing infection processes [63].

What about the other two choices? From Chapter 2, we expect the choices (ii) and (iii) to correspond to the type reproduction number for the host population, T_H , and for the vector population, T_V , respectively. Indeed, with reference to the notation of Section 3.1.1, [86] shows that under (ii) (or equivalently (iii)), the following holds

$$B = B_1(\mathcal{M} - B_2)^{-1} = (B_1\mathcal{M}^{-1})(\mathcal{I}_X - B_2\mathcal{M}^{-1}).$$

Note that this relation is in accordance with the definition of the type reproduction number in the autonomous case [117], see also [11].

Observe that the method presented in this chapter can be used to also compute T_H and T_V . Here we only use the Fourier method, as no jump-discontinuities arise in the derivatives of the model parameters. Figure 3.5.5 shows infinite order of convergence for the approximations of R , T_H and T_V , respectively, for $\delta = 0.8$. In Figure 3.5.6, we plot R_0 , T_H and T_V as functions of δ . Note the well-known relation between T and R_0 , i.e., $T = \sqrt{R_0}$, for models of the form (3.5.3) [9].

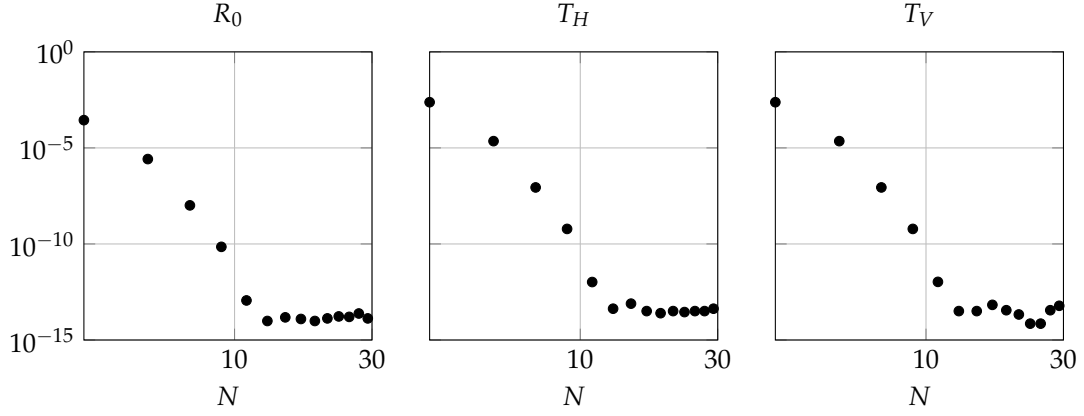


Figure 3.5.5: Example 2. Log-log plot for increasing N of the Fourier approximation of R_0 (left), T_H (center) and T_V (right) with $d = c_0 = 1$, $k = 1.5$ and $\delta = 0.8$. Infinite order of convergence is observed, in agreement with Theorem 2.3.4. The reference values $R_0 \approx 4.289089516936638$ and $T_H = T_V \approx 18.396288884295764$ are obtained with $N = 150$. Original figure from [24].

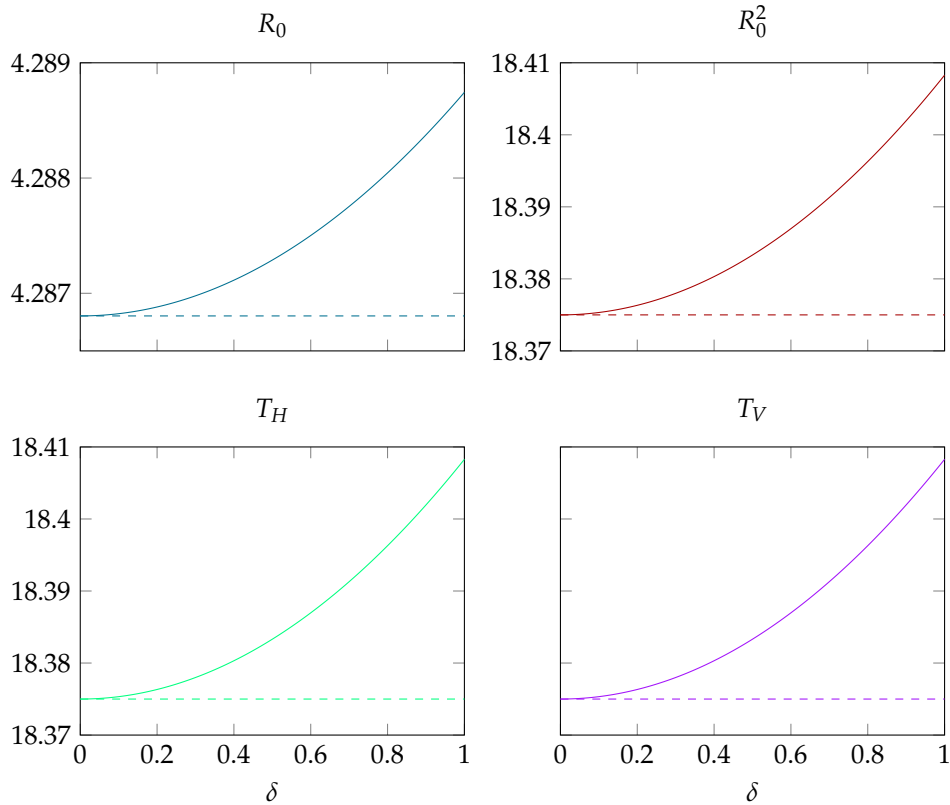


Figure 3.5.6: Example 2. Basic reproduction number R_0 (top left), squared basic reproduction number R_0^2 (top right), type reproduction number for the host population T_H (below left), and type reproduction number for the vector population T_V (below right) as functions of δ . The dashed lines represent the same quantities computed for the model with time-averaged coefficients. Original figure from [24].

4

Control reproduction numbers for epidemic models with mass testing strategies

The aim of this chapter is to give a definition of the control reproduction number, R_c , for a class of compartmental epidemic models with mass testing strategies starting from the general definition in (I.3.1), and to derive an efficient numerical method for its computation. The content of this chapter is mainly taken from the work [120] by the author, M. Sabbatino and A. Pugliese. Part of the content presented in this chapter will also appear in M. Sabbatino's Ph.D thesis.

The test-and-isolate policy, generally coupled with contact tracing, is one of the several NPIs (Non-Pharmaceutical Interventions) that were developed during the COVID-19 epidemic. We refer to [14, 47, 115] for some studies on its effectiveness in different countries. To better understand the potential and the limitations of a test-trace-isolate strategy, several models have been developed that include testing and isolation in combination with several other features important for the spread of SARS-CoV-2, e.g., pre-symptomatic infection, a realistic structure of contact networks, combination with other NPIs or with vaccination [77, 105, 129, 142].

In this chapter, inspired by [105] and with the aim of obtaining useful general insights from the theoretical analysis of test-and-isolate strategies alone [123] (which may be then extended to more complex models), we consider compartmental models of SIR and SEIR type with a realistic testing strategy, in which individuals are tested at fixed intervals of time and isolated if positive (see Section 4.1 for a precise definition).¹ The resulting models are described by systems of impulsive ODEs, for which we derive thresholds quantities that determines whether an epidemic can be controlled under the testing procedure (including also adherence to testing, ratio of false negatives, and compliance with isolation instructions) or not.

Note that for similar models [105] characterize R_c as the spectral radius of an operator obtained via an extension of the NGM method [58, 63].

In this chapter, instead, we give a formal characterization for R_c starting from the general definition in (I.3.1) and arguing in terms of “probabilities of still being infectious at a given time”. In particular, noting that newly infected individuals are structured by the time t since last testing at the moment of infection, we explicitly compute the kernel k in (I.3.1). The resulting NGO acts on a space of L^1 -integrable functions over the mass testing period interval, $[0, \tau]$, $\tau \geq 0$. Explicit expressions for R_c can be obtained for the considered SIR-type models. Yet, for the SEIR models numerical approximations are required. Hence, we present a method to approximate R_c based on the pseudospectral discretization of the NGO. We rigorously investigate the convergence of the

¹The considered models neglect some important features of a real epidemic, such as heterogeneity of the population and of the contact patterns, and include several other simplifying assumptions, like the exponential distribution of infectious and exposed states. Nevertheless, we believe that the results can still provide some insights on the conditions for a test-and-isolate policy to be effective.

method, and we present numerical results showing that $R_c = 1$ is a threshold for the stability of the DFE.

The content of the chapter is organized as follows. In Section 4.1, we introduce mass testing and isolation in a class of compartmental models. With reference to these models, in Section 4.2 we give conditions for an epidemic to be controllable under the mass testing strategy. In Section 4.3 we give the definition of the control reproduction number. The numerical method is presented in Section 4.5, while the convergence proof is presented in Section 4.6. Section 4.7 contains details about the implementation. Finally, Section 4.8 contains numerical results.

4.1 Compartmental models with mass testing events

In this section, we add mass testing and isolation to the compartmental SIR and SEIR model.

We assume that all individuals are tested at mass testing events with intervals of length $\tau > 0$ between them. At each testing event, a fraction $1 - p$ of the infected individuals is identified, and isolated, where $p \in (0, 1)$ represents the probability of not being tested, plus the probability of being tested and false negative, plus the probability of being tested and positive but not isolated.

Since the isolated individuals no longer participate in the infection process, we assume that they move to the removed compartment.

We assume that the population is large enough to neglect stochasticity, and is isolated, spatially homogeneous and closed. Moreover, we assume that there is no turnover, i.e., there are no births and deaths.

SIR model with general mass testing

Let $S(t)$, $I(t)$ and $R(t)$ denote the number of individuals who are susceptible, infectious and removed, respectively, at time $t \geq 0$. The model reads as follows

$$\begin{cases} S'(t) = -\lambda(t)S(t), \\ I'(t) = \lambda(t)S(t) - \gamma I(t), \\ R'(t) = \gamma I(t), \\ I(nT_+) = pI(nT_-), \end{cases} \quad n \in \mathbb{N}, \quad (4.1.1)$$

where

$$\lambda(t) := \beta \frac{I(t)}{P}, \quad t \geq 0, \quad (4.1.2)$$

is the force of infection, $P = S + I + R = \text{const}$ is the total population, β is the transmission rate and γ is the recovery rate; see Figure 4.1.1. As P does not depend on time, we can then neglect the variable $R(t)$ in (4.1.1), obtaining

$$\begin{cases} S'(t) = -\lambda(t)S(t), \\ I'(t) = \lambda(t)S(t) - \gamma I(t), \\ I(nT_+) = pI(nT_-), \end{cases} \quad n \in \mathbb{N}. \quad (4.1.3)$$

Observe that, in each interval $(n\tau, (n+1)\tau)$, $n \in \mathbb{N}$, the dynamic of (4.1.3) is described by the usual SIR model. Hence, the solutions of the system are continuous in the interior of each of these intervals, but they have jump-discontinuities at $t = n\tau$, $n \in \mathbb{N}$, due to the isolation procedure.

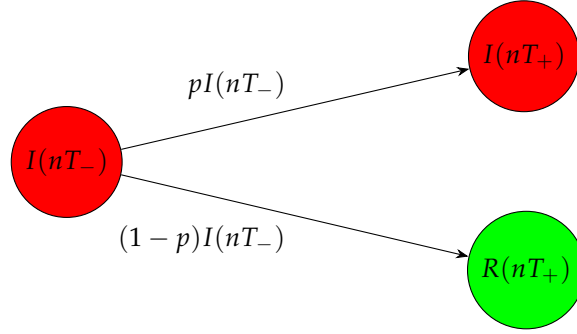


Figure 4.1.1: Flow chart representing the mass testing and isolation event at $t = nT$, for $n \in \mathbb{N}$. Here I denotes the number of infectious individuals and R the number of removed individuals.

SEIR model with general mass testing: exposed cannot be identified

In this section, we assume that, upon infection, individuals enter a latent phase in which they are not yet infectious. Then, the infectiousness is acquired at a rate σ , where $1/\sigma$ describes the mean length of the period spent in the latent phase by an individual after infection. Note that, in this context, a realistic assumption is that individuals do not test positive immediately after the infection. Here, for the sake of simplicity, we assume that the non-detectable individuals are exactly those in the class E , i.e., we identify the possibility of being identified through a test with being infectious.

Let $S(t)$, $E(t)$, $I(t)$ and $R(t)$ denote the number of individuals who are susceptibles, exposed (infected but not yet infectious), infectious and removed, respectively, at time $t \geq 0$, and let $P(t) = S(t) + E(t) + I(t) + R(t) = \text{const}$. The model reads

$$\begin{cases} S'(t) = -\lambda(t)S(t), \\ E'(t) = \lambda(t)S(t) - \sigma E(t), \\ I'(t) = \sigma E(t) - \gamma I(t), \\ R'(t) = \gamma I(t), \\ I(nT_+) = pI(nT_-), \end{cases} \quad n \in \mathbb{N}, \quad (4.1.4)$$

where λ is defined as in (4.1.2). Again, as P is constant, we neglect the equation for R in (4.1.4), obtaining

$$\begin{cases} S'(t) = -\lambda(t)S(t), \\ E'(t) = \lambda(t)S(t) - \sigma E(t), \\ I'(t) = \sigma E(t) - \gamma I(t), \\ I(nT_+) = pI(nT_-), \end{cases} \quad n \in \mathbb{N}. \quad (4.1.5)$$

4.1.1 Compartmental models with alternate mass testing events

In the previous section we considered models in which all individuals are tested at fixed interval of times. Anyway, there may be cases in which not all individuals can be tested in the same days (e.g., people may submit to testing only when needed, or it may be either impossible or too expensive to run all tests at the same time). In [105], the authors list several examples in which, during the COVID epidemic, tests were prescribed twice a week, every week or every other week.

For this reason, in this section we consider models that try to capture the effect of having scattered tests. Following [105], we assume that the population is split into k groups and every τ/k days a different group is tested, proceeding cyclically, so that each group is tested every τ days.

In particular, here we consider a simple case in which there are only 2 groups (namely 1 and 2) of the same size $\frac{P}{2}$, that are indistinguishable and mix randomly. We assume that every individual is tested at intervals of length $\frac{\tau}{2}$, so that every $\frac{\tau}{2}$ there are testing sessions in which individuals of alternately either group 1 or group 2 are tested and isolated if positive.

We assume that the total population is constant and is subdivided into compartments according to the stage of infection and the group to which it belongs (1 or 2).

SIR model with two groups tested alternately

Let $S_j(t)$, $I_j(t)$ and $R_j(t)$ denote the number of individuals of group $j = 1, 2$ who are susceptible, infectious and removed, respectively. We assume that the individuals 1 are tested at time $n\tau$, while the individuals 2 are tested at time $(n + \frac{1}{2})\tau$, for $n \in \mathbb{N}$. Between each testing event, the model dynamics is described by the following system of differential equations

$$\begin{cases} S'_j(t) = -\lambda(t)S_j(t), \\ I'_j(t) = \lambda S_j(t) - \gamma I_j(t), \end{cases} \quad t \in \left((2n + q - 1)\frac{\tau}{2}, (2n + q)\frac{\tau}{2}\right), \quad n \in \mathbb{N}, \quad j, q = 1, 2, \quad (4.1.6)$$

where

$$\lambda(t) := \beta \frac{I_1(t) + I_2(t)}{P}, \quad t \geq 0, \quad (4.1.7)$$

is the force of infection and β, γ are defined as in (4.1.1). We neglect the equations for R_j , $j = 1, 2$, as irrelevant for the overall dynamics. The testing events are modelled as

$$\begin{cases} I_1(n\tau_+) = pI_1(n\tau_-), & n \in \mathbb{N}, \\ I_2((n + \frac{1}{2})\tau_+) = pI_2((n + \frac{1}{2})\tau_-), & n \in \mathbb{N}. \end{cases}$$

SEIR model with two groups tested alternately

Let $S_j(t)$, $E_j(t)$, $I_j(t)$ and $R_j(t)$ denote the number of individuals of group $j = 1, 2$ who are susceptibles, exposed, infectious and removed, respectively. Between each testing event, the model dynamics is described by the following system of differential equations

$$\begin{cases} S'_j(t) = -\lambda(t)S_j(t), \\ E'_j(t) = \lambda S_j(t) - \sigma E_j(t), \\ I'_j(t) = \sigma E_j(t) - \gamma I_j(t), \end{cases} \quad t \in \left((2n + q - 1)\frac{\tau}{2}, (2n + q)\frac{\tau}{2}\right), \quad n \in \mathbb{N}, \quad j, q = 1, 2, \quad (4.1.8)$$

where λ is defined as in (4.1.7) and σ is defined as in (4.1.1). We neglect the equations for R_j , $j = 1, 2$, as irrelevant for the overall dynamics. The testing events are instead modelled as

$$\begin{cases} I_1(n\tau_+) = pI_1(n\tau_-), & n \in \mathbb{N}, \\ I_2((n + \frac{1}{2})\tau_+) = pI_2((n + \frac{1}{2})\tau_-), & n \in \mathbb{N}. \end{cases}$$

4.2 Conditions for epidemic outbreak or extinction

In this section, we derive conditions to determine if, at the beginning of an epidemic, an outbreak may occur or not. To do so, we look at the linearized equations for the infected individuals around

the DFE. In particular, for the cases with alternate testing, we make the approximation $S_1 \approx \frac{p}{2}$ and $S_2 \approx \frac{p}{2}$. These conditions will be used later on in the chapter for comparison with the results obtained by looking at the control reproduction number. As the focus of this chapter is on the definition and the (numerical) computation of R_c , we omit the details of the computations for which we refer to [120].

SIR model with general testing For the SIR model, the linearized equation for the infected individuals reads

$$\begin{cases} I'(t) = \beta I(t) - \gamma I(t), \\ I(n\tau_+) = pI(n\tau_-), \end{cases} \quad n \in \mathbb{N}. \quad (4.2.1)$$

Solving (4.2.1) in each interval $[n\tau, (n+1)\tau]$, we obtain

$$I((n+1)\tau_+) = pe^{(\beta-\gamma)\tau} I(n\tau_+), \quad n \in \mathbb{N}.$$

Hence, the condition for epidemic control is given by

$$pe^{\gamma(R_0-1)\tau} < 1, \quad (4.2.2)$$

where $R_0 = \beta/\gamma$ is the basic reproduction number for the S(E)IR model in the absence of interventions.

SEIR model with general testing For the SEIR model, the linearized equations for the infected individuals read

$$\begin{cases} E' = \beta I - \sigma E, \\ I' = \sigma E - \gamma I, \\ I(n\tau_+) = pI(n\tau_-), \end{cases} \quad n \in \mathbb{N}. \quad (4.2.3)$$

Solving (4.2.3) in each interval $[n\tau, (n+1)\tau]$, we obtain the discrete system

$$\begin{pmatrix} E((n+1)\tau_+) \\ I((n+1)\tau_+) \end{pmatrix} = \begin{pmatrix} 1 & 0 \\ 0 & p \end{pmatrix} e^{A\tau} \begin{pmatrix} E(n\tau_+) \\ I(n\tau_+) \end{pmatrix}, \quad (4.2.4)$$

where

$$A := \begin{pmatrix} -\sigma & \beta \\ \sigma & -\gamma \end{pmatrix}.$$

Conditions for epidemic control are determined looking at conditions that guarantees that the spectral radius of the matrix

$$T := \begin{pmatrix} 1 & 0 \\ 0 & p \end{pmatrix} e^{AT}$$

is less than one. In [120], this is done by using the Jury condition² [82, pp. 324, Proposition C.1] which gives the following result.

Proposition 4.2.1. *Let $\lambda_{1,2}$ denote the eigenvalues of A , and let $\Delta := 4\sigma\beta + (\sigma - \gamma)^2$, and let C denote the positive constant³*

$$C := e^{-(\sigma+\gamma)\frac{\tau}{2}} \left(\cosh\left(\frac{\sqrt{\Delta}\tau}{2}\right) + \frac{\sigma - \gamma}{\sqrt{\Delta}} \sinh\left(\frac{\sqrt{\Delta}\tau}{2}\right) - e^{-(\sigma+\gamma)\frac{\tau}{2}} \right).$$

²The Jury condition ensures that the spectral radius of a 2×2 matrix T is less than one if and only if the following conditions hold: $\det(T) < 1$ and $|\operatorname{tr}(T)| < \det(T) + 1$.

³The proof that C is a positive constant can be found in the appendix of [120]

Then

$$[T]_{11} = \frac{(\gamma - \sigma)(e^{\lambda_1 T} - e^{\lambda_2 T})}{2\sqrt{\Delta}} + \frac{e^{\lambda_1 T} + e^{\lambda_2 T}}{2},$$

and the following conditions hold:

- If $[T]_{11} \geq 1$, the control of the epidemic is impossible for any value of p ,
- if $[T]_{11} < 1$, there exist $p^* = \min \left\{ 1, \frac{1 - [T]_{11}}{C} \right\}$ such that if $p < p^*$, the epidemic can be controlled by testing.

It is easy to see that $p^* = 1 \iff R_0 \leq 1$. Yet, interpreting the condition $p < p^*$ is not easy, given the complicated expression of p^* .

SIR model with alternate testing For the SIR model with alternate testing, the linearized equations for the infected individuals around the DFE read

$$\begin{cases} I'_j(t) = \frac{\beta}{2} (I_1(t) + I_2(t)) - \gamma I_j(t), & j = 1, 2, \\ I_1(n\tau_+) = p I_1(n\tau_-), & n \in \mathbb{N}, \\ I_2((n + \frac{1}{2})\tau_+) = p I_2((n + \frac{1}{2})\tau_-), & n \in \mathbb{N}. \end{cases} \quad (4.2.5)$$

Solving (4.2.5) in each interval $[n\tau, (n + \frac{1}{2})\tau]$, we obtain the discrete system

$$\begin{pmatrix} I_1((n + 1)\tau_+) \\ I_2((n + 1)\tau_+) \end{pmatrix} = T \begin{pmatrix} I_1(n\tau_+) \\ I_2(n\tau_+) \end{pmatrix}, \quad (4.2.6)$$

where T is a 2×2 matrix whose components are given by

$$\begin{aligned} T_{11} &= \frac{p(1+p)}{4} (e^{(\beta-\gamma)\tau} + e^{-\gamma\tau}) + \frac{p(1-p)}{2} e^{(\frac{\beta}{2}-\gamma)\tau} \\ T_{12} &= \frac{p(1+p)}{4} (e^{(\beta-\gamma)\tau} - e^{-\gamma\tau}) \\ T_{21} &= \frac{(1+p)}{4} (e^{(\beta-\gamma)\tau} + e^{-\gamma\tau}) \\ T_{22} &= \frac{(1+p)}{4} (e^{(\beta-\gamma)\tau} + e^{-\gamma\tau}) + \frac{(1-p)}{2} e^{(\frac{\beta}{2}-\gamma)\tau}. \end{aligned}$$

Conditions for epidemic control are obtained by imposing that $\rho(T) < 1$. Using again the Jury condition, one arrives through lengthy computations at the following result.

Proposition 4.2.2. • if $(e^{\beta\tau/2} - 1)e^{-\gamma\tau/2} > 2$ the epidemic grows for any value of p ;

- if $R_0 \leq 1$, the epidemic is controlled for any value of p ;
- if the previous conditions do not hold, then if p satisfies

$$p < p^* := \frac{2 - e^{-\frac{\gamma}{2}\tau} (e^{\frac{\beta}{2}\tau} - 1)}{e^{-\frac{\gamma}{2}\tau} (e^{\frac{\beta}{2}\tau} - 1) + 2e^{(\frac{\beta}{2}-\gamma)\tau}},$$

the number of infectives will decrease to 0, otherwise if $p > p^*$ the epidemic initially grows.

SEIR model with alternate testing For the SEIR model with alternate testing, the linearization reads

$$\begin{cases} E'_j(t) = \frac{\beta}{2} (I_1(t) + I_2(t)) - \sigma E_j(t), & j = 1, 2, \\ I'_j(t) = \sigma E_j(t) - \gamma I_j(t), & j = 1, 2, \\ I_1(n\tau_+) = p I_1(n\tau_-), & n \in \mathbb{N}, \\ I_2((n + \frac{1}{2})\tau_+) = p I_2((n + \frac{1}{2})\tau_-), & n \in \mathbb{N}. \end{cases} \quad (4.2.7)$$

Unfortunately, for (4.2.7) we are not able to find an explicit expression like in previous cases. Anyway, one can still characterize the stability of the DFE through conditions on the spectral radius of the discrete-time evolution operator associated to (4.2.7) and use numerical computations for exploiting when the spectral radius is less than one.

4.3 Control reproduction number for models with general testing events

In this section, we derive a characterization of the control reproduction number R_c (i.e., the reproduction number in the presence of interventions) for the (linearized) models with general mass testing events (4.2.1) and (4.2.3) starting from the general definition in Section I.3.1.

To do so, we note that in these models newly infected individuals are distinguished by the time t since last testing at the time in which they were infected. Indeed, the potential of an individual to infect others depends on t , as it determines the time that infectious individuals have before the next testing. Thus, denoting by τ the time between to consecutive tests, the operator $\mathcal{K}$ in (I.3.1) becomes

$$(\mathcal{K}\phi)(t) := \int_0^\tau k(t, s)\phi(s) ds, \quad t \in [0, \tau], \quad (4.3.1)$$

where ϕ is a function that represents the density of the distribution with respect to the time since last testing of individuals. The control reproduction number is the spectral radius of $\mathcal{K}$, i.e., $R_c := \rho(\mathcal{K})$.

We are left with the determination of the kernel $k(t, s)$, which represents the expected number of infectives of type t generated by an infective of type s over its whole infectious period. To do this, we note that individuals who were infected at time s in the testing cycle can still contribute to new infections at time t if and only if they are still infectious and have not been tested and isolated. With this in mind, we specialize the derivation of the kernel k for the SIR model (4.2.1) and the SEIR model (4.2.3).

4.3.1 Control reproduction number for the SIR model with general testing

In this section, we derive the kernel $k(t, s)$ for the SIR model. To do this, we need to compute the probability of being infectious at time $t \geq 0$ if infected at time 0 in the absence of interventions, which is given by $e^{-\gamma t}$, $t \geq 0$. Hence, using the memoryless properties of the exponential distribution, we obtain

$$k(t, s) = \beta e^{-\gamma(t-s)} \chi_{[0, t]}(s) + p e^{-\gamma(\tau-s)} k(t, 0). \quad (4.3.2)$$

Note that k is the sum of two contributions: the first term on the right-hand side of (4.3.2) represents the expected number of infectives generated before the first testing event; the second term, instead, represents the probability of still being infective after the testing event, times the expected number of infectives generated t time after the testing event (note in fact that $p e^{-\gamma(\tau-s)}$ is the probability of having survived up to time τ if infected at time s , times the probability of not have been tested and isolated).

Now, setting $s = 0$ in (4.3.2), we have⁴

$$k(t, 0) = \beta \frac{e^{-\gamma t}}{1 - pe^{-\gamma \tau}},$$

from which we get

$$k(t, s) = \beta e^{-\gamma(t-s)} \left(\chi_{[0,t]}(s) + \frac{pe^{-\gamma \tau}}{1 - pe^{-\gamma \tau}} \right). \quad (4.3.3)$$

Then, inserting (4.3.3) in (4.3.1), we get

$$(\mathcal{K}\psi)(t) = \beta e^{-\gamma t} \left(\int_0^t e^{\gamma s} \psi(s) ds + \frac{pe^{-\gamma \tau}}{1 - pe^{-\gamma \tau}} \int_0^\tau e^{\gamma s} \psi(s) ds \right), \quad t \in [0, \tau],$$

which is a positive operator acting on the space $L^1([0, \tau], \mathbb{R})$. The control reproduction number, R_c , is characterized as the spectral radius of $\mathcal{K}$. Note that $\mathcal{K}$ is an integral operator of mixed Fredholm-Volterra type. Moreover, it is easy to see that it is compact. Hence, the Krein-Rutmann theorem ensures that R_c is a dominant eigenvalue with associated a nonnegative eigenfunction.

In this case, one can easily obtain that the eigenfunction associated to R_c is

$$\phi(t) = e^{(\frac{\beta}{R_c} - \gamma)t}, \quad t \in [0, \tau],$$

and from this deduce that

$$R_c = \frac{R_0}{1 - \frac{\log(p)}{\gamma \tau}}, \quad (4.3.4)$$

where $R_0 = \beta/\gamma$. Note that R_c tends to R_0 as τ goes to infinity, while it tends to 0 as τ goes to 0. From (4.3.4), we get the condition for epidemic control

$$R_c \leq 1 \iff p \leq e^{-(R_0-1)\gamma \tau}. \quad (4.3.5)$$

Note that this is the same condition obtained in (4.2.1).

4.3.2 Control reproduction number for the SEIR model with general testing

In this section we extend the idea of Section 4.3.1 to the SEIR model. To do so, as for the SIR model, we need to compute the probability of being infectious at time t if exposed at time 0 in the absence of interventions. Using again the memoryless properties of the exponential distribution, we obtain⁵

$$\Gamma(t) := \sigma \int_0^t e^{-\sigma s} e^{-\gamma(t-s)} ds = \begin{cases} \frac{\sigma}{\gamma - \sigma} (e^{-\sigma t} - e^{-\gamma t}), & \sigma \neq \gamma, \\ \gamma t e^{-\gamma t}, & \sigma = \gamma. \end{cases}$$

From this, we get

$$k(t, s) = \beta \Gamma(t-s) \chi_{[0,t]}(s) + e^{-\sigma(\tau-s)} k(t, 0) + p \Gamma(\tau-s) k_I(t, 0). \quad (4.3.6)$$

The first term represents the infections produced before the first testing event, the second those produced afterwards if the individual is still exposed at the first testing event, and the third those produced after the first testing if the individual is infectious at the testing but does not get isolated. The term k_I can be determined by proceeding as in Section 4.3.1, obtaining

$$k_I(t, 0) = \frac{\beta e^{-\gamma t}}{1 - pe^{-\gamma \tau}}.$$

⁴Note that $k(t, 0) = \beta e^{-\gamma t} \sum_{j=0}^{\infty} (pe^{-\gamma \tau})^j$.

⁵The term $\sigma e^{-\sigma t}$ gives the probability density function of the event “not being removed before time $t \geq 0$.”

Hence, we get

$$k(t, s) = \beta \Gamma(t - s) \chi_{[0, t]}(s) + e^{-\sigma(\tau - s)} k(t, 0) + p \Gamma(\tau - s) \frac{\beta e^{-\gamma t}}{1 - p e^{-\gamma \tau}}. \quad (4.3.7)$$

Then, setting $s = 0$ in (4.3.7), we can solve for $k(t, 0)$ obtaining

$$k(t, 0) = \beta \frac{\Gamma(t) + \Gamma(\tau) \frac{p e^{-\gamma t}}{1 - p e^{-\gamma \tau}}}{1 - e^{-\sigma \tau}}.$$

Finally, we find

$$k(t, s) = \beta \left(\Gamma(t - s) \chi_{[0, t]}(s) + c(t, s) \right), \quad \tau, s \in [0, \tau], \quad (4.3.8)$$

where

$$c(t, s) := \Gamma(\tau - s) \frac{p e^{-\gamma t}}{1 - p e^{-\gamma \tau}} + e^{-\sigma(\tau - s)} \frac{\Gamma(t) + \Gamma(\tau) \frac{p e^{-\gamma t}}{1 - p e^{-\gamma \tau}}}{1 - e^{-\sigma \tau}}, \quad t, s \in [0, \tau].$$

Then, inserting (4.3.8) in (4.3.1), we get

$$(\mathcal{K}\psi)(t) := \beta \left(\int_0^t \Gamma(t - s) \psi(s) ds + \int_0^\tau c(t, s) \psi(s) ds \right).$$

which is a positive operator acting on $L^1([0, T], \mathbb{R})$. As in the case of the SIR model, $\mathcal{K}$ is an integral operator of mixed Volterra-Fredholm type. Yet, differently from Section 4.3.1, finding an explicit expression for R_c in this case is not an easy task. Hence, we have to resort to numerical computations to compute R_c .

4.4 Control reproduction number for models with alternate testing events

In this section, we extend the idea of Section 4.3 to the case of the (linearized) models with alternate testing events (4.2.5) and (4.2.7).

To do so, let us note that now newly infected individuals of a certain group (either 1 or 2) are distinguished by the time t since the last testing event of their own group at the time in which they were infected. Indeed, the potential of an individual of either group 1 or 2 to infect others depends on t , as it determines the time that infectious individuals have before the next testing of their group. Thus, denoting by τ the time between two consecutive tests of the same group, which we assume to be the same for group 1 and 2, the operator $\mathcal{K}$ in (I.3.1) can be recast again as in (4.3.1) and $R_c := \rho(\mathcal{K})$.

As before, we are faced with the computation of the kernel k in Equation (4.3.1). Since now we have two groups, 1 and 2, for each of these groups we have to compute $k_{ij}(t, s)$, i.e., the expected number of individuals of group i and type t generated by an individual of group j and type s during its whole infectious period. Then, k will be a 2×2 matrix

$$k(t, s) = \begin{pmatrix} k_{11}(t, s) & k_{12}(t, s) \\ k_{21}(t, s) & k_{22}(t, s) \end{pmatrix}, \quad t, s \in [0, \tau].$$

We start by noting that, since the two groups are identical, the probability for an individual of group i to have a contact with another individual of group i , is $1/2$, $i = 1, 2$.⁶ Hence, it is not difficult to see that

$$k_{11}(t, s) = \frac{1}{2} \tilde{k}(t, s), \quad (4.4.1)$$

⁶Of course, if the total population is not equally divided in two groups, but is divided according to $P_1 = (1 - x)P$ and $P_2 = xP$, for $x \in (0, 1)$, the contact probabilities respectively become $\frac{1}{1-x}$ and $\frac{1}{x}$.

where $\tilde{k}$ is the kernel obtained for the corresponding case with general mass testing.

To compute $k_{12}(\tau, s)$, we have to separately consider, because of the difference in testing times between the two groups, the case $t \in (0, \tau/2)$ and $t \in (\tau/2, \tau)$. If $t \in (0, \tau/2)$, an individual of group 1 can have been infected by individuals of group 2 of type s , with $s \in (0, t + \tau/2)$, before their first testing. Hence,

$$k_{12}(\tau, s) = \frac{1}{2} \tilde{k}(t + \tau/2, s), \quad \tau \in (0, \tau/2).$$

If $t \in (\tau/2, \tau)$, an individual of group 1 may have been infected, before their first testing, only by individuals of group 2 of type s with $s \in (0, t - \tau/2)$. Hence, one obtains

$$k_{12}(\tau, s) = \frac{1}{2} \tilde{k}(t - \tau/2, s), \quad \tau \in (\tau/2, \tau).$$

Finally, since the two groups and their contacts are identical, by symmetry we have $k_{22}(\tau, s) = k_{11}(\tau, s)$ and $k_{21}(\tau, s) = k_{12}(\tau, s)$. Hence, summarizing what above, we have

$$k(t, s) = \frac{1}{2} \begin{pmatrix} \tilde{k}(t, s), & \tilde{k}(\zeta(t), s) \\ \tilde{k}(\zeta(t), s), & \tilde{k}(t, s) \end{pmatrix}, \quad t, s \in [0, \tau], \quad (4.4.2)$$

where

$$\zeta(t) := \begin{cases} t + \frac{\tau}{2}, & \text{if } t \in (0, \frac{\tau}{2}), \\ t - \frac{\tau}{2}, & \text{if } t \in (\frac{\tau}{2}, \tau). \end{cases} \quad (4.4.3)$$

From (4.3.1) and (4.4.2), we obtain that $\mathcal{K}$ is a positive operator acting on the space $L^1([0, \tau]^2, \mathbb{R}^2)$, and is defined, for $\psi := (\psi_1; \psi_2)$, as

$$(\mathcal{K}\psi)(t) := \begin{pmatrix} \int_0^\tau (\tilde{k}(t, s)\psi_1(s) + \tilde{k}(\zeta(t), s)\psi_2(s)) \, ds \\ \int_0^\tau (\tilde{k}(\zeta(t), s)\psi_1(s) + \tilde{k}(t, s)\psi_2(s)) \, ds \end{pmatrix}, \quad t \in [0, \tau]. \quad (4.4.4)$$

It is easy to see that for the SIR and SEIR model, $\mathcal{K}$ is a compact operator. Moreover, it is strongly positive, i.e., $\mathcal{K}\psi > 0$ for $\psi > 0$. Hence, the Krein-Rutmann theorem ensures that there exists a unique real eigenvalue of $\mathcal{K}$ associated to a positive eigenfunction, see [88, Proposition 10.9, 99].

Let us note that the search for eigenvalues and eigenvectors of $\mathcal{K}$ can be simplified. Indeed, if η is an eigenfunction with eigenvalue λ of the strongly positive operator $\mathcal{Q}: L^1([0, \tau], \mathbb{R}) \rightarrow L^1([0, \tau], \mathbb{R})$ defined as

$$(\mathcal{Q}\eta)(t) := \int_0^\tau (\tilde{k}(t, s) + \tilde{k}(\zeta(t), s)) \eta(s) \, ds, \quad (4.4.5)$$

then the vector function $(\eta; \eta)$ is an eigenfunction of $\mathcal{K}$ with eigenvalue λ . Hence, R_c can equivalently be computed as the unique positive eigenvalue of $\mathcal{Q}$ corresponding to a positive eigenfunction. Eventually, note that $\mathcal{Q}$ can be seen as the restriction of $\mathcal{K}$ to the space $\{(\psi_1, \psi_2) \in L^1([0, \tau], \mathbb{R}^2) \mid \psi_1 = \psi_2\}$. Hence, in the following, with abuse of notation, we denote $\mathcal{Q}$ by $\mathcal{K}$ and η by ψ .

As for the case with general testing, one can explicitly derive an expression for R_c and the relevant eigenfunction for the SIR model with alternate testing. In fact, one can check by direct substitution that

$$\psi(t) := \begin{cases} Ce^{(\frac{\beta}{R_c} - \gamma)t}, & t \in (0, \frac{\tau}{2}), \\ Ce^{(\frac{\beta}{R_c} - \gamma)(t - \frac{\tau}{2})}, & t \in (\frac{\tau}{2}, \tau) \end{cases} \quad (4.4.6)$$

is a positive eigenfunction for $\mathcal{K}$ with relevant eigenvalue

$$R_c = \frac{R_0 \gamma T}{2} \left[\log \left(\frac{1 + q(1+z)^2 + 2z}{1 + q(1+z)^2} \right) \right]^{-1}, \quad (4.4.7)$$

where $z := e^{\gamma \frac{\tau}{2}}$, and q is defined as

$$q := \frac{pe^{-\gamma\tau}}{1 - pe^{-\gamma\tau}}.$$

Direct substitution shows that the condition $p = p^*$, for p^* defined as in Theorem 4.2.2, holds if and only if $R_c = 1$, i.e., the information on the stability boundaries are the same.

As for the SEIR model with alternate testing, finding an explicit expression for R_c is not an easy task. Hence, numerical methods enter the scene.

4.5 Generalization and numerical approach

Let us note that, for the models considered so far, the NGO takes the form of an integral operator of mixed Volterra-Fredholm type. This is due to the heterogeneity introduced in the model by the mass testing event. Although we presented the derivation of the NGO only for the SIR and the SEIR models, we expect that, in the case of $d \geq 1$ equations describing the dynamics of the infected individuals near the DFE in the presence of general mass testing events, the NGO will be an integral operator $\mathcal{K}: L^1([0, \tau], \mathbb{R}^d) \rightarrow L^1([0, \tau], \mathbb{R}^d)$ of the following type

$$(\mathcal{K}\psi)(t) := B \left(\int_0^t F(t-s)\psi(s) ds + \int_0^\tau G(t,s)\psi(s) ds \right) \quad (4.5.1)$$

where $B \in \mathbb{R}^{d \times d}$, $F \in \text{Lip}^0([0, \tau], \mathbb{R}^{d \times d})$ and $G \in \text{Lip}^0([0, \tau]^2, \mathbb{R}^{d \times d})$.⁷ Moreover, we expect that the extension to the case of models with alternate mass testing, will lead to a modification of (4.5.1) by including the effect of a piecewise linear function as the one in (4.4.3).

For this reason, in this section, we introduce a numerical method to approximate the control reproduction number of models that can be recast in the framework described in (4.5.1). As in the previous chapters, to obtain an approximation $R_{c,N}$ of R_c , we derive a finite-dimensional approximation $\mathcal{K}_N$ of $\mathcal{K}$, and we approximate the eigenvalues of the latter through those of the former. This is achieved by pseudospectral collocation. For the use of pseudospectral methods in Volterra and Fredholm equations, we refer to [41]. Notice that, since we are interested in the spectral theory, here we enlarge our attention to complex-valued functions.

4.5.1 Discretization of $\mathcal{K}$

Let us observe that the eigenfunctions of $\mathcal{K}$ are continuous, hence we can restrict our attention to the subspace $Y := C([0, \tau], \mathbb{C}^d)$ of $X := L([0, \tau], \mathbb{C}^d)$, where point evaluation is well-defined.

Given a positive integer N , we consider the space $Y_{N-1} \subset Y$ of algebraic polynomials on $[0, \tau]$ of degree at most $N-1$ and taking values in $\mathbb{C}^d$. Let $\Theta_N := \{a_1 < \dots < a_N\}$ denote a mesh of N points in $(0, \tau)$. We define restriction and prolongation operators respectively as

$$\mathcal{R}_N: Y \rightarrow \mathbb{C}^{dN}, \quad \mathcal{R}_N\psi := (\psi(t_1); \dots; \psi(t_N)),$$

and

$$\mathcal{P}_{N-1}: \mathbb{C}^{dN} \rightarrow Y_{N-1}, \quad \mathcal{P}_{N-1}\Psi := \sum_{i=1}^N \ell_i \Psi.$$

⁷Note that the choice of requiring F and G to be Lipschitz is not restrictive as, in the case of compartmental models, we expect F and G to be even more regular.

where $\Psi := (\Psi_1; \dots; \Psi_N)$, for $\Psi_i \in \mathbb{C}^d$, $i = 1, \dots, N$, and $\{\ell_i\}_{i=1}^N$ is the Lagrange polynomial basis relevant to Θ_N . Observe that

$$\mathcal{R}_N \mathcal{P}_{N-1} = \mathcal{I}_{\mathbb{C}^{dN}}, \quad \mathcal{P}_{N-1} \mathcal{R}_N = \mathcal{L}_{N-1},$$

where $\mathcal{L}_{N-1}: Y \rightarrow Y_{N-1}$ is the Lagrange interpolation operator relevant to Θ_N .

Then, we derive the finite-dimensional approximation $\mathcal{K}_N: \mathbb{C}^{dN} \rightarrow \mathbb{C}^{dN}$ of $\mathcal{K}$ as

$$\mathcal{K}_N := \mathcal{R}_N \mathcal{K} \mathcal{P}_{N-1}. \quad (4.5.2)$$

We make the following assumption.

Assumption 4.1. Θ_N is the mesh of Chebyshev zeros in $[0, \tau]$.

The discrete eigenvalue problem is solved by using the standard MATLAB function `eig`.

4.5.2 Piecewise extension for models with two groups alternately tested

The method presented in Section 4.5.1 can be adapted to approximate R_c in models for which the NGO can be recast as follows

$$(\mathcal{K}\psi)(t) = \frac{1}{2}B \left(\int_0^t F(t-s)\psi(s) \, ds + \int_0^{\zeta(t)} F(\zeta(t)-s)\psi(s) \, ds \right. \\ \left. + \int_0^\tau (G(t,s) + G(\zeta(t),s)) \psi(s) \, ds \right), \quad \tau \in [0, \tau],$$

where f is defined as in (4.4.3); see for instance (4.4.4) and (4.4.5). To conveniently deal with the jump-discontinuity at $t = \tau/2$, we have to resort to a piecewise approach. More in details, let $\Theta_{N,j} := \{t_{1,j} < \dots < t_{m,j}\}$ denote a mesh of points in $(\frac{(j-1)\tau}{2}, \frac{j\tau}{2})$, $j = 1, 2$. We consider the space

$$\tilde{Y} := \left\{ \psi \in L^1([0, \tau], \mathbb{C}^d) \mid \psi|_{\left(\frac{k\tau}{2}, \frac{(k+1)\tau}{2}\right)} \text{ is continuous, } k = 0, 1, \right. \\ \left. \text{and } \lim_{\tau \rightarrow 0^+} \psi(t), \lim_{\tau \rightarrow \frac{\tau}{2}^\pm} \psi(t), \lim_{\tau \rightarrow T^-} \psi(t) \text{ exist finite} \right\},$$

and we define restriction and prolongation operators respectively as

$$\tilde{\mathcal{R}}_N: \tilde{Y} \rightarrow \mathbb{C}^{2dN}, \quad \tilde{\mathcal{R}}_N \psi := (\psi(t_{1,1}); \dots; \psi(t_{N,1}); \psi(t_{1,2}), \dots; \psi(t_{N,2})),$$

and

$$\tilde{\mathcal{P}}_{N-1}: \mathbb{C}^{2dN} \rightarrow \tilde{Y}, \quad \tilde{\mathcal{P}}_{N-1} \Psi := \sum_{i=1}^N \ell_{i,1} \chi_{[0, \frac{\tau}{2}]} \Psi_{i,1} + \sum_{i=1}^N \ell_{i,2} \chi_{[\frac{\tau}{2}, \tau]} \Psi_{i,2},$$

where $\Psi := (\Psi_{1,1}; \dots; \Psi_{N,1}; \Psi_{1,2}; \dots; \Psi_{N,2})$. Then, we define $\tilde{\mathcal{K}}_N: \mathbb{C}^{2dN} \rightarrow \mathbb{C}^{2dN}$ of $\mathcal{K}$ as

$$\tilde{\mathcal{K}}_N := \tilde{\mathcal{R}}_N \tilde{\mathcal{K}} \tilde{\mathcal{P}}_{N-1}. \quad (4.5.3)$$

Note that $\tilde{\mathcal{P}}_{N-1}$ has a jump-discontinuity at $t = \frac{\tau}{2}$, which is in accordance with the fact that we are approximating a function with the same property. Note moreover that, although here we restricted to the case of a single jump-discontinuity point, the method can be further extended to account for the case of more discontinuity points.

4.6 Convergence analysis

In this section, we investigate the convergence of the eigenvalue(s) (and the corresponding eigenvectors) of $\mathcal{K}_N$ to those of $\mathcal{K}$ via the spectral approximation theory of [45]. To this aim, we define the operator

$$\mathcal{P}_{N-1}\mathcal{K}_N\mathcal{R}_N: Y \rightarrow Y,$$

which has the same nonzero eigenvalues with the same geometric and partial multiplicities of $\mathcal{K}_N$, see Theorem 1.3.1. Observe that $\mathcal{P}_{N-1}\mathcal{K}_N\mathcal{R}_N = \mathcal{L}_{N-1}\mathcal{K}\mathcal{L}_{N-1}$. Hence, since

$$\text{Range}(\mathcal{L}_{N-1}) \subset Y_{N-1},$$

Theorem 1.3.2 ensures that $\mathcal{L}_{N-1}\mathcal{K}\mathcal{L}_{N-1}$ has the same nonzero eigenvalues with the same geometric and partial multiplicities, and the same eigenfunctions as the operator $\hat{\mathcal{K}}_N := \mathcal{L}_{N-1}\mathcal{K}$. Thus, we have the following result that follows immediately from the fact that $\mathcal{L}_{N-1}\mathcal{K} - \mathcal{K} = (\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{K}$ is compact for every $N \geq \bar{N}$.

Theorem 4.6.1. *Let $\lambda \in \mathbb{C}$ be an isolated nonzero eigenvalue of $\mathcal{K}$ with finite algebraic multiplicity m and ascent l and let Δ be a neighborhood of λ such that λ is the sole eigenvalue of $\mathcal{K}$ in Δ . Then there exists $\bar{N}$ such that, for $N \geq \bar{N}$, $\hat{\mathcal{K}}_N$ has in Δ exactly m eigenvalues $\lambda_{N,j}$, $j = 1, \dots, m$, counting their multiplicities. Moreover,*

$$\max_{j=1, \dots, m} |\lambda_{N,j} - \lambda| = O(\varepsilon_N^{1/l})$$

for

$$\varepsilon_N := \|\mathcal{L}_{N-1}\mathcal{K} - \mathcal{K}\|_{Y \leftarrow E_\lambda}$$

and E_λ the generalized eigenspace of λ . Finally, for any $j = 1, \dots, m$ and for any eigenvector $\psi_{N,j}$ of $\hat{\mathcal{K}}_N$ relevant to $\lambda_{N,j}$ such that $\|\psi_{N,j}\|_Y = 1$, we have

$$\text{dist}(\psi_{N,j}, \ker(\lambda\mathcal{I}_Y - \mathcal{K})) = O(\varepsilon_N^{1/l}),$$

where dist is the distance in the space Y between an element and a subspace.

Proof. Let Lip^0 be endowed with the usual Lipschitz norm. Observe that $\mathcal{K}: Y \rightarrow \text{Lip}^0([0, \tau], \mathbb{C}^d)$ is bounded. Thus from Assumption 4.1 and Theorem 1.1.6, we have that there exists a constant $C > 0$ independent of N such that

$$\begin{aligned} \|(\mathcal{L}_{N-1} - \mathcal{I}_Y)\mathcal{K}\|_{Y \leftarrow Y} &\leq \|\mathcal{L}_{N-1} - \mathcal{I}_Y\|_{Y \leftarrow \text{Lip}^0([0, \tau], \mathbb{C}^d)} \|\mathcal{K}\|_{\text{Lip}^0([0, \tau], \mathbb{C}^d) \leftarrow Y} \\ &\leq C \frac{\log N}{N} \|\mathcal{K}\|_{\text{Lip}^0([0, \tau], \mathbb{C}^d) \leftarrow Y}, \end{aligned}$$

which tends to 0 as $N \rightarrow \infty$. Then, thesis follows as in the proof of Theorem 2.3.3. $\square$

The analysis is now completed with a bound on the error on the eigenvalues depending on the regularity of F, G .

Assumption 4.2.

- (i) $F \in \text{Lip}^s([0, \tau], \mathbb{R}^{d \times d})$ and $G \in \text{Lip}_\tau^s([0, \tau]^2, \mathbb{R}^{d \times d})$ for some integer $s \geq 0$,
- (ii) $F \in C^\infty([0, \tau], \mathbb{R}^{d \times d})$ and $G \in C^\infty([0, \tau]^2, \mathbb{R}^{d \times d})$,
- (iii) F, G are real analytic.

Corollary 4.6.2. *Let Assumption 4.1 and Assumption 4.2 hold. Let $\lambda, \lambda_{N,i}, i = 1, \dots, s, E_\lambda$ and ε_N be as in Theorem 2.3.3. Then*

$$\varepsilon_N = O(\rho_N),$$

where

$$\rho_N := \begin{cases} N^{-(s+1)} \log N & \text{under Assumption 4.2 (i),} \\ N^{-r} \log N & \text{for every integer } r \geq 1 \text{ under Assumption 4.2 (ii),} \\ p^{-N} \log N & \text{for some constant } p > 1 \text{ under Assumption 4.2 (iii).} \end{cases}$$

Proof. Let us observe that

(i) $\mathcal{K}(E_\lambda) \subset \text{Lip}^p([0, \tau], \mathbb{C}^d)$ under Assumption 4.2 (i),

(ii) $\mathcal{K}(E_\lambda) \subset C^\infty([0, \tau], \mathbb{C}^d)$ under Assumption 4.2 (ii),

(iii) $\mathcal{K}(E_\lambda)$ consists of analytic functions under Assumption 4.2 (iii).

Then, the thesis follows by proceeding as in the proof of Corollary 2.3.4. $\square$

4.7 Implementation issues

Here we give an explicit description of the entries of the matrix $\mathcal{K}_N$. For the sake of simplicity, we restrict to the case $d = 1$. Thanks to the cardinal property of the Lagrange polynomials in (1.1.3), it is easy to see that the entries of the matrix $\mathcal{K}_N$ are explicitly given by

$$[\mathcal{K}_N]_{i,j} := B \left(\int_0^{t_i} F(t_i - s) \ell_j(s) ds + \int_0^\tau G(t_i, s) \ell_j(s) ds \right), \quad i, j = 1, \dots, N. \quad (4.7.1)$$

When the integrals in (4.7.1) cannot be computed analytically, we approximate them via the Fejer's first rule quadrature with N nodes [139].

In this case, the bounds in Corollary 4.6.2 are preserved under the following regularity conditions [53, pp. 85, 131].

Assumption 4.3.

(i) $c(\tau, \cdot), \Gamma \in \text{Lip}^s([0, a^+], \mathbb{R}^{d \times d})$ for some integer $s \geq 0$, for every $\tau \in [0, \tau]$,

(ii) $c(\tau, \cdot), \Gamma \in C^\infty([0, a^+], \mathbb{R}^{d \times d})$, for every $\tau \in [0, \tau]$,

(iii) $c(\tau, \cdot), \Gamma$ are real analytic for every $\tau \in [0, \tau]$,

4.7.1 Implementation for models with alternate testing

Here we give an explicit description of the entries of the matrix $\tilde{\mathcal{K}}_N$ in (4.5.3). Again, for simplicity, we restrict to the case $d = 1$. It is easy to see that $\tilde{\mathcal{K}}_N$ may be explicitly rewritten as $\tilde{\mathcal{K}}_N = \kappa_1 + \kappa_2 + \kappa_3$, where $\kappa_1, \kappa_2, \kappa_3: \mathbb{C}^{2N} \rightarrow \mathbb{C}^{2N}$ are defined as

$$[\kappa_1]_{i+Nh,j+Nk} := \frac{1}{2} B \int_{k\frac{\tau}{2}}^{(k+1)\frac{\tau}{2}} \bar{G}(t_{i,h+1}, s) \ell_{j,k+1}(s) ds, \quad i, j = 1, \dots, N, \quad h, k = 0, 1,$$

where $\bar{G}(t, s) := G(t, s) + G(\zeta(t), s)$, for $t, s \in [0, \tau]$,

$$[\kappa_2]_{i+Nh,j+Nk} := \begin{cases} \frac{1}{2} B \int_{h\frac{\tau}{2}}^{t_{i,h+1}} F(t_{i,h+1} - s) \ell_{j,h+1}(s) ds, & i, j = 1, \dots, N, \quad h = 0, 1, \quad k = h, \\ \frac{1}{2} B \int_0^{\frac{\tau}{2}} F(t_{i,2} - s) \ell_{j,1}(s) ds, & i, j = 1, \dots, N, \quad h = 1, \quad k = 0, \\ 0, & \text{otherwise,} \end{cases}$$

and

$$[\kappa_3]_{i+hN, j+kN} := \begin{cases} [\kappa_2]_{i+N, j}, & i, j = 1, \dots, N, \quad h = k = 0, \\ [\kappa_2]_{i, j}, & i, j = 1, \dots, N, \quad h = 1, \quad k = 0, \\ [\kappa_2]_{i, j+N}, & i, j = 1, \dots, N, \quad h = 0, \quad k = 1, \\ 0, & \text{otherwise.} \end{cases}$$

4.8 Numerical results

In this section, we experimentally validate the theoretical results in Section 4.6 by applying the method to the models presented in Section 4.1.1 and we numerically illustrate the dependence of R_c on the model parameters for the four models. We start by observing that, in Figure 4.8.1, infinite convergence order occurs for all the 4 models, which is in perfect accordance with the results of Section 4.6, as the model parameters are (piecewise) C^∞ functions. This is expected as the main ingredients in the construction of the NGO are the probabilities of moving from one state to another, which are generally described by smooth functions, see for example [98, Section 3]. Hence, the kernels involved in (4.5.1) are typically (piecewise) analytic functions.

Figure 4.8.2 shows the behavior of R_c as a function of p for the four models. Note that, while extinction of an epidemic is always possible in the SIR model with general testing by taking p small enough, the same does not hold for the other models. In particular, note that for this choice of the parameters (with $R_0 = 3$), it is impossible to control an epidemic if the interval between tests is larger or equal to approximately the mean length of the infectious period, i.e., $\gamma T \geq 1$.

Introducing either alternate testing events or the impossibility to detect exposed individuals makes control more difficult with respect to the case of the SIR model with general testing. Yet, the combination of these two features does not seem to have a big impact on the amount of interventions to apply to control the epidemic. Observe in fact that the results for the SEIR model with general testing are only slightly different from the case with alternating testing events. Yet, among the considered examples, the SEIR model with alternate testing is the one giving more “restrictive” conditions for control.

Additionally, an interesting fact we observed in [120] is that the mean length of the latent phase σ has a very minor effect on the value of R_c .

Finally, Figure 4.8.3 shows the level curves for $R_c = 1$ as functions of β and p for $\gamma T = 0.5, 1, 1.5$. Note that the results for the SEIR model with general testing events are consistent with the conditions in Theorem 4.2.1. As a matter of fact, the same picture was obtained in [120] by looking at the stability boundaries for the discrete evolution operators discussed in (4.2) (which were numerically computed in the case of the SEIR model with alternated testing events). This confirms, in our case, the correct definition and derivation for the NGOs and R_c in Section 4.3.

Remark 4.8.1. For the classical SIR and SEIR models, one can determine the so called final size, i.e., the total number of individuals that will be infected during the outbreak. This quantity is strictly related to R_0 [57]. In fact, under the assumption that nobody is immune at the beginning of an epidemic, if we denote by $z := 1 - \frac{S_\infty}{S_0}$ the fraction of individuals that eventually gets infected, we have

$$1 - z = e^{-R_0 z - (1-z)\left(1 - \frac{S_0}{N}\right)}. \quad (4.8.1)$$

Such a relation does not hold in general for model with heterogeneities [6]. Yet, in [120] we numerically investigated (using the method presented in this chapter) if such a relation may hold for the models considered in this chapter. It turned out that, although the relation in (4.8.1) is presumably not exact, it provides very good approximation for the final sizes (numerically computed as $1 - \lim_{t \rightarrow +\infty} S(t)$).

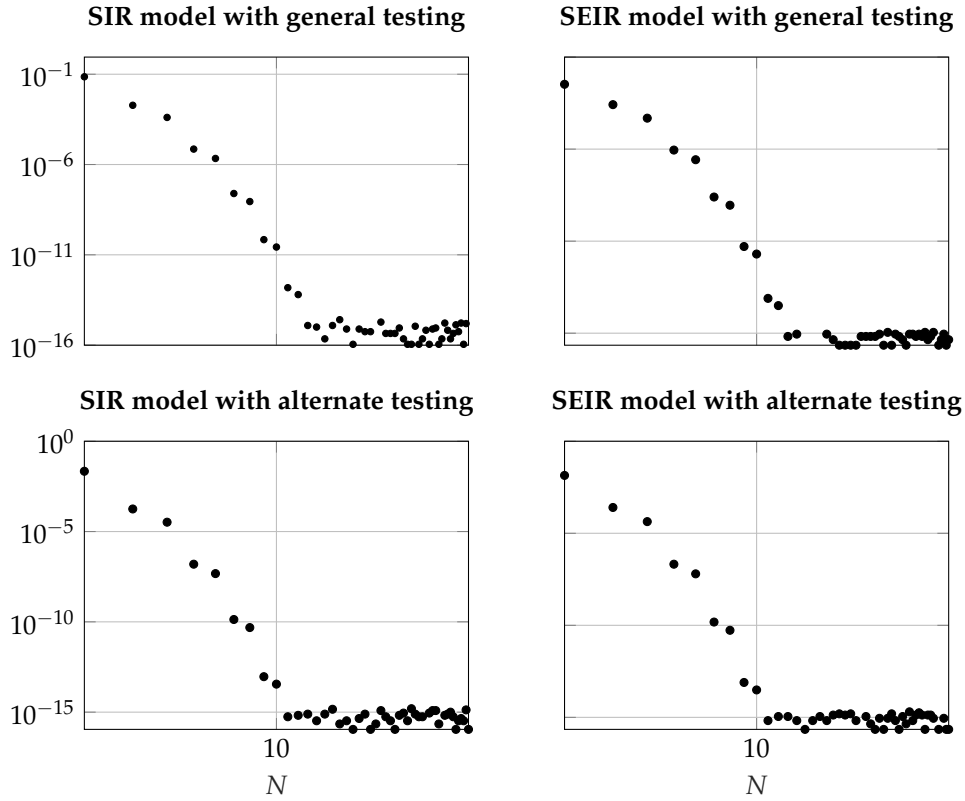


Figure 4.8.1: Log-log plot for increasing N of the approximation of R_c for the SIR model with general testing (upper row, left), for the SEIR model with general testing (upper row, right), for the SIR model with alternate testing (lower row, left) and for the SEIR model with alternate testing (lower row, right), $\tau = 2$, $\beta = 1$, $\gamma = 1$ and $\sigma = 1$. The errors for the SIR model are computed with respect to the values obtained from the theoretical expressions (4.3.4) and (4.4.7) for $p = 0.5$. The errors for the SEIR model are computed with respect to the value $R_c = R_0 = \beta/\gamma$, which holds for $p = 1$. Infinite order of convergence is observed in all the panels.

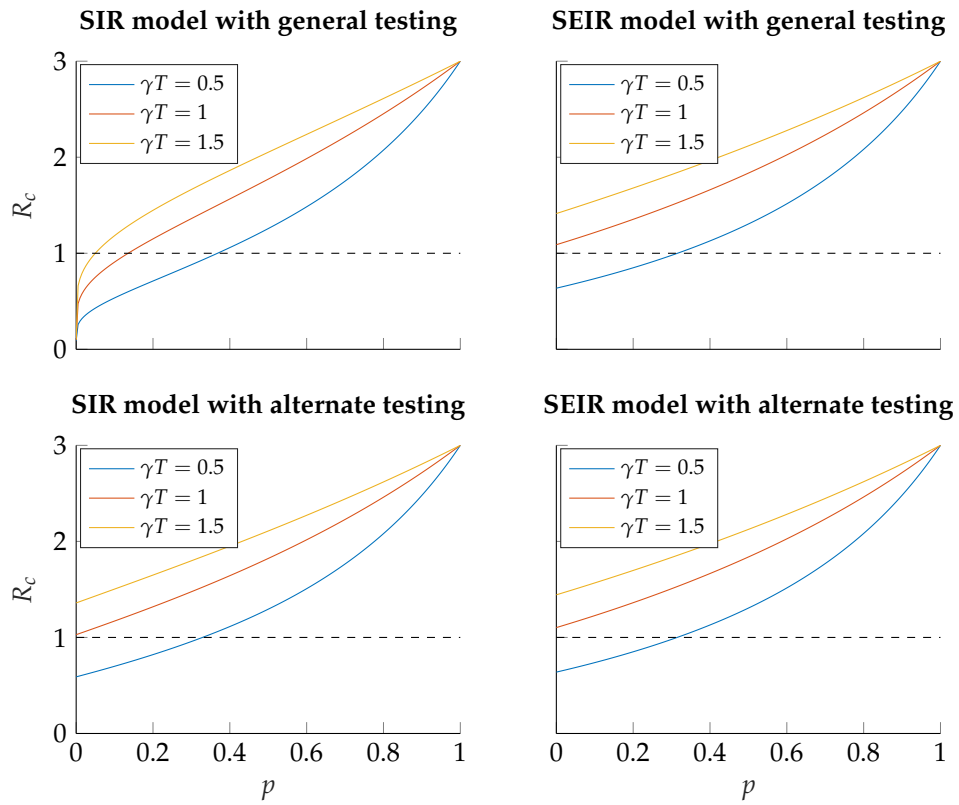


Figure 4.8.2: R_c as a function of p for the SIR model with general testing (upper row, left), for the SEIR model with general testing (upper row, right), for the SIR model with alternate testing (lower row, left) and for the SEIR model with alternate testing (lower row, right), $R_0 = 3$, $\sigma = 1.2\gamma$, and $\gamma T = 0.5, 1, 1.5$. For the SIR models, R_c has been computed using the formulas in (4.3.4) and (4.4.7). Obtained with $N = 30$. Original figure from [120].

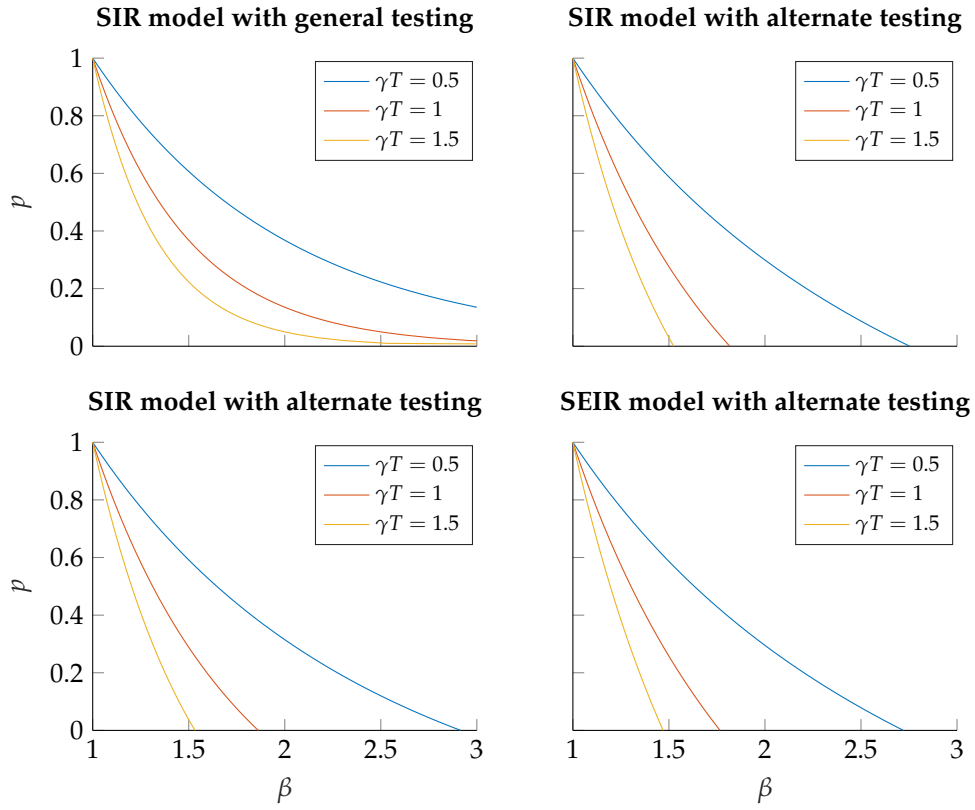


Figure 4.8.3: Level curves $R_c = 1$ as functions of β and p for the SIR model with general testing (upper row, left), for the SEIR model with general testing (upper row, right), for the SIR model with alternate testing (lower row, left) and for the SEIR model with alternate testing (lower row, right), for $\gamma T = 0.5, 1, 1.5$ and $\sigma = 1.2\gamma$. Obtained with $N = 30$. Original figure from [120].

Age-structured models with nonlocal diffusion

The aim of this chapter is to present a numerical method for the linear stability analysis of age-structured population models with nonlocal diffusion. The content of this chapter is mainly taken from the work by the author, D. Breda and R. Vermiglio [26].

Age-structured epidemic models with spatial diffusion are often formulated as IPDEs with nonlocal boundary conditions in which the diffusive term is represented by the Laplace operator (see [51] and the references in [96]). However, the latter describes the random spread of individuals in adjacent spatial positions, thus it is not suitable for describing, e.g., the spread of a disease via long-distance traveling [103]. In recent years, many authors [19, 97, 103, 106, 140, 141, 143] have considered nonlocal (convolution) diffusion operators of the form

$$\int_{\Omega} J(x-y) [u(y) - u(x)] dy \quad (5.0.1)$$

in order to describe the long-distance dispersal of a population u in a region $\Omega \subseteq \mathbb{R}^n$, where $J(x-y)$ is interpreted as the probability of jumping from position $y \in \Omega$ to $x \in \Omega$ [69]. Thus, in (5.0.1), the convolution $\int_{\Omega} J(x-y)u(y) dy$ represents the rate at which individuals are arriving at position $x \in \Omega$ from other places while $\int_{\Omega} J(y-x)u(x) dy$ represents the rate at which individuals are leaving location x to travel to other sites.

These and similar models have been intensively studied in a series of recent papers [65, 93, 94, 95, 96, 133], where the authors developed the relevant theory of the associated semigroups of solution operators, their asymptotic behavior, their spectral properties, as well as asynchronous exponential growth and nonlinear dynamics. Moreover, in [92] the authors investigated how age-structured models with Laplace diffusion can be approximated by models involving nonlocal diffusion. All these aspects are well understood when the evolution is considered on abstract spaces, leading to deal with infinite-dimensional dynamical systems. Consequently, when practical computations are required, numerical approximations enter the scene.

In this chapter, in view of investigating the stability of linear age-structured population models with nonlocal diffusion of Dirichlet type, we propose to approximate the (leading part of the) spectrum of the infinitesimal generator associated to the relevant semigroup of solution operators by reduction to finite dimension. This is achieved by combining a spectral projection in space with a pseudospectral collocation in age after integrating the state on the age interval in order to gain on regularity. Then we also extend to the Neumann case. We rigorously prove the convergence of the approximating eigenvalues to the exact ones in the case of separable model coefficients, and we experimentally validate the obtained results on some test cases. Further numerical tests are presented also for the general instance. This work extends the method proposed in [37] (in which the authors consider the case of Laplace diffusion) to the case of age-structured models with spatial-dependent coefficients.

The chapter is organized as follows. In Section 5.1, we present the prototype age-structured model with Dirichlet nonlocal diffusion of interest and the relevant assumptions. In Section 5.2 we

illustrate the abstract setting and the reformulation via integration of the age-state. The numerical approach is proposed in Section 5.3. In Section 5.4 we develop the convergence analysis. In Section 6.4 we provide some details about the implementation of the method, while Section 5.6 contains numerical experiments. In Section 5.7 we discuss some results for models with Neumann nonlocal diffusion.

5.1 Age-structured models with Dirichlet nonlocal diffusion

Let $u(t, a, x)$ denote the density of the population at time $t \geq 0$, age $a \in [0, a^+]$ and position $x \in \Omega$, where $a^+ \in (0, \infty)$ and $\Omega \subseteq \mathbb{R}^n$ is open, bounded and connected with C^1 boundary.

Age-structured models with Dirichlet nonlocal diffusion take the form [96]

$$\left\{ \begin{array}{ll} d\mathcal{D}u(t, a, x) = d \int_{\mathbb{R}^n} J(x-y)[u(t, a, y) - u(t, a, x)] dy - \mu(a, x)u(t, a, x), & t > 0, \quad a \in [0, a^+], \quad x \in \Omega, \\ u(t, 0, x) = \int_0^{a^+} \beta(a, x)u(t, a, x) da, & t > 0, \quad x \in \Omega, \\ u(t, a, x) = 0, & t > 0, \quad a \in [0, a^+], \quad x \in \mathbb{R}^n \setminus \Omega, \\ u(0, a, x) = u_0(a, x), & a \in [0, a^+], \quad x \in \Omega, \end{array} \right. \quad (5.1.1)$$

where $\mathcal{D}$ is defined as in (I.2.6), and $\beta, \mu: [0, a^+] \times \Omega \rightarrow \mathbb{R}$ and $d > 0$ describe birth, mortality, and diffusion, respectively. The kernel $J: \mathbb{R}^n \rightarrow \mathbb{R}$ is a C^0 , compactly supported¹ nonnegative radial function satisfying

$$\int_{\mathbb{R}^n} J(x) dx = 1, \quad J(x) \geq 0, \quad J(0) > 0.$$

Note that $J(x-y) = J(y-x)$ and $\int_{\mathbb{R}^n} J(x-y) dy = 1$ for a.a. $x \in \mathbb{R}^n$. Moreover, the diffusion takes place in the whole $\mathbb{R}^n$, but u vanishes outside Ω , thus the integrals in (5.1.1) can be considered in Ω instead of $\mathbb{R}^n$. As common in the literature [69, 88], u is an L^1 -function in age and an L^2 -function in space, and thus we introduce the space $U := L^1([0, a^+], L^2(\Omega, \mathbb{R}))^2$ equipped with the norm

$$\|\phi\|_U := \int_0^{a^+} \|\phi(a, \cdot)\|_{L^2(\Omega, \mathbb{R})} da.$$

Following these observations, given $u_0 \in U$, we say that u is a mild solution of (5.1.1) if $u \in C^0([0, +\infty), U)$, u is extended by zero in $\mathbb{R}^n \setminus \Omega$, and satisfies

$$\left\{ \begin{array}{ll} \mathcal{D}u(t, a, x) = d(\mathcal{J}u - u)(t, a, x) - \mu(a, x)u(t, a, x), \\ u(t, 0, x) = \int_0^{a^+} \beta(a, x)u(t, a, x) da, \\ u(0, a, x) = u_0(a, x), \end{array} \right. , \quad (5.1.2)$$

for $t \geq 0$, $a \in [0, a^+]$, $x \in \Omega$, in the sense of [96, Theorem 2.3] where, for brevity, we introduce $\mathcal{J}: U \rightarrow U$ defined as

$$\mathcal{J}\phi(a, x) := \int_{\Omega} J(x-y)\phi(a, y) dy.$$

Also, from the biological point of view, we write

$$\mu(a, x) = \mu_0(a) + \mu_1(a, x),$$

¹The hypothesis that J has compact support can be actually relaxed if one supposes Ω to be bounded [95].

²For simplicity we write $u(t, a, x)$ for $u(t)(a)(x)$ and we adopt a similar notation hereafter. Moreover, in general, when we write $(a, x) \in [0, a^+] \times \Omega$, we implicitly mean a.e..

where μ_0 represents the natural mortality and μ_1 describes how the spatial position of individuals affects the mortality depending on the age.

The following requirements are necessary to proceed with the analysis [65].

Assumption 5.1.

- (i) $\mu_0 \in L^1_{\text{loc}}([0, a^+], \mathbb{R})$ is positive and $\int_0^{a^+} \mu_0(a) da = +\infty$;
- (ii) $\mu_1 \in L^\infty([0, a^+], C(\overline{\Omega}, \mathbb{R}))$ is nonnegative;
- (iii) $\beta \in L^\infty([0, a^+], C(\overline{\Omega}, \mathbb{R}))$ is nonnegative.

By defining $\tilde{u}$ through $u(t, a, x) = \Pi_0(a)\tilde{u}(t, a, x)$ [81, 88] for the natural survival probability

$$\Pi_0(a) := e^{-\int_0^a \mu_0(\alpha) d\alpha}, \quad a \in [0, a^+],$$

(5.1.2) becomes

$$\begin{cases} \mathcal{D}\tilde{u}(t, a, x) = d(\mathcal{J}\tilde{u} - \tilde{u})(t, a, x) - \mu_1(a, x)\tilde{u}(t, a, x), \\ \tilde{u}(t, 0, x) = \int_0^{a^+} \beta(a, x)\Pi_0(a)\tilde{u}(t, a, x) da, \\ \tilde{u}(0, a, x) = \tilde{u}_0(a, x), \end{cases} \quad (5.1.3)$$

for $t > 0$, $a \in [0, a^+]$ and $x \in \Omega$, where $\tilde{u}_0 := \Pi_0^{-1}u_0$. In view of asymptotic stability, (5.1.2) and (5.1.3) are equivalent since Π_0 is bounded thanks to Assumption 5.1 (i).

5.2 Abstract setting

According to [94, 96], (5.1.3) can be seen as the abstract Cauchy problem

$$\begin{cases} \tilde{u}'(t) = \mathcal{A}\tilde{u}(t), & t > 0, \\ \tilde{u}(0) = \tilde{u}_0 \in D(\mathcal{A}), \end{cases} \quad (5.2.1)$$

where $\mathcal{A}: D(\mathcal{A}) \subseteq U \rightarrow U$ is defined by

$$\mathcal{A}\phi(a, x) := d(\mathcal{J}\phi - \phi)(a, x) - \partial_a\phi(a, x) - \mu_1(a, x)\phi(a, x),$$

$$D(\mathcal{A}) := \left\{ \phi \in U \mid \partial_a\phi \in U \text{ and } \phi(0, x) = \int_0^{a^+} \beta(a, x)\Pi_0(\alpha)\phi(\alpha, x) d\alpha \right\}. \quad (5.2.2)$$

Note that if $\tilde{u}_0 \in D(\mathcal{A})$ then $\tilde{u}$ is a classical solution in the sense of [96, Theorem 2.3]. Under Assumption 5.1, $\mathcal{A}$ generates the strongly continuous semigroup of bounded positive linear solution operators $\{T(t)\}_{t \geq 0}$ in U given by $T(t)\tilde{u}_0 := \tilde{u}(t)$. Moreover, its spectrum determines the stability of the null solution since the spectral bound $s(\mathcal{A})$ of $\mathcal{A}$ coincides with the growth bound of the generated semigroup. However, unlike the case of Laplace diffusion, $\{T(t)\}_{t \geq 0}$ is not eventually compact. This makes the stability analysis more involved since the spectrum of $\mathcal{A}$ is not necessarily just point spectrum. Nevertheless, sufficient conditions on the model coefficients are given in [65] (see definition (3.2) and Theorem 4.8 therein, to which we refer for a complete illustration) for the existence of a *principal* eigenvalue, i.e., a simple isolated real eigenvalue λ_0 strictly to the right of all the other spectral values of $\mathcal{A}$ (and with positive eigenfunction). Hence, under such conditions, $s(\mathcal{A}) = \lambda_0$ and thus everything reduces to computing the latter.

In view of analyzing the stability of (5.1.3), based on the above considerations, we propose to numerically approximate the principal eigenvalue λ_0 of $\mathcal{A}$. To this aim, inspired by [27] and Chapter 2, we introduce the following equivalent reformulation, which allows one to gain in regularity and to better deal with the condition characterizing newborns in $D(\mathcal{A})$.

Let $v(t) := \mathcal{S}\tilde{u}(t)$ for $\mathcal{S}: U \rightarrow V$ defined as

$$\mathcal{S}\phi(a, x) := \int_0^a \phi(\alpha, x) \, d\alpha$$

and

$$V := \left\{ \psi \in U \mid \psi(a, x) = \int_0^a \phi(\alpha, x) \, d\alpha \text{ for some } \phi \in U \right\}$$

equipped with $\|\psi\|_V := \|\partial_a \psi\|_U$ (note that $\psi(0, x) = 0$ a.e. in Ω). $\mathcal{S}$ determines an isomorphism between U and V with inverse $\mathcal{S}^{-1}\psi = \partial_a \psi$. Then $\tilde{u}$ is a solution of (5.2.1) in U if and only if v is a solution of

$$\begin{cases} v'(t) = \mathcal{B}v(t), & t > 0, \\ v(0) = v_0 \in V, \end{cases}$$

in V , where $v_0 := \mathcal{S}\tilde{u}_0$ and $\mathcal{B} := \mathcal{S}\mathcal{A}\mathcal{S}^{-1}$ with domain $D(\mathcal{B}) = \mathcal{S}D(\mathcal{A}) \subset V$. Explicitly,

$$\mathcal{B}\psi(a, x) = d(\mathcal{J}\psi - \psi)(a, x) + \mathcal{K}\psi(a, x) \quad (5.2.3)$$

for $\mathcal{K}: D(\mathcal{B}) \rightarrow V$ given by

$$\mathcal{K}\psi(a, x) := -\partial_a \psi(a, x) + \int_0^{a^+} \beta(\alpha, x) \Pi_0(\alpha) \partial_a \psi(\alpha, x) \, d\alpha - \int_0^a \mu_1(\alpha, x) \partial_a \psi(\alpha, x) \, d\alpha$$

and

$$D(\mathcal{B}) = \{ \psi \in V \mid \partial_a \psi \text{ is absolutely continuous in } a \}.$$

Since $\sigma(\mathcal{B}) = \sigma(\mathcal{A})$ [67, Section 2.1] and $\sigma_p(\mathcal{B}) = \sigma_p(\mathcal{A})$ (See Proposition 1.3.1), in order to approximate λ_0 we propose to discretize $\mathcal{B}$ instead of $\mathcal{A}$, given that the domain condition for $\mathcal{B}$ is now trivial and the original boundary condition on the newborns has moved to the action of $\mathcal{K}$.

5.2.1 Rates independent of the space variable

In this section, we work under the hypothesis that β and μ_1 depend only on age.

Assumption 5.2. $\beta(a, x) = \beta(a)$ and $\mu_1(a, x) = \mu_1(a)$ for a.a. $x \in \Omega$.

It follows from [96] that $\sigma(\mathcal{A}) = \sigma_p(\mathcal{A})$. Consequently, $\sigma(\mathcal{B}) = \sigma_p(\mathcal{B})$. Moreover, as we illustrate next, $\sigma(\mathcal{B})$ can be characterized through separate eigenvalue problems in age and space, respectively.

To this aim, as far as age-dependency is considered, let $\mathcal{K}^a: D(\mathcal{K}^a) \subseteq V^a \rightarrow V^a$ for

$$\mathcal{K}^a f(a) := -f'(a) + \int_0^{a^+} \beta(\alpha) \Pi_0(\alpha) f'(\alpha) \, d\alpha - \int_0^a \mu_1(\alpha) f'(\alpha) \, d\alpha,$$

$$D(\mathcal{K}^a) := \{ f \in V^a \mid f' \text{ is absolutely continuous} \}$$

and

$$V^a := \left\{ f \in L^1([0, a^+], \mathbb{R}) \mid f(a) = \int_0^a \varphi(\alpha) \, d\alpha \text{ for some } \varphi \in L^1([0, a^+], \mathbb{R}) \right\}.$$

It can be shown that $\mathcal{K}^a$ is the generator of an eventually compact strongly continuous semigroup of bounded positive linear operators on V^a [7, Appendix A]. Thus its spectrum consists of only eigenvalues which are at most countable and either are isolated or they accumulate at $-\infty$. Moreover, it can be shown that $\gamma_0 := s(\mathcal{K}^a)$ is actually an eigenvalue of $\mathcal{K}^a$. Let then $\{\gamma_i\}_{i=0}^\infty$ be the eigenvalues of $\mathcal{K}^a$ and let us arrange them as $\gamma_0 > \operatorname{Re} \gamma_1 \geq \operatorname{Re} \gamma_2 \geq \dots$ ³.

³Note that the eigenvalues of $\mathcal{K}^a$ coincide with those of the operator in [96, Theorem 2.2]. See also [7, Appendix A].

As far as space-dependency is considered, let $\mathcal{J}^x: L^2(\Omega, \mathbb{R}) \rightarrow L^2(\Omega, \mathbb{R})$ be defined as

$$\mathcal{J}^x g(x) := \int_{\Omega} J(x-y)g(y) \, dy.$$

Under the assumptions on J , $\mathcal{J}^x$ is compact and self-adjoint and the following result on its eigenvalues holds [69].

Proposition 5.2.1. *$\mathcal{J}^x$ has only real eigenvalues smaller than 1, say $\{\theta_j\}_{j=0}^{\infty}$ ordered as $1 > \theta_0 > \theta_1 \geq \theta_2 \geq \dots$ and they accumulate at 0. Moreover, θ_0 is the unique eigenvalue associated to a positive eigenfunction $g_0 \in L^2(\Omega, \mathbb{R})$, it is simple and positive.*

Now, if $\lambda \in \sigma(\mathcal{B})$ with eigenfunction $\psi \in D(\mathcal{B})$, i.e.,

$$\mathcal{B}\psi = \lambda\psi,$$

then, under Assumption 5.2, it is shown in [96] that $\psi(a, x) = f(a)g(x)$ for f an eigenfunction of $\mathcal{K}^a$ and g an eigenfunction of $\mathcal{J}^x$. Moreover, the following result holds [96].

Theorem 5.2.2. *Let $\{\gamma_i\}_{i=0}^{\infty}$ and $\{\theta_j\}_{j=0}^{\infty}$ be the eigenvalues of $\mathcal{K}^a$ and $\mathcal{J}^x$, respectively. Then:*

- (i) $\sigma(\mathcal{B}) = \{\gamma_i + \theta_j - 1\}_{i,j=0}^{\infty}$;
- (ii) $\lambda_0 := \gamma_0 + \theta_0 - 1$ is the principal eigenvalue of $\mathcal{B}$, it has positive eigenfunction

$$\psi_0(a, x) = \left(\int_0^a e^{-\gamma_0 \alpha} e^{-\int_0^{\alpha} \mu_1(s) \, ds} \, d\alpha \right) g_0(x)$$

and $s(\mathcal{B}) = \lambda_0$.

5.3 The numerical approach

The aim of the numerical method described next is that of approximating (the rightmost) part of $\sigma_p(\mathcal{B})$ through the eigenvalues of a matrix discretizing $\mathcal{B}$. We have in mind domains $\Omega \subset \mathbb{R}^n$ which are (or can be mapped to) rectangles and we propose to combine a spectral projection in space with a pseudospectral collocation in age.

As for the spectral projection in space, we restrict to the case $\Omega = (-l, l)$, $l > 0$, for the sake of simplicity.⁴ Let $\{P_j\}_{j=0}^{\infty}$ be the Legendre orthonormal basis for $L^2(\Omega, \mathbb{R})$, M be a positive integer and $V_M^x := \text{Span}\{P_0, \dots, P_M\}$. We define restriction and prolongation operators respectively as

$$\mathcal{R}_M^x: L^2(\Omega, \mathbb{R}) \rightarrow \mathbb{R}^{M+1}, \quad \mathcal{R}_M^x g = (g_0; \dots; g_M),$$

where $g_j := \langle g, P_j \rangle_{L^2(\Omega, \mathbb{R})}$ for all $j = 0, \dots, M$ and

$$\mathcal{P}_M^x: \mathbb{R}^{M+1} \rightarrow V_M^x, \quad \mathcal{P}_M^x G = \sum_{j=0}^M P_j G_j,$$

where $G := (G_0; \dots; G_M)$. Observe that

$$\mathcal{R}_M^x \mathcal{P}_M^x = \mathcal{I}_{\mathbb{R}^{M+1}}, \quad \mathcal{P}_M^x \mathcal{R}_M^x = \pi_M,$$

where $\pi_M: L^2(\Omega, \mathbb{R}) \rightarrow V_M^x$ is the projection operator $\pi_M g = \sum_{j=0}^M P_j g_j$.

As for the pseudospectral collocation in age, let N be a positive integer, $\Theta_N := \{a_1 < \dots < a_N\}$ be the mesh of Chebyshev zeros in $[0, a^\dagger]$, and let V_N^a be the space of algebraic polynomials on

⁴Extension to rectangular domains typically rely on the tensorial product of univariate orthonormal bases [44].

$[0, a^\dagger]$ of degree at most N and taking value zero at $a = 0$. We define restriction and prolongation operators respectively as

$$\mathcal{R}_N^a: V^a \rightarrow \mathbb{R}^N, \quad \mathcal{R}_N^a f = (f(a_1); \dots; f(a_N))$$

and

$$\mathcal{P}_N^a: \mathbb{R}^N \rightarrow V^a, \quad \mathcal{P}_N^a F = \sum_{i=1}^N \ell_i F_i,$$

where $F := (F_1; \dots; F_N)$ and $\{\ell_i\}_{i=0}^N$ is the Lagrange algebraic polynomial basis relevant to $\Theta_{0,N} := \{0\} \cup \Theta_N$. Observe that

$$\mathcal{R}_N^a \mathcal{P}_N^a = \mathcal{I}_{\mathbb{R}^N}, \quad \mathcal{P}_N^a \mathcal{R}_N^a = \mathcal{L}_N,$$

where $\mathcal{L}_N: V^a \rightarrow V_N^a$ is the Lagrange interpolation operator relevant to $\Theta_{0,N}$.

A finite-dimensional approximation $\mathcal{B}_{N,M}: \mathbb{R}^{N(M+1)} \rightarrow \mathbb{R}^{N(M+1)}$ of $\mathcal{B}$ is obtained as

$$\mathcal{B}_{N,M} := \mathcal{R}_N^a \mathcal{R}_M^x \mathcal{B} \mathcal{P}_M^x \mathcal{P}_N^a,^5$$

which, according to (5.2.3), reads

$$\mathcal{B}_{N,M} = d \mathcal{R}_N^a \mathcal{R}_M^x (\mathcal{J}^x - \mathcal{I}_V) \mathcal{P}_M^x \mathcal{P}_N^a + \mathcal{R}_N^a \mathcal{R}_M^x \mathcal{K}^a \mathcal{P}_M^x \mathcal{P}_N^a. \quad (5.3.1)$$

Note that, under Assumption 5.2, (5.3.1) reduces to

$$\mathcal{B}_{N,M} = d(\mathcal{J}_M^x - \mathcal{I}_{\mathbb{R}^{M+1}}) \otimes \mathcal{I}_{\mathbb{R}^N} + \mathcal{I}_{\mathbb{R}^{M+1}} \otimes \mathcal{K}_N^a \quad (5.3.2)$$

for

$$\mathcal{J}_M^x: \mathbb{R}^{M+1} \rightarrow \mathbb{R}^{M+1}, \quad \mathcal{J}_M^x := \mathcal{R}_M^x \mathcal{J}^x \mathcal{P}_M^x$$

and

$$\mathcal{K}_N^a: \mathbb{R}^N \rightarrow \mathbb{R}^N, \quad \mathcal{K}_N^a := \mathcal{R}_N^a \mathcal{K}^a \mathcal{P}_N^a. \quad (5.3.3)$$

Thus, in this case, computing separately the eigenvalues of $\mathcal{J}_M^x$ and those of $\mathcal{K}_N^a$ represents an efficient alternative to compute directly the eigenvalues of (5.3.1). Indeed,

$$\sigma(\mathcal{B}_{N,M}) = \{\gamma + \theta - 1 \mid \theta \in \sigma(\mathcal{J}_M^x) \text{ and } \gamma \in \sigma(\mathcal{K}_N^a)\} \quad (5.3.4)$$

follows from [80, Theorem 4.4.5] and represents the numerical counterpart of Theorem 5.2.2 (i).

In the following section we provide a rigorous convergence analysis of the eigenvalues of (5.3.2) to those of $\mathcal{B}$. In fact, under Assumption 5.2 it is known that $\mathcal{B}$ has only point spectrum and that $\lambda_0 = s(\mathcal{B})$ (see Theorem 5.2.2 (ii)). This convergence analysis is not suitable for the general case in which $\sigma(\mathcal{B})$ is not necessarily just point spectrum. Even if a principal eigenvalue $\lambda_0 = s(\mathcal{B})$ is guaranteed to exist [65], studying the convergence properties of its approximation may require an ad-hoc treatment, which is out of the scope of this chapter. Nevertheless, in Section 5.6 we provide some encouraging numerical results also for this case, as we comment therein.

5.4 Convergence analysis

The following analysis holds under Assumption 5.2 and is based on separately proving the convergence of the eigenvalues of $\mathcal{J}_M^x$ to those of $\mathcal{J}^x$ as $M \rightarrow \infty$ (Section 5.4.1) and the convergence of the eigenvalues of $\mathcal{K}_N^a$ to those of $\mathcal{K}^a$ as $N \rightarrow \infty$ (Section 5.4.2). Then (5.3.4) provides the final result on the convergence of the eigenvalues of $\mathcal{B}_{N,M}$ to those of $\mathcal{B}$ as $N, M \rightarrow \infty$ (Section 5.4.3).

⁵Observe that in exact arithmetic this is equivalent to $\mathcal{R}_M^x \mathcal{R}_N^a \mathcal{B} \mathcal{P}_N^a \mathcal{P}_M^x$.

5.4.1 Convergence in space

The following result is based on the compactness of $\mathcal{J}^x$ and the spectral approximation theory of [45].

Theorem 5.4.1. *Let $\theta \in \mathbb{R}$ be an isolated nonzero eigenvalue of $\mathcal{J}^x$ with finite algebraic multiplicity m and ascent l and let Δ be a neighborhood of θ such that θ is the sole eigenvalue of $\mathcal{J}^x$ in Δ . Then there exists $\overline{M}$ such that, for $M \geq \overline{M}$, $\mathcal{J}_M^x$ has in Δ exactly m eigenvalues $\theta_{M,j}$, $j = 1, \dots, m$, counting their multiplicities. Moreover,*

$$\max_{j=1, \dots, m} |\theta_{M,j} - \theta| = O(\varepsilon_M^{1/l})$$

for

$$\varepsilon_M := \|\pi_M^x \mathcal{J}^x - \mathcal{J}^x\|_{L^2(\Omega, \mathbb{R}) \leftarrow \mathcal{M}_\theta}$$

and $\mathcal{M}_\theta$ the generalized eigenspace of θ . Finally, for any $j = 1, \dots, m$ and for any eigenvector $g_{M,j}$ of $\pi_M^x \mathcal{J}^x$ relevant to $\theta_{M,j}$ such that $\|g_{M,j}\| = 1$, we have

$$\text{dist}(g_{M,j}, \ker(\theta \mathcal{I}_{L^2(\Omega, \mathbb{R})} - \mathcal{J}^x)) = O(\varepsilon_M^{1/l}),$$

where dist is the distance in the space $L^2(\Omega, \mathbb{R})$ between an element and a subspace.

Proof. We first observe that $\mathcal{J}_M^x$ has the same nonzero eigenvalues with the same algebraic and geometric multiplicities of $\pi_M^x \mathcal{J}^x$, see Proposition 1.3.1. As for the latter, the compactness of $\mathcal{J}_x$, the pointwise convergence of π_M^x to $\mathcal{I}_{L^2(\Omega, \mathbb{R})}$ [40, Theorem 5.9] and [100, Theorem 10.6] give $\|\pi_M^x \mathcal{J}^x - \mathcal{J}^x\|_{L^2(\Omega, \mathbb{R}) \leftarrow L^2(\Omega, \mathbb{R})} \rightarrow 0$ as $M \rightarrow \infty$. Then, the thesis follows from [45, Proposition 2.3 and Proposition 4.1]. $\square$

The analysis is now completed with a bound on the error on the eigenvalues depending on the regularity of $\mathcal{J}^x$.

Assumption 5.3. $\mathcal{J}^x \in H^k(\Omega, \mathbb{R})$ for some integer $k > 0$.

Corollary 5.4.2. *Let θ and $\theta_{M,j}$, $j = 1, \dots, m$, be as in Theorem 5.4.1. Under Assumption 5.3*

$$\max_{j=1, \dots, m} |\theta_{M,j} - \theta| = O\left(\frac{1}{M^{k/l}}\right).$$

Proof. Assumption 5.3 implies that $\mathcal{M}_\theta \subset H^k(\Omega, \mathbb{R})$. Then, from Theorem 5.4.1 and [44, p. 309, Formula (9.7.11)], for every $g \in \mathcal{M}_\theta$ there exists $C > 0$ such that

$$\|(\pi_M \mathcal{J}^x - \mathcal{J}^x)g\|_{L^2(\Omega, \mathbb{R})} \leq C \cdot \frac{1}{M^k} \cdot \|\mathcal{J}^x g\|_{H^k(\Omega, \mathbb{R})} = C \cdot \frac{1}{M^k} \cdot \|\mathcal{J}^x\|_{H^k(\Omega, \mathbb{R})} \cdot \|g\|_{H^k(\Omega, \mathbb{R})}$$

holds. $\square$

5.4.2 Convergence in age

The following analysis is based on [31, Section 4], to which we refer for the general results, see also Chapter 3. Here we only need to construct the characteristic equation associated to $\mathcal{K}^a$, its discrete counterpart associated to $\mathcal{K}_N^a$ and provide a bound on the relevant collocation error depending on one among the following regularity conditions on μ_1 .

Assumption 5.4.

- (i) $\mu_1 \in C^s([0, a^+], \mathbb{R})$ for some integer $s \geq 0$;
- (ii) $\mu_1 \in C^\infty([0, a^+], \mathbb{R})$;

(iii) μ_1 is real analytic.

Let $\gamma \in \mathbb{C}$ and $f \in D(\mathcal{K}^a)$ be such that

$$\mathcal{K}^a f = \gamma f.$$

By setting $\eta := f'$ we get

$$-\eta(a) + \int_0^{a^+} \beta(\alpha) \Pi_0(\alpha) \eta(\alpha) d\alpha - \int_0^a \mu_1(\alpha) \eta(\alpha) d\alpha = \gamma \int_0^a \eta(\alpha) d\alpha. \quad (5.4.1)$$

Thus γ is an eigenvalue for $\mathcal{K}^a$ if and only if

$$1 - \hat{\mathcal{K}}^a(\gamma) = 0$$

for

$$\hat{\mathcal{K}}^a(\gamma) := \int_0^{a^+} \beta(\alpha) \Pi(\alpha) e^{-\int_0^\alpha \mu_1(s) ds - \gamma \alpha} d\alpha. \quad (5.4.2)$$

Note that (5.4.1) can be seen in the framework of

$$q + \mathcal{S}(\gamma + \mu_1)q = \alpha \quad (5.4.3)$$

with general $\alpha, \gamma \in \mathbb{C}$, which admits a unique solution $q = q(\cdot, \gamma, \alpha)$ thanks to standard results on Volterra integral equations [71, Theorem 9.3.6]. In particular

$$\mathcal{I}_{L^1([0, a^+], \mathbb{R})} + \mathcal{S}(\gamma + \mu_1): L^1([0, a^+], \mathbb{R}) \rightarrow L^1([0, a^+], \mathbb{R})$$

is invertible with bounded inverse thanks to Assumption 5.1 (i). In fact, q is the derivative η of an eigenfunction f of $\mathcal{K}^a$ when $\gamma \in \sigma(\mathcal{K}^a)$ (and $\alpha = \int_0^{a^+} \beta(\alpha) \Pi_0(\alpha) \eta(\alpha) d\alpha$ follows from the domain of $\mathcal{K}^a$).

Similarly, let $\gamma \in \mathbb{C}$ and $f_N \in V_N^a$ be such that

$$\mathcal{K}_N^a F = \gamma F$$

for $F := (f_N(a_1); \dots; f_N(a_N))$. By setting $\eta_N := f'_N$ we get, for $i = 1, \dots, N$,

$$-\eta_N(a_i) + \int_0^{a^+} \beta(\alpha) \Pi_0(\alpha) \eta_N(\alpha) d\alpha - \int_0^{a_i} \mu_1(\alpha) \eta_N(\alpha) d\alpha = \gamma \int_0^{a_i} \eta_N(\alpha) d\alpha.$$

If $q_N = q_N(\cdot; \gamma, \alpha)$ is the polynomial collocating (5.4.3) at A_N , we get that γ is an eigenvalue of $\mathcal{K}_N^a$ if and only if

$$1 - \hat{\mathcal{K}}_N^a(\gamma) = 0$$

for

$$\hat{\mathcal{K}}_N^a(\gamma) := \int_0^{a^+} \beta(\alpha) \Pi_0(\alpha) q_N(\alpha; \gamma, 1) d\alpha. \quad (5.4.4)$$

Note that $q_N(\cdot; \gamma, 1) = \eta_N(\cdot; \gamma, 1)$ when $\gamma \in \sigma(\mathcal{K}_N^a)$.

Now we show that q_N exists and is unique and we give an upper bound for $\|q_N(\cdot; \gamma, \alpha) - q(\cdot; \gamma, \alpha)\|_{L^1([0, a^+], \mathbb{R})}$. Since q_N is a polynomial of degree $N - 1$, it can be reconstructed exactly at N nodes through the Lagrange interpolation operator $\tilde{\mathcal{L}}_{N-1}$ relevant to A_N . Then

$$q_N + \tilde{\mathcal{L}}_{N-1} [\mathcal{S}(\gamma + \mu_1)q_N] = \alpha \quad (5.4.5)$$

follows straightforwardly from (5.4.3) and

$$e_N + \tilde{\mathcal{L}}_{N-1} \mathcal{S}(\gamma + \mu_1)e_N = r_N \quad (5.4.6)$$

follows by setting $e_N := q_N - q$ and $r_N := (\mathcal{I}_{L^1([0, a^+], \mathbb{R})} - \tilde{\mathcal{L}}_{N-1})\mathcal{S}(\gamma + \mu_1)q$ (we avoid to write the dependence of e_N and r_N on α and γ , unless explicitly required).

Proposition 5.4.3. *Under Assumption 5.1 (ii) there exists a positive integer $\bar{N}$ such that, for $N \geq \bar{N}$, (5.4.6) has a unique solution e_N and*

$$\|e_N\|_{L^1([0,a^+],\mathbb{R})} \leq 2|\alpha|\varepsilon_N \left\| \left(\mathcal{I}_{L^1([0,a^+],\mathbb{R})} + \mathcal{S}(\gamma + \mu_1) \right) \right\|_{L^1([0,a^+],\mathbb{R}) \leftarrow L^1([0,a^+],\mathbb{R})}^{-1},$$

where

$$\varepsilon_N = \begin{cases} O(N^{-(s+1)} \log N) & \text{under Assumption 5.4 (i);} \\ O(N^{-(r+1)} \log N) & \text{for every integer } r \geq 1 \text{ under Assumption 5.4 (ii);} \\ O(p^{-N} \log N) & \text{for some constant } p > 1 \text{ under Assumption 5.4 (iii).} \end{cases}$$

Proof. By observing that $\text{Range}(\mathcal{S}) \subset AC([0,a^+],\mathbb{R})$, we have that

$$\|\mathcal{I}_{AC([0,a^+],\mathbb{R})} - \tilde{\mathcal{L}}_{N-1}\|_{L^1([0,a^+],\mathbb{R}) \leftarrow AC([0,a^+],\mathbb{R})} \rightarrow 0, \quad N \rightarrow \infty$$

thanks to Corollary 1.1.15, thus we can apply the Banach perturbation Lemma [100, Theorem 10.1] to get

$$\|e_N\|_{L^1([0,a^+],\mathbb{R})} \leq 2 \left\| \left(\mathcal{I}_{L^1([0,a^+],\mathbb{R})} + \mathcal{S}(\gamma + \mu_1) \right) \right\|_{L^1([0,a^+],\mathbb{R}) \leftarrow L^1([0,a^+],\mathbb{R})}^{-1} \cdot \|r_N\|_{L^1([0,a^+],\mathbb{R})}.$$

Then

$$\|r_N\|_{L^1([0,a^+],\mathbb{R})} \leq a^+ \|r_N\|_\infty \leq (1 + \Lambda_{N-1}) \mathcal{E}_{N-1}(\mathcal{S}(\gamma + \mu_1)q)$$

follows from Theorem 1.1.10, where Λ_{N-1} is the Lebesgue constant relevant to Θ_N and $\mathcal{E}_{N-1}(\cdot)$ is defined as in (1.1.1). The final bound follows since q depends linearly on α , the choice of Θ_N guarantees $\Lambda_{N-1} = O(\log N)$ and estimates for $\mathcal{E}_{N-1}(\mathcal{S}(\gamma + \mu_1)q)$ can be obtained from Theorem 1.1.7 and Theorem 1.1.10. $\square$

The final result follows by comparing $\hat{\mathcal{K}}^a$ in (5.4.2) with $\hat{\mathcal{K}}_N^a$ in (5.4.4).

Theorem 5.4.4. *Let γ be a non zero eigenvalue of $\mathcal{K}^a$ with finite algebraic multiplicity m and let Δ be a neighborhood of γ such that γ is the sole eigenvalue of $\mathcal{K}^a$ in Δ . Under Assumption 5.1 there exists $\bar{N} \in \mathbb{N}$ such that, for $N \geq \bar{N}$, $\mathcal{K}_N^a$ has in Δ exactly m eigenvalues $\gamma_{N,i}$, $i = 1, \dots, m$, counting their multiplicities. Moreover,*

$$\max_{i=1,\dots,m} |\gamma_{N,i} - \gamma| \leq \rho(N)$$

with

$$\rho(N) = \begin{cases} O((N^{-(s+1)} \log N)^{1/m}) & \text{under Assumption 5.4 (i);} \\ O((N^{-(r+1)} \log N)^{1/m}) & \text{for every integer } r \geq 1 \\ & \text{under Assumption 5.4 (ii);} \\ O((p^{-N} \log N)^{1/m}) & \text{for some constant } p > 1 \\ & \text{under Assumption 5.4 (iii).} \end{cases}$$

Proof. The thesis follows from

$$\begin{aligned} |\hat{\mathcal{K}}_N^a(\gamma) - \hat{\mathcal{K}}^a(\gamma)| &\leq \int_0^{a^+} |\beta(\alpha) \Pi_0(\alpha)| \cdot |q_N(\alpha; \gamma, 1) - q(\alpha; \gamma, 1)| d\alpha \\ &\leq a^+ \|\beta \Pi_0\|_{L^\infty([0,a^+],\mathbb{R})} \|e_N(\cdot; \gamma, 1)\|_{L^1([0,a^+],\mathbb{R})} \end{aligned}$$

by using Proposition 5.4.3 and (eventually) by applying Rouché's Theorem as in [31, Section 4]. $\square$

Remark 5.4.5. The convergence result of Theorem 5.4.4 is preserved in the case one uses a straightforward piecewise collocation approach in presence of possible discontinuities of β and μ_1 (or of their derivatives). Note that the MATLAB demos available at <http://cdlab.uniud.it/software> that we use to make all the tests in sections 5.6 and 5.7 implement this piecewise alternative.

5.4.3 Final convergence result

Summarizing the above results, the main theorem follows as a corollary.

Theorem 5.4.6. *Let Assumption 5.3 hold. Let $\lambda \in \sigma(\mathcal{B})$, $\gamma \in \sigma(\mathcal{K}^a)$ and $\theta \in \sigma(\mathcal{J}^x)$ be such that $\lambda = \gamma + \theta - 1$. Suppose that γ is a nonzero eigenvalue of $\mathcal{K}^a$ with finite algebraic multiplicity m_γ and let Δ_γ be a neighborhood of γ such that γ is the sole eigenvalue of $\mathcal{K}^a$ in Δ_γ . Moreover, suppose that $\theta \in \mathbb{R}$ is an isolated nonzero eigenvalue of $\mathcal{J}^x$ with finite algebraic multiplicity m_θ , ascent l_θ and Δ_θ is a neighborhood of θ such that θ is the sole eigenvalue of $\mathcal{J}^x$ in Δ_θ .*

Then there exist $\bar{N}, \bar{M} \in \mathbb{N}$ such that, for $N \geq \bar{N}$ and $M \geq \bar{M}$, $\mathcal{K}_N$ has in Δ_γ exactly m_γ eigenvalues $\gamma_{N,i}$, $i = 1, \dots, m_\gamma$, counting their multiplicities, and $\mathcal{J}_M^x$ has in Δ_θ exactly m_θ eigenvalues $\theta_{M,j}$, $j = 1, \dots, m_\theta$, counting their multiplicities, and

$$\max_{\substack{i=1,\dots,m_\gamma \\ j=1,\dots,m_\theta}} |\lambda - (\gamma_{N,i} + \theta_{M,j} - 1)| \leq \rho_\gamma(N) + \rho_\theta(M)$$

with

$$\rho_\gamma(N) = \begin{cases} O((N^{-(s+1)} \log N)^{1/m_\gamma}) & \text{under Assumption 5.4 (i);} \\ O((N^{-(r+1)} \log N)^{1/m_\gamma}) & \text{for every integer } r \geq 1 \\ & \text{under Assumption 5.4 (ii);} \\ O((p^{-N} \log N)^{1/m_\gamma}) & \text{for some constant } p > 1 \\ & \text{under Assumption 5.4 (iii);} \end{cases}$$

$$\text{and } \rho_\theta(M) = O\left(M^{-\frac{k}{l_\theta}}\right).$$

5.5 Implementation

Here we describe how to explicitly construct the entries of the matrices representing the discretized operators obtained in Section 5.3.

Let $(i; j) := (i - 1)(M + 1) + j$ for $i = 1, \dots, N$ and $j = 0, \dots, M + 1$. Thanks to the cardinal property of the Lagrange polynomials $\ell_h(a_i) = \delta_{ih}$, $i, h = 0, \dots, N$, and to the orthonormality of $\{P_j\}_{j=0}^\infty$, the action of $\mathcal{B}_{N,M}$ on $\Psi = (\Psi_0; \dots; \Psi_{N(M+1)}) \in \mathbb{R}^{N(M+1)}$ reads

$$\begin{aligned} [\mathcal{B}_{N,M}\Psi]_{(i;j)} &= d \sum_{k=0}^M \left[\int_{\Omega} (\mathcal{J}^x P_k - P_k)(x) P_j(x) dx \right] \Psi_{(i;k)} - \sum_{h=1}^N \ell'_h(a_i) \Psi_{(h;j)} \\ &+ \sum_{h=1}^N \sum_{k=0}^M \left[\int_{\Omega} P_k(x) \left(\int_0^{a^\dagger} \beta(\alpha, x) \Pi_0(\alpha) \ell'_h(\alpha) d\alpha \right) P_j(x) dx \right] \Psi_{(h;k)} \\ &- \sum_{h=1}^N \sum_{k=0}^M \left[\int_{\Omega} P_k(x) \left(\int_0^{a_i} \mu_1(\alpha, x) \ell'_h(\alpha) d\alpha \right) P_j(x) dx \right] \Psi_{(h;k)}. \end{aligned}$$

In particular, the matrix expression for $\mathcal{B}_{N,M}$ reads

$$\mathcal{B}_{N,M} = d(\mathcal{J}_M^x - \mathcal{I}_{\mathbb{R}^{M+1}}) \otimes \mathcal{I}_{\mathbb{R}^N} - \mathcal{I}_{\mathbb{R}^{M+1}} \otimes \mathcal{D}_N^a + \mathcal{H}_{N,M} - \mathcal{W}_{N,M}$$

where, for $i, h = 1, \dots, N$ and $j, k = 0, \dots, M$,

$$\begin{aligned} [\mathcal{J}_M^x]_{j,k} &:= \int_{\Omega} \mathcal{J}^x P_k(x) P_j(x) dx, \\ [\mathcal{D}_N^a]_{i,h} &:= \ell'_h(a_i), \end{aligned} \tag{5.5.1}$$

$$[\mathcal{H}_{N,M}]_{(ij),(h,k)} := \int_{\Omega} P_k(x) \left(\int_0^{a^\dagger} \beta(\alpha, x) \Pi_0(\alpha) \ell'_h(\alpha) d\alpha \right) P_j(x) dx, \quad (5.5.2)$$

$$[\mathcal{W}_{N,M}]_{(ij),(h,k)} := \int_{\Omega} P_k(x) \left(\int_0^{a_i} \mu_1(\alpha, x) \ell'_h(\alpha) d\alpha \right) P_j(x) dx. \quad (5.5.3)$$

Observe that $\mathcal{J}_M^x$ is symmetric since $\mathcal{J}^x$ is self-adjoint. Moreover, under Assumption 5.2, one can write $\mathcal{H}_{N,M} = \mathcal{I}_{\mathbb{R}^{M+1}} \otimes \mathcal{H}_N^a$ and $\mathcal{W}_{N,M} = \mathcal{I}_{\mathbb{R}^{M+1}} \otimes \mathcal{W}_N^a$, where, for $i, h = 1, \dots, N$,

$$\begin{aligned} [\mathcal{H}_N^a]_{i,h} &:= \int_0^{a^\dagger} \beta(a) \Pi_0(a) \ell'_h(a) da, \\ [\mathcal{W}_N^a]_{i,h} &:= \int_0^{a_i} \mu_1(a) \ell'_h(a) da. \end{aligned}$$

Clearly, $\mathcal{K}_N^a$ in (5.3.3) reads

$$\mathcal{K}_N^a = -\mathcal{D}_N^a + \mathcal{H}_N^a - \mathcal{W}_N^a.$$

Finally, if the integrals in (5.5.1), (5.5.2) and (5.5.3) (or the following ones) cannot be computed analytically, we approximate them numerically. We use the Gauss-Legendre quadrature with $M+1$ nodes for the integrals in space, the Fejer's first rule quadrature with N points for the integrals in age in $[0, a^\dagger]$ and the i -th row of the inverse of the differentiation matrix $\mathcal{D}_N^a$ for the integrals in $[0, a_i]$, $i = 1, \dots, N$ [60]. Of course the relevant quadrature errors must be suitably taken into account in bounding the final error on the eigenvalues. The results in [131] and [53, pp. 85] ensure that Theorem 5.4.6 still holds under regularity assumptions on the model coefficients. We also remark that by using Gauss-Legendre quadrature, the spectral discretization in space becomes equivalent to collocating at the Legendre-Gauss zeros [44, Section 3.2.5].

5.6 Numerical results

The following test cases concern model (5.1.2). In particular the first one confirms Theorem 5.4.6 under Assumption 5.2. The second one experimentally shows that similar results are preserved even without Assumption 5.2 but still under the conditions of [65]. Both concern $\Omega = (-l, l)$ for $l > 0$. In the final third case, we consider a circular domain (that indeed can be mapped into a rectangle as assumed at the beginning of Section 5.3).

Example 1 Inspired by [23, 97, 103], we consider $a^\dagger = 1$,

$$\beta(a, x) = \beta(a) = 8(1 - \ln R) \chi_{[\frac{1}{2}, a^\dagger]}(a), \quad \mu_0(a) = \frac{1}{a^\dagger - a}, \quad \mu_1(a, x) \equiv 0$$

and

$$J(x) = \begin{cases} ke^{-\frac{1}{4-x^2}} & \text{if } x \in (-2, 2) \\ 0 & \text{otherwise} \end{cases}$$

with $R > 0$ and $k = \left(\int_{-2}^2 e^{-\frac{1}{4-x^2}} dx \right)^{-1}$. With these choices Assumption 5.2 holds, thus we compute the eigenvalues of $\mathcal{K}_N^a$ and $\mathcal{J}_M^x$ separately. We use $N = M$. Moreover, $\Pi_0(a) = 1 - a$ and, for $R = 1$, $\gamma_0 = 0$.⁶ Finally, since β is piecewise defined, we resort to the piecewise approach mentioned in Remark 5.4.5.

⁶This can be derived as in [23] by observing that the characteristic equation for $\mathcal{K}^a$ reads

$$1 = \int_{\frac{1}{2}}^1 8(1 - \log R)(1 - a)e^{-\lambda a} da.$$

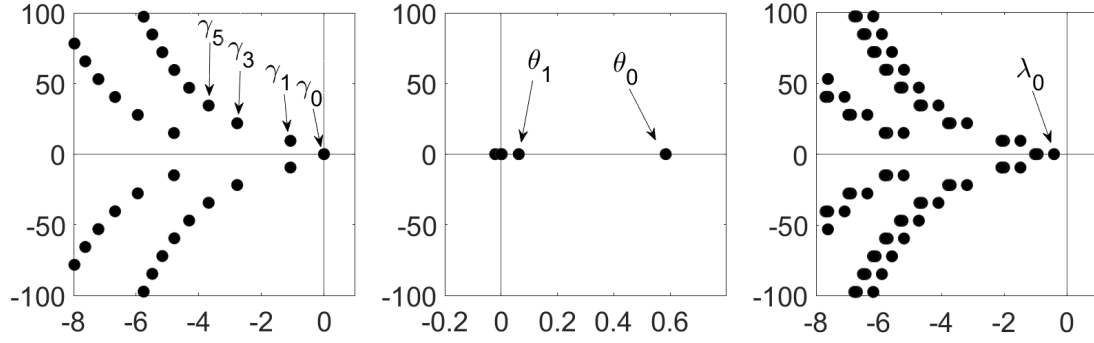


Figure 5.6.1: Example 1: computed spectra in the complex plane with $l = 1$ and $d = 1$ for $\mathcal{K}^a$ (left), $\mathcal{J}^x$ (center) and $\mathcal{B}$ (right) with $N = M = 100$. Original figure from [26].

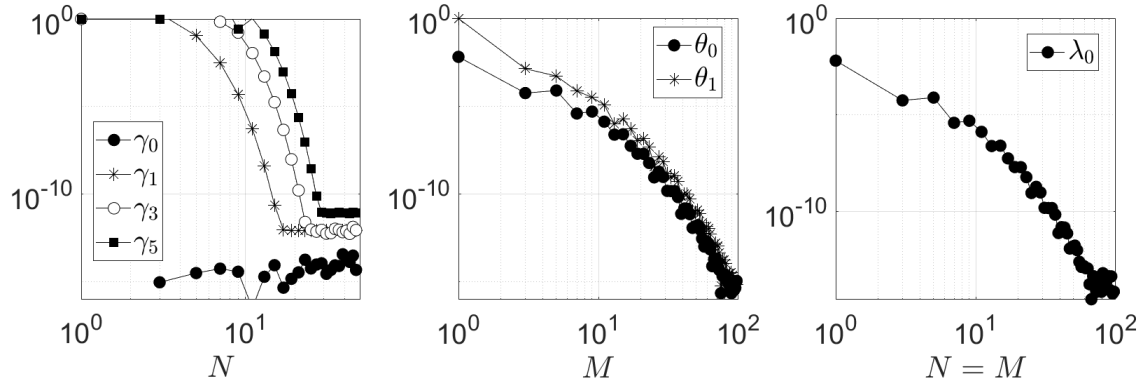


Figure 5.6.2: Example 1: errors in computing $\gamma_0, \gamma_1, \gamma_3, \gamma_5$ (left), θ_0, θ_1 (center) and λ_0 (right) with $l = 1$ and $d = 1$ for increasing values of N and M . The reference values $\gamma_1 \approx -1.070249248997922 + 9.438599419667414i$, $\gamma_3 \approx -2.772533303698945 + 21.842287295644464i$, $\gamma_5 \approx -3.683984412603065 + 34.410428157635607i$ are obtained with $N = 1000$; the reference values $\theta_0 \approx 0.584294111974084$ and $\theta_1 \approx 0.062556017866521$ are obtained with $M = 1000$. Original figure from [26].

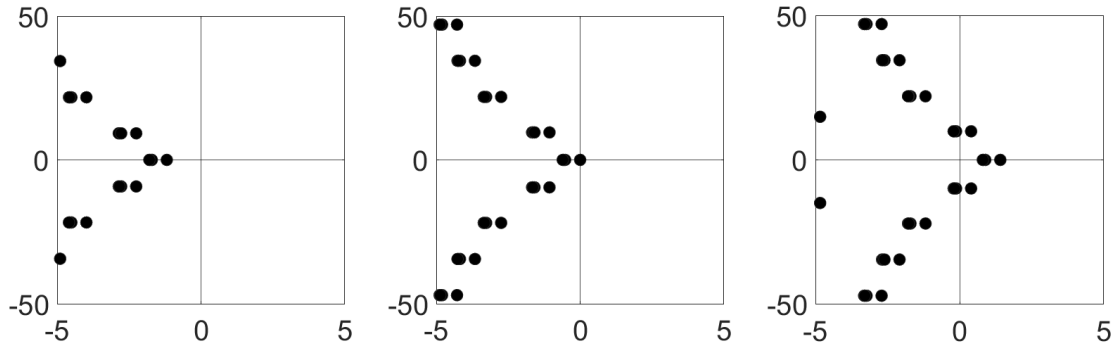


Figure 5.6.3: Example 1: computed spectra of $\mathcal{B}$ in the complex plane with $l = 1, d = 1$ and $R = 1.5$ (left), $R \approx 0.7277628676660066$ (center) and $R = 0.1$ (right) with $N = M = 100$. Original figure from [26].

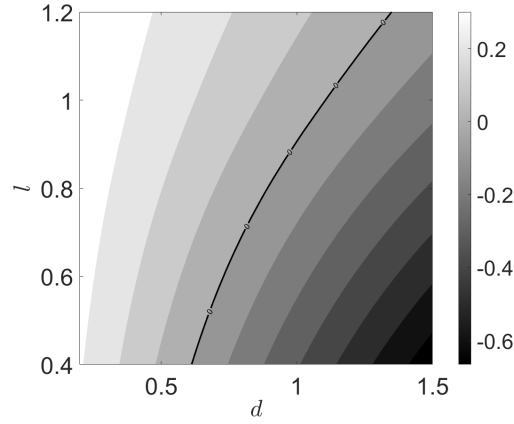


Figure 5.6.4: Example 1: level curves for λ_0 as a function of (d, l) and stability boundary (thick line) with $R = 0.7$ and $N = M = 30$. Original figure from [26].

Computed spectra are shown in Figure 5.6.1 for $l = 1$ and $d = 1$. For the same values, the convergence behavior is illustrated in Figure 5.6.2, which confirms Corollary 5.4.2 and Theorem 5.4.4 showing also how the error constants are affected by $|\gamma|$ and $|\theta|$.

In Figure 5.6.3 we perform a bifurcation analysis of the null equilibrium with respect to R , with $l = 1$ and $d = 1$, finding a transcritical bifurcation at $R \approx 0.7277628676660066$ (correspondingly $\gamma_0 \approx 0.415705888025916$). Level curves of λ_0 as a function of (d, l) are reported in Figure 5.6.4. The principal eigenvalue is a decreasing function of d and an increasing function of l , confirming the results in [65].

Example 2 We consider $a^\dagger = 1$,

$$\beta(a, x) = \beta_0 \chi_{[\frac{1}{2}, a^\dagger]}(a)(2 - x^2), \quad \mu_0(a) = \frac{1}{a^\dagger - a}, \quad \mu_1(a, x) = \frac{1}{1 + x^2}$$

and

$$J(x) = \pi^{-\frac{1}{2}} e^{-x^2}$$

with $\beta_0 > 0$.

Differently from Example 1, β and μ_1 depend also on x . Yet, these choices satisfy the conditions of [65]. Again, we use the piecewise approach with $N = M$.

Figure 5.6.5 shows the computed spectrum of $\mathcal{B}$ (left) and the convergence diagram for the first two rightmost eigenvalues λ_0 and λ_1 (right) with $\beta_0 = 8$ and $d = l = 1$. Figure 5.6.6 and Figure 5.6.7 show the computed eigenfunctions of $\mathcal{B}$ and $\mathcal{A}$, respectively, for λ_0 and λ_1 . In Figure 5.6.7 (left) we observe a positive eigenfunction with a simple dominant real eigenvalue, i.e., λ_0 , whereas in Figure 5.6.7 (right) the eigenfunction of λ_1 changes sign. Note that in Figure 5.6.6 (left) the corresponding eigenfunction of $\mathcal{B}$ is increasing and vanishes only for $a = 0$ as it is relevant to the age-integrated state, whereas in Figure 5.6.7 (right) the eigenfunction of λ_1 is not monotone. Accordingly to the theory of [65], this suggests that the proposed approach correctly approximates the principal eigenvalue λ_0 . Eventually, Figure 5.6.8 shows the level curves of λ_0 as a function of (d, l) . As in Example 1, λ_0 is a decreasing function of d and an increasing function of l , confirming again the results in [65].

Example 3 We consider $a^\dagger = 1, d = 1$,

$$\beta(a, x) = \beta(a) = \beta_0 \chi_{[\frac{1}{2}, a^\dagger]}(a), \quad \mu_0(a) = \frac{1}{a^\dagger - a}, \quad \mu_1(a, x) \equiv 0,$$

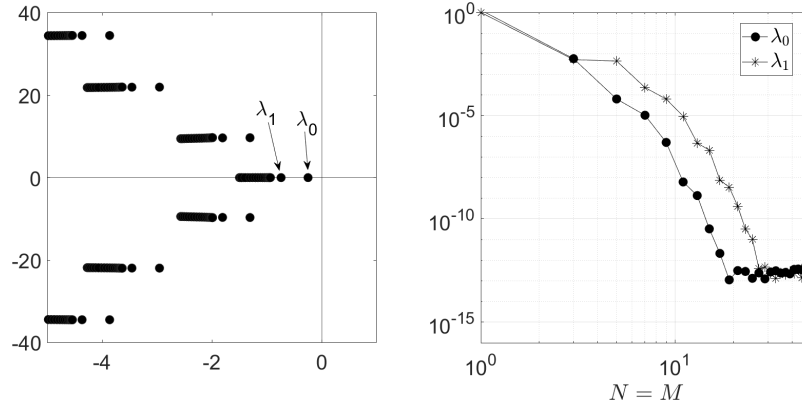


Figure 5.6.5: Example 2: spectrum of $\mathcal{B}$ in the complex plane computed with $N = M = 50$ (left) and convergence diagram for the first two rightmost eigenvalues λ_0 and λ_1 (right) with $\beta_0 = 8$ and $d = l = 1$. The reference values $\lambda_0 \approx -0.248872934970194$ and $\lambda_1 \approx -0.739612643296491$ are obtained with $N = M = 100$. Original figure from [26].

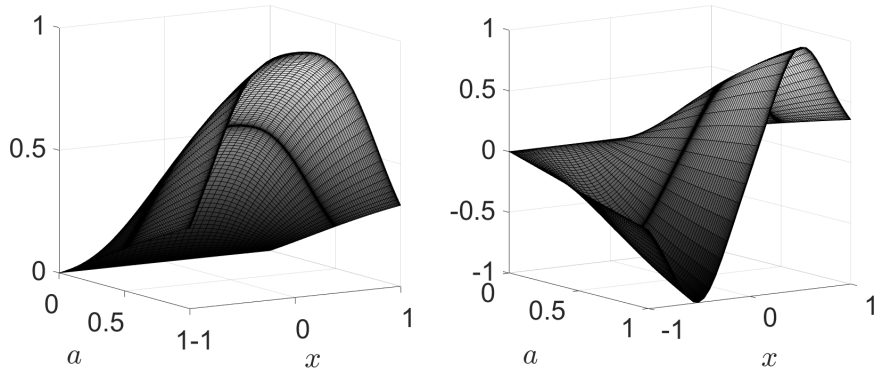


Figure 5.6.6: Example 2: computed eigenfunctions of $\mathcal{B}$ relevant to λ_0 (left) and λ_1 (right) with $\beta_0 = 8, d = l = 1$ and $N = M = 50$. Original figure from [26].

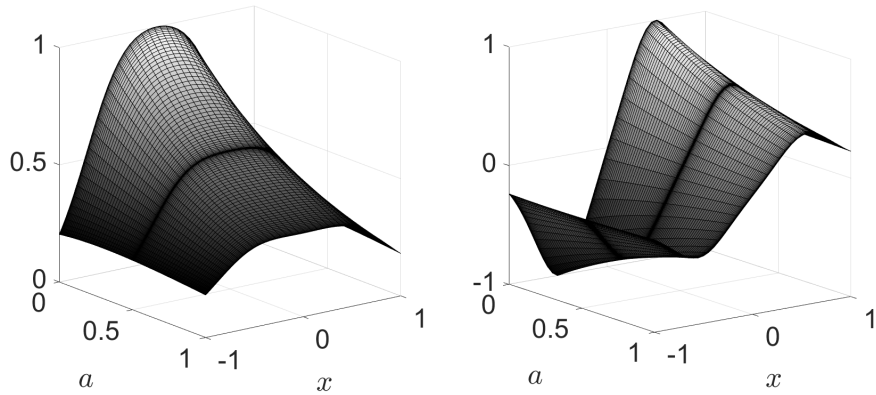


Figure 5.6.7: Example 2: computed eigenfunctions of $\mathcal{A}$ relevant to λ_0 (left) and λ_1 (right) with $\beta_0 = 8, d = l = 1$ and $N = M = 50$. Original figure from [26].

$$J(x) = \pi^{-1} e^{-\|x\|_2^2}$$

and $\Omega := \{x \in \mathbb{R}^2 \mid \|x\|_2 < R\}$ for $R > 0$. By using polar coordinates the diffusion operator $\tilde{\mathcal{J}}^x$ on $AC_0([0, a^\dagger], L^2([0, R] \times [0, 2\pi], \mathbb{R}))$ reads

$$\tilde{\mathcal{J}}^x \tilde{\psi}(a, r, \theta) = \int_0^R \int_0^{2\pi} J(r \cos \theta - \rho \cos \varphi, r \sin \theta - \rho \sin \varphi) \tilde{\psi}(a, \rho, \varphi) \rho \, d\varphi \, d\rho.$$

Observe that with these choices Assumption 5.2 holds. Again, we use the piecewise approach with $N = M$ (note that, being $\Omega \subset \mathbb{R}^2$, here M represents the degree of the univariate polynomials in both directions of the tensorial approach). Figure 5.6.9 shows the computed spectrum of $\mathcal{B}$ (left) and the convergence diagram for the first two rightmost eigenvalues λ_0 and λ_1 (right) with $\beta_0 = 8$ and $R = 1$. Figure 5.6.10 shows the level curves of λ_0 as a function of (d, l) , which again confirm the results of [65].

5.7 Nonlocal diffusion of Neumann type

Now we briefly consider models with nonlocal diffusion of Neumann type, i.e., models in which the diffusion is limited to a certain region $\Omega \subset \mathbb{R}^n$ [95]. The prototype model is

$$\left\{ \begin{array}{ll} \mathcal{D}u(t, a, x) = d \int_{\Omega} J(x - y) [u(t, a, y) - u(t, a, x)] \, dy \\ \quad - \mu(a, x) u(t, a, x), & t > 0, a \in [0, a^\dagger], x \in \Omega, \\ u(t, 0, x) = \int_0^{a^\dagger} \beta(\hat{a}, x) u(t, \hat{a}, x) \, d\hat{a}, & t > 0, x \in \Omega, \\ u(0, a, x) = u_0(a, x), & a \in [0, a^\dagger], x \in \Omega, \end{array} \right. \quad (5.7.1)$$

where $\mathcal{D}$ is defined as in (I.2.6). Again, the semigroup generated by (5.7.1) is not eventually compact in general, yet stability is still governed by the spectral bound $s(\mathcal{A})$ of the relevant infinitesimal generator $\mathcal{A}$ (which can be derived as in Section 5.2). Moreover, $s(\mathcal{A})$ can be shown to be its principal eigenvalue under suitable assumptions [95].

By replacing $\mathcal{J} - \mathcal{I}_U$ with $\mathcal{J} - \mathcal{C}$ for $\mathcal{C}: U \rightarrow U$ defined as

$$\mathcal{C}\phi(a, x) := \phi(a, x) \int_{\Omega} J(x - y) \, dy$$

and by proceeding as in sections 5.2 and 5.3, we can reformulate (5.7.1) by integration of the age-state and derive a similar numerical approximation for the spectrum of the infinitesimal generator.

Anyway, let us remark that a decomposition as in Theorem 5.2.2 has not been proved to hold true for the case of Neumann diffusion, although it is easy to see that

$$\sigma_p(\mathcal{K}^a) + \sigma_p(\mathcal{J}^x - \mathcal{C}^x) \subseteq \sigma_p(\mathcal{B}),$$

where $\mathcal{C}^x: L^2(\Omega, \mathbb{R}) \rightarrow L^2(\Omega, \mathbb{R})$ is defined as

$$\mathcal{C}^x g(x) := g(x) \int_{\Omega} J(x - y) \, dy.$$

Nevertheless, in [95, Theorem 4.1] it is proved that if $\lambda_0 \in \sigma_p(\mathcal{A})$ is associated with a positive eigenfunction ϕ , then λ_0 is the principal eigenvalue of $\mathcal{A}$. Holding this true, we can still characterize the principal eigenvalue of $\mathcal{B}$ under Assumption 5.2. In fact the Neumann eigenvalue problem

$$-(\mathcal{J}^x - \mathcal{C}^x)g(x) = \theta g(x)$$

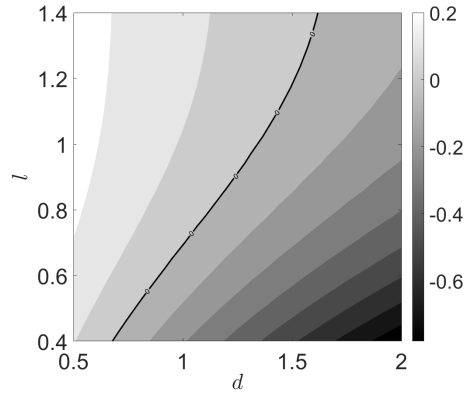


Figure 5.6.8: Example 2: level curves for λ_0 as a function of (d, l) and stability boundary (thick line) with $\beta_0 = 10$ and $N = M = 30$. Original figure from [26].

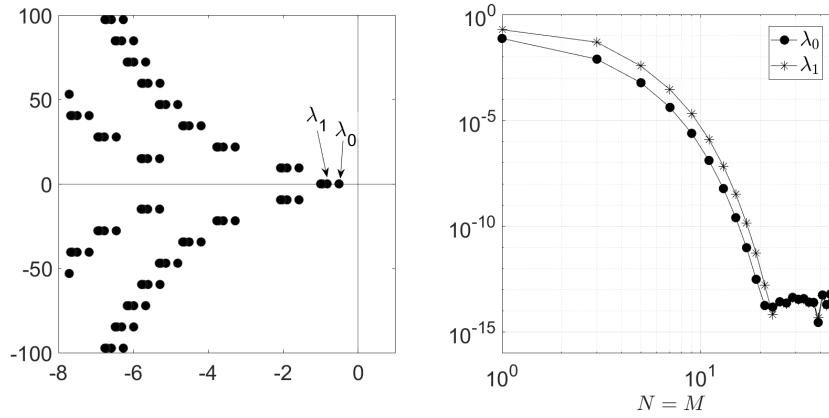


Figure 5.6.9: Example 3: spectrum of B in the complex plane computed with $N = M = 50$ (left) and convergence diagram for the first two rightmost eigenvalues λ_0 and λ_1 (right) with $\beta_0 = 8$, $d = R = 1$. The reference values $\lambda_0 \approx -0.508459905995625$ and $\lambda_1 \approx -0.827016421828640$ are obtained with $N = M = 100$. Original figure from [26].

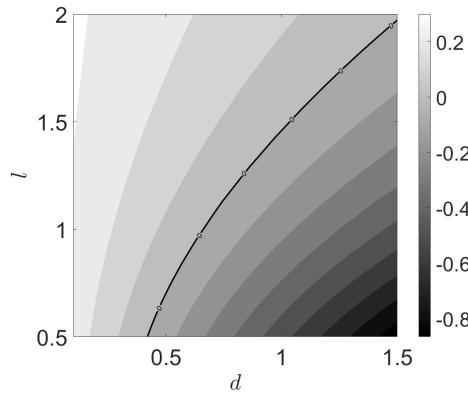


Figure 5.6.10: Example 3: level curves of λ_0 as a function of (d, R) and stability boundary (thick line) with $\beta_0 = 10$ and $N = M = 30$. Original figure from [26].

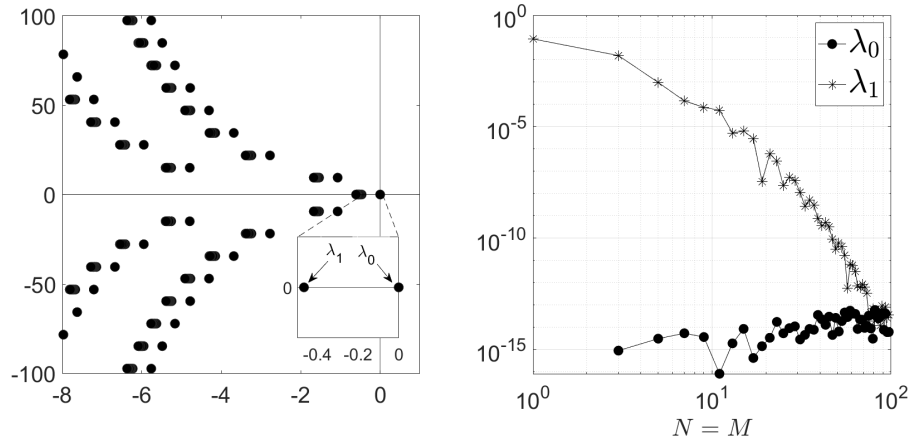


Figure 5.7.1: Nonlocal diffusion of Neumann type: spectrum of $\mathcal{B}$ in the complex plane computed with $N = M = 100$ (left) and convergence diagram for the first two rightmost eigenvalues λ_0 and λ_1 (right) with $d = l = 1$. The reference value $\lambda_1 \approx -0.467278026690667$ is obtained with $N = M = 1000$. Original figure from [26].

has principal eigenvalue $\theta_0 = 0$ with g_0 constant [119]. Thus $s(\mathcal{B}) = \lambda_0 = \gamma_0 - \theta_0 = \gamma_0$ with associated eigenfunction $\psi(a, x) = f_0(a)$, where f_0 is the eigenfunction for $\mathcal{K}^a$ relevant to the principal eigenvalue γ_0 . Finally, a decomposition like (5.3.4) holds for the discretized problem.

In light of the above results, we can proceed as in Section 5.4 to prove that, under Assumption 5.2, the eigenvalues of $\mathcal{B}_{N,M}$ converge to those of $\mathcal{B}$ (in particular λ_0 is approximated by a converging sequence of eigenvalues). The proof again consists in considering the separated eigenvalue problems for $\mathcal{K}_N^a$ and $\mathcal{J}_M^x - \mathcal{C}_M^x$. While the convergence analysis relevant to $\mathcal{K}_N^a$ remains unchanged, a slight modification is required for the space counterpart. Indeed, $\mathcal{J}^x - \mathcal{C}^x$ is not compact in general, but being bounded and self-adjoint, Theorem 5.4.1 and Theorem 5.4.2 remain valid thanks to the strong stability guaranteed by a (Galerkin-type) spectral projection method as the one presented in Section 5.3 [46, Section 4].

As a numerical test, we consider the same coefficients of Example 1 in Section 5.6, thus ensuring Assumption 5.2. Figure 5.7.1 shows the computed spectrum of $\mathcal{B}$ (left, recall that $\gamma_0 = 0$) and the convergence diagram for λ_0 and λ_1 . The error for λ_0 is at the machine precision already for small values of $N = M$ while the error for λ_1 decreases with infinite order (observe that the relevant eigenfunction is of class C^∞).

6

Age-structured models with an additional age

The aim of this last chapter is to present a numerical method for the linear stability analysis of age-structured population models with an additional age. The content of this chapter is mainly taken from the work [7] by the author, A. Andò, D. Liessi and F. Scarabel.

In the previous chapters, we considered models with either a single structure or where the age-structure was coupled to a spatial variable. Here, we consider models structured by two ages, e.g., demographic and infection age, which are motivated by applications to infectious disease dynamics, see for example [87].

For linear population models with two age structures, it has been proved that the stability of the null equilibrium is determined by the spectrum of the infinitesimal generator associated to the relevant solution semigroup [91, 134]. Nevertheless, investigating the stability of this equilibrium is not easy in general due to the complicated structure of the infinitesimal generator and its domain.

Hence, in this chapter we propose a numerical method to approximate this spectrum. To conveniently deal with the conditions in the domain of the generator, inspired by [121] we reformulate the problem via integration of the age-state variables. The advantages of this approach are mainly twofold: on the one hand, the transformed operator acts on a space of absolutely continuous functions (rather than the original space L^1), hence point evaluation, as well as polynomial interpolation and collocation are natural; on the other hand, the domain of the transformed operator is characterized by a trivial condition (specifically, a zero boundary condition), which substantially simplifies the numerical implementation.

As far as we know, there is currently no other numerical method available for this problem. We demonstrate the applicability of the new method with several numerical tests, illustrating the convergence of the approximated eigenvalues to the exact ones. An application to an epidemic model is discussed as well.

The content of the chapter is organized as follows. In Section 6.1, we introduce the prototype model. In Section 6.2 we illustrate the abstract framework and the reformulation of the infinitesimal generator in terms of the integrated state. In Section 6.3 we present the numerical approach. In Section 6.4 we give details about the implementation. Section 6.5 contains numerical tests and an application to an epidemiological model structured by demographic and infection age [87].

6.1 The prototype model

Let $u(t, a, \tau)$ denote the density of the population at time $t \geq 0$ and ages $a, \tau \in \Omega := [0, a^+] \times [0, \tau^+]$, where $a^+, \tau^+ \in (0, +\infty)$ denote the maximal ages of the individuals. The model consists of a first order hyperbolic PDE

$$\partial_t u(t, a, \tau) + \partial_a u(t, a, \tau) + \partial_\tau u(t, a, \tau) = -\mu(a, \tau)u(t, a, \tau), \quad t \geq 0, \quad (a, \tau) \in \Omega, \quad (6.1.1)$$

coupled with the nonlocal boundary conditions

$$u(t, a, 0) = \iint_{\Omega} \alpha(a, \xi, s) u(t, \xi, s) d\xi ds =: K_{\alpha}(u(t, \cdot, \cdot))(a), \quad t \geq 0, \quad a \in [0, a^+] \quad (6.1.2)$$

$$u(t, 0, \tau) = \iint_{\Omega} \beta(\tau, \xi, s) u(t, \xi, s) d\xi ds =: K_{\beta}(u(t, \cdot, \cdot))(\tau), \quad t \geq 0, \quad \tau \in [0, \tau^+] \quad (6.1.3)$$

where $\mu(a, \tau)$ is the per capita removal rate of individuals with ages (a, τ) , while $\alpha(a, \xi, s)$ and $\beta(\tau, \xi, s)$ describe the per capita rates at which individuals with ages (ξ, s) produce new individuals with ages $(a, 0)$ and $(0, \tau)$, respectively.

Following [91, Assumption 2.1], we make the following assumption.¹

Assumption 6.1.

- (i) $\mu \in L^1_{\text{loc}}([0, a^+] \times [0, \tau^+], \mathbb{R})$ is nonnegative and bounded away from zero,
- (ii) $\alpha \in L^{\infty}([0, a^+] \times \Omega, \mathbb{R})$ is nonnegative,
- (iii) $\beta \in L^{\infty}([0, \tau^+] \times \Omega, \mathbb{R})$ is nonnegative.

6.2 Abstract setting

Under Assumption 6.1, for every $u_0 \in U := L^1(\Omega, \mathbb{R})$, the IBVP defined by (6.1.1)–(6.1.3) and $u(0, \cdot, \cdot) = u_0$ admits a unique solution $u(t, \cdot, \cdot) \in U$, $t \geq 0$. Moreover, the family of linear solution operators $\{T(t)\}_{t \geq 0}$ in U given by $T(t)u_0 := u(t, \cdot, \cdot)$ forms a strongly continuous semigroup of bounded positive operators, see [91, Theorem 2.3] or [134, Theorem 3.1].

Additionally, if μ , α and β are Lipschitz continuous on the interior of their domains, then $\{T(t)\}_{t \geq 0}$ is eventually compact and has asynchronous exponential growth [91, Sections 4 and Section 5.2]. The infinitesimal generator of $\{T(t)\}_{t \geq 0}$ is the operator $\mathcal{A}: D(\mathcal{A}) \subset U \rightarrow U$ defined as [91, Remark 2.3]

$$\begin{aligned} \mathcal{A}\phi(a, \tau) &:= -\partial_a \left[\phi(a, \tau) + \partial_{\tau} \int_0^a \phi(\xi, \tau) d\xi \right] - \mu(a, \tau)\phi(a, \tau) \\ &= -\partial_{\tau} \left[\phi(a, \tau) + \partial_a \int_0^{\tau} \phi(a, s) ds \right] - \mu(a, \tau)\phi(a, \tau), \quad \phi \in D(\mathcal{A}), \end{aligned} \quad (6.2.1)$$

where $D(\mathcal{A})$ satisfies the inclusion²

$$\begin{aligned} D(\mathcal{A}) \subset \left\{ \phi \in U \mid \mu\phi \in U, \right. \\ (a, \tau) \mapsto \int_0^a \phi(\xi, \tau) d\xi \text{ is absolutely continuous in } \tau, \text{ for a.a. } a \in [0, a^+], \\ (a, \tau) \mapsto \left[\phi(a, \tau) + \partial_{\tau} \int_0^a \phi(\xi, \tau) d\xi \right] \text{ is absolutely continuous in } a, \text{ for a.a. } \tau \in [0, \tau^+], \\ \left. \lim_{a \rightarrow 0^+} \left[\phi(a, \tau) + \partial_{\tau} \int_0^a \phi(\xi, \tau) d\xi \right] = K_{\beta}(\phi)(\tau) \text{ for a.e. } \tau \in [0, \tau^+], \right\} \end{aligned}$$

¹Note that, in [91] μ is assumed to be L^1 on its domain. Here we make a different choice to allow for unbounded mortality, see Section I.2.1. Following [81, 88], it is not difficult to show that the results of [91] still holds.

²As we assumed that μ can be unbounded at the maximum ages, to have a well-posed infinitesimal generator we added a condition on $\mu\phi$ in its domain in (6.2.2).

$$\begin{aligned}
(a, \tau) &\mapsto \int_0^\tau \phi(a, s) \, ds \text{ is absolutely continuous in } a, \text{ for a.a. } \tau \in [0, \tau^+], \\
(a, \tau) &\mapsto \left[\phi(a, \tau) + \partial_a \int_0^\tau \phi(a, s) \, ds \right] \text{ is absolutely continuous in } \tau, \text{ for a.a. } a \in [0, a^+], \\
\lim_{\tau \rightarrow 0^+} \left[\phi(a, \tau) + \partial_a \int_0^\tau \phi(a, s) \, ds \right] &= K_\alpha(\phi)(a) \text{ for a.e. } a \in [0, a^+], \\
\partial_a \left[\phi(a, \tau) + \partial_\tau \int_0^a \phi(\xi, \tau) \, d\xi \right] &\in U, \\
\partial_\tau \left[\phi(a, \tau) + \partial_a \int_0^\tau \phi(a, s) \, ds \right] &\in U \Big\},
\end{aligned} \tag{6.2.2}$$

while [134, Remark 6.1] claims that equality holds. If $\phi \in D(\mathcal{A})$ is sufficiently smooth, then the action of $\mathcal{A}$ simplifies and can be expressed as

$$\mathcal{A}\phi = -(\partial_a \phi + \partial_\tau \phi + \mu \phi).$$

From [49, Theorem 9.5] and [67, Theorem VI.1.15], it follows that the stability of the null equilibrium is determined by the sign of $s(\mathcal{A})$. Moreover, [91, Proposition 5.6] ensures that $\sigma(\mathcal{A})$ contains eigenvalue only, and $\lambda_0 := s(\mathcal{A})$ is the dominant eigenvalue of $\mathcal{A}$. Additionally, it is simple.

In view of analyzing the stability of (6.1.1)–(6.1.3), based on the above considerations, we propose to numerically approximate λ_0 . To this aim, we introduce the following equivalent reformulation, which allows one to gain in regularity and to better deal with the conditions characterizing $D(\mathcal{A})$.

We consider the space

$$V := \left\{ \psi: \Omega \rightarrow \mathbb{R} \mid \psi(a, \tau) = \int_0^a \int_0^\tau \phi(\xi, s) \, ds d\xi \text{ for some } \phi \in U \right\},$$

which is a Banach space if endowed with norm $\|\psi\|_V := \|\partial_a \partial_\tau \psi\|_U$. Then, the operator $\mathcal{S}: U \rightarrow V$ defined as

$$\mathcal{S}\phi(a, x) := \int_0^a \int_0^\tau \phi(\xi, s) \, ds d\xi, \quad (a, \tau) \in \Omega,$$

determines an isomorphism between U and V with inverse $\mathcal{S}^{-1}\psi = \partial_a \partial_\tau \psi$. Then the operator $\mathcal{B} := \mathcal{S}\mathcal{A}\mathcal{S}^{-1}$ with domain $D(\mathcal{B}) = \mathcal{S}D(\mathcal{A})$ satisfies $\sigma(\mathcal{B}) = \sigma(\mathcal{A})$ [67, Section 2.1] and $\sigma_p(\mathcal{B}) = \sigma_p(\mathcal{A})$, see Proposition 1.3.1. Furthermore, from [91, Proposition 3.1], noting that in that proof $\chi = A\phi + \mu\phi$, for $\psi \in D(\mathcal{B})$, we can write

$$\begin{aligned}
\mathcal{B}\psi(a, \tau) &= -\partial_a \psi(a, \tau) - \partial_\tau \psi(a, \tau) \\
&\quad + \int_0^a K_\alpha(\partial_\tau \partial_a \psi)(\zeta) \, d\zeta + \int_0^\tau K_\beta(\partial_\tau \partial_a \psi)(\eta) \, d\eta \\
&\quad - \int_0^a \int_0^\tau \mu(\zeta, \eta) \partial_\tau \partial_a \psi(\zeta, \eta) \, d\eta d\zeta.
\end{aligned} \tag{6.2.3}$$

Hence, in order to approximate λ_0 , we propose to discretize $\mathcal{B}$ instead of $\mathcal{A}$, given that the domain condition for $\mathcal{B}$ is now trivial.

6.3 The numerical approach

The aim of the numerical method described next is that of approximating (the rightmost) part of $\sigma_p(\mathcal{B})$ through the eigenvalues of a matrix discretizing $\mathcal{B}$. To do so, we resort to pseudospectral collocation in both the age-variables with a tensorial approach.

For N, M positive integers, let $V_{N,M}$ denote the space of bivariate algebraic polynomials on Ω of degree at most N in the first variable and at most M in the second variable, taking value 0 at

$a = 0$ and $\tau = 0$. Let $\Theta_N^a = \{a_1 < \dots < a_N\}$ denote the mesh of N Chebyshev zeros in $(0, a^+)$, and let $\Theta_M^\tau = \{\tau_1 < \dots < \tau_M\}$ denote the mesh of M Chebyshev zeros in $(0, \tau^+)$. We define restriction and prolongation operators respectively as

$$\mathcal{R}_{N,M}: V \rightarrow \mathbb{R}^{NM}, \quad \mathcal{R}_{N,M}\psi = (\psi(a_1, \tau_1); \dots; \psi(a_1, \tau_N); \psi(a_2, \tau_1); \dots; \psi(a_N, \tau_M)),$$

and

$$\mathcal{P}_{N,M}: \mathbb{R}^{NM} \rightarrow V_{NM}, \quad \mathcal{P}_{N,M}\Psi = \sum_{i=1}^N \sum_{j=1}^M \ell_{N,i}^a \ell_{M,j}^\tau \Psi_{(i-1)M+j},$$

where $\Psi := (\Psi_1; \dots; \Psi_{NM})$, $\{\ell_{N,i}^a\}_{i=0}^N$ is the Lagrange basis relevant to $\Theta_{0,N}^a := \{0\} \cup \Theta_N^a$ and $\{\ell_{M,j}^\tau\}_{j=0}^M$ is the Lagrange basis relevant to $\Theta_{0,M}^\tau := \{0\} \cup \Theta_M^\tau$. Then, the finite-dimensional approximation $\mathcal{B}_{N,M}: \mathbb{R}^{NM} \rightarrow \mathbb{R}^{NM}$ of $\mathcal{B}$ is obtained as

$$\mathcal{B}_{N,M} := \mathcal{R}_{N,M} \mathcal{B} \mathcal{P}_{N,M}.$$

The discrete eigenvalue problem is solved by using the standard MATLAB function `eig`.

6.4 Implementation

Now, we describe how to explicitly construct the entries of the matrices representing the discretized operator obtained in Section 6.3.

Let $(i; j) := (i-1)M + j$, for $i = 1, \dots, N$ and $j = 1, \dots, M$, we have

$$\begin{aligned} [\mathcal{B}_{N,M}\Psi]_{(i;j)} &= - \sum_{h=1}^N (\ell_{N,h}^a)'(a_i) \Psi_{(h;j)} - \sum_{k=1}^M (\ell_{M,k}^\tau)'(\tau_j) \Psi_{(i;k)} \\ &\quad + \int_0^{a_i} K_\alpha \left(\sum_{h=1}^N \sum_{k=1}^M (\ell_{N,h}^a)'(\ell_{M,k}^\tau)' \Psi_{(h;k)} \right) (\zeta) d\zeta \\ &\quad + \int_0^{\tau_j} K_\beta \left(\sum_{h=1}^N \sum_{k=1}^M (\ell_{N,h}^a)'(\ell_{M,k}^\tau)' \Psi_{(h;k)} \right) (\eta) d\eta \\ &\quad - \int_0^{a_i} \int_0^{\tau_j} \mu(\zeta, \eta) \sum_{h=1}^N \sum_{k=1}^M (\ell_{N,h}^a)'(\zeta) (\ell_{M,k}^\tau)'(\eta) \Psi_{(h;k)} d\eta d\zeta, \end{aligned}$$

for $i = 1, \dots, N$ and $j = 1, \dots, M$. Using the linearity of K_α and K_β , it is easy to characterize the entries of the matrix $\mathcal{B}_{N,M}$. Let $\mathcal{D}_N^a \in \mathbb{R}^{N \times N}$ and $\mathcal{D}_M^\tau \in \mathbb{R}^{M \times M}$ be defined as

$$\begin{aligned} [\mathcal{D}_N^a]_{i,j} &= (\ell_{N,j}^a)'(a_i), \quad i, j = 1, \dots, N \\ [\mathcal{D}_M^\tau]_{i,j} &= (\ell_{M,j}^\tau)'(\tau_i), \quad i, j = 1, \dots, M. \end{aligned}$$

In other words, $\mathcal{D}_N^a$ and $\mathcal{D}_M^\tau$ are the part of the differentiation matrices relevant to $\Theta_{0,N}^a$ and $\Theta_{0,M}^\tau$, respectively, deleting the first row and the first column. Then, we can write

$$\mathcal{B}_{N,M} = -\mathcal{D}_N^a \otimes \mathcal{I}_{\mathbb{R}^M} - \mathcal{I}_{\mathbb{R}^N} \otimes \mathcal{D}_M^\tau + \mathcal{K}_{N,M}^\alpha + \mathcal{K}_{N,M}^\beta - \mathcal{U}_{N,M}$$

where $\mathcal{K}_{N,M}^\alpha, \mathcal{K}_{N,M}^\beta, \mathcal{U}_{N,M} \in \mathbb{R}^{NM \times NM}$ are defined as

$$[\mathcal{K}_{N,M}^\alpha]_{(i;j), (h;k)} = \int_0^{a_i} K_\alpha((\ell_{N,h}^a)'(\ell_{M,k}^\tau)')(\zeta) d\zeta, \quad (6.4.1)$$

$$[\mathcal{K}_{N,M}^\beta]_{(i;j), (h;k)} = \int_0^{\tau_j} K_\beta((\ell_{N,h}^a)'(\ell_{M,k}^\tau)')(\eta) d\eta, \quad (6.4.2)$$

	C^∞	Lip^2	Lip^1	Lip^0	Discontinuous
Ω	$[0, 1] \times [0, 2]$	$[0, 1] \times [0, 2]$	$[0, 1] \times [0, 2]$	$[0, 1] \times [0, 2]$	$[0, 1] \times [0, 2]$
$\alpha_1(a)$	e^{-a^2}	$a^2 a $	$-a a $	$ a $	1
$\beta_1(\tau)$	e^τ	$\tau^2 \tau $	$\tau \tau $	$ \tau $	0
$\gamma(\xi, \sigma)$	$\ \alpha\beta\ _U^{-1}$	$\frac{5}{8}$	$\frac{6}{7}$	$\frac{3}{4}$	2
$\mu(a, \tau)$	1	1	1	1	1
λ_0	-1	-1	-1	-1	-1
$\phi(a, \tau)$	$e^{-a^2+\tau}$	$(a - \tau)^2 a - \tau $	$(a - \tau) a - \tau $	$ a - \tau $	$\chi_{[0, +\infty[}(a - \tau)$

Table 6.5.1: Parameters and resulting eigenvalue and eigenfunction used in the numerical tests of Section 6.5 relevant to model (6.1.1)–(6.1.3).

$$[\mathcal{U}_{N,M}]_{(i;j),(h;k)} = \int_0^{a_i} \int_0^{\tau_j} \mu(\zeta, \eta) (\ell_{N,h}^a)'(\zeta) (\ell_{M,k}^\tau)'(\eta) d\eta d\zeta, \quad (6.4.3)$$

for $i, k = 1, \dots, N$ and $j, h = 1, \dots, M$.

If the integrals in (6.4.1)–(6.4.3) cannot be computed analytically, we approximate them numerically. We use the Fejer's first rule quadrature for the integrals in $[0, a^\dagger]$ and $[0, \tau^\dagger]$ with N and M nodes, respectively, and the i -th row of the inverse of the differentiation matrices $\mathcal{D}_a$ and $\mathcal{D}_\tau$ for the integrals in $[0, a_i]$ and $[0, \tau^\dagger]$, $i = 1, \dots, N$, $j = 1, \dots, M$ [60].

6.5 Numerical results

In this Section, we present several numerical experiments to investigate how the spectrum of the finite-dimensional operator $\mathcal{B}_{N,M}$ approximates the spectrum of $\mathcal{B}$. For this purpose, we select several parameter sets for which λ_0 and the relevant eigenfunction ϕ of $\mathcal{A}$ are explicitly known, and we study the convergence of the approximated eigenvalues of $\mathcal{B}_{N,M}$ to the analytic ones.

For each example we study the behavior for increasing $N = M$ of the absolute error on the known eigenvalue λ_0 . In all examples we choose

$$\alpha(a, \xi, s) = \alpha_1(a) \gamma(\xi, s), \quad \beta(\tau, \xi, s) = \beta_1(\tau) \gamma(\xi, s)$$

in the boundary conditions (6.1.2)–(6.1.3), in order to simplify finding an explicit eigenfunction.

We remark that the parameters are chosen in order to have an analytically known eigenfunction with certain smoothness properties, without regard to any specific biological interpretation. The choices of the parameters and the resulting eigenvalue and eigenfunction are listed in Table 6.5.1. For the relevant eigenfunctions, we also describe the degree of regularity.

The left panel of Figure 6.5.1 shows infinite convergence order, in accordance with the fact that the relevant eigenfunction is of class C^∞ .

The right panel of Figure 6.5.1 shows the approximation error in the case of non C^∞ eigenfunctions. Finite convergence order is observed in all the cases. In particular, the convergence order increases with the regularity of the eigenfunction. The convergence is of almost order 2 also in the case of a discontinuous eigenfunction. This can be explained by the fact that we are actually collocating the eigenvalue problem for $\mathcal{B}$, which means that the eigenvalues are the same as $\mathcal{A}$, but the eigenfunctions correspond to (double) integrals of the eigenfunctions of $\mathcal{A}$. Hence, in the case of ϕ discontinuous, we are actually approximating a function which has two degrees of smoothness more. This is an important advantage of the reformulation via integration of the state, as the method performs well even in the presence of discontinuous problems.

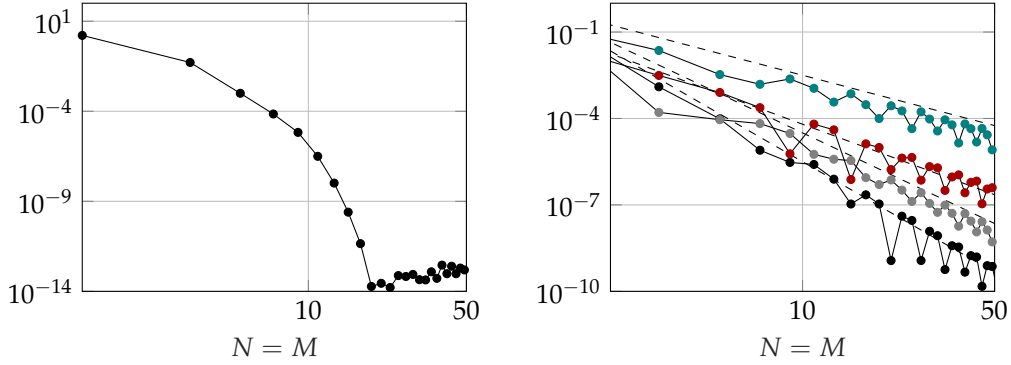


Figure 6.5.1: Loglog plot for increasing $N = M$ of the approximation error on λ . Left: infinite convergence order is observed for the case C^∞ . Right: finite convergence order is observed for the case Lip^2 (black), Lip^1 (gray), Lip^0 (red) and discontinuous (green). The slopes of the dashed lines are $-2.5, -3.5, -4.5, -5.5$. Original figure from [7].

6.5.1 Applications to the Kermack-McKendrick model with demography

We consider the epidemic model proposed in [87] (to which we refer for the details), where the infected individuals are structured by demographic age $a \in [0, a^+]$ and infection age $\tau \in [0, \tau^+]$. Assuming that the host population is at demographic equilibrium (see Section I.2.1), the linearized equation for the infected individuals around the DFE reads

$$\begin{cases} \mathcal{D}i(t, \tau, a) = -(\mu(a) + \gamma(\tau))i(t, \tau, a), & t \geq 0, \quad (a, \tau) \in \Omega, \\ i(t, a, 0) = w_0(a) \int_0^{a^+} \int_0^{\xi} \beta(\tau) i(t, \xi, \tau) d\tau d\xi, & t \geq 0, \quad a \in [0, a^+], \\ i(t, 0, \tau) = 0 & t \geq 0, \quad \tau \in [0, \tau^+], \end{cases} \quad (6.5.1)$$

where $i(t, a, \tau)$ denotes the density of infectious individuals at time $t \geq 0$, demographic age $a \in [0, a^+]$ and infection age $\tau \in [0, \tau^+]$,

$$\mathcal{D}i(t, a, \tau) := \partial_t i(t, a, \tau) + \partial_a i(t, a, \tau) + \partial_\tau i(t, a, \tau),$$

$\beta(\tau)$ is the infection age-specific infection rate, $\gamma(\tau)$ is the infection age-specific recovery rate, $\mu(a)$ is the demographic age-specific mortality rate, and

$$w_0(a) := \frac{\Pi(a)}{\int_0^{a^+} \Pi(\xi) d\xi}, \quad a \in [0, a^+]$$

is the (stable) age-profile of the host population, where

$$\Pi(a) := e^{-\int_0^a \mu(\xi) d\xi}, \quad a \in [0, a^+]$$

is the survival probability function, see (I.2.3).

Following [87, Section 4.2], the basic reproduction number is given by

$$R_0 = \int_0^{a^+} \Phi(a) w_0(a) da, \quad (6.5.2)$$

for

$$\Phi(a) := \int_0^{\min\{a^+-a, \tau^+\}} \beta(\tau) \Gamma(\tau) \frac{\Pi(a+\tau)}{\Pi(a)} d\tau, \quad (6.5.3)$$

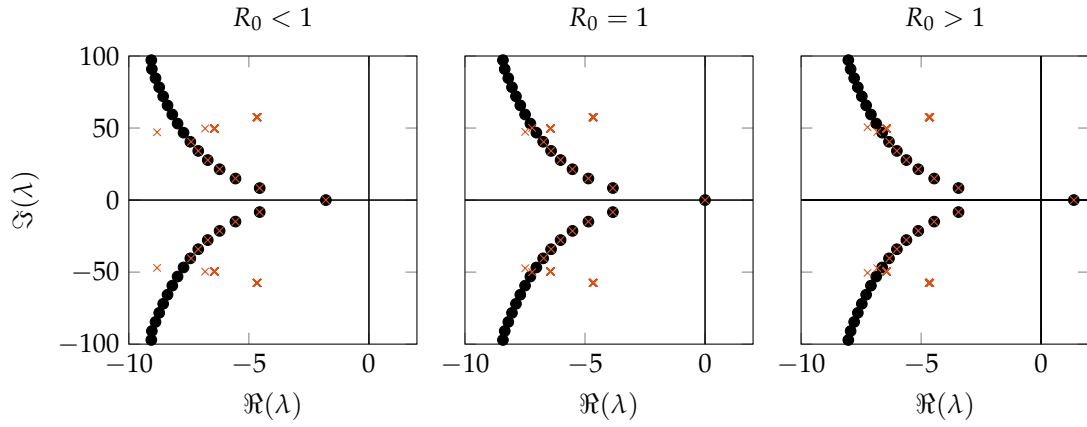


Figure 6.5.2: Computed spectra of $\mathcal{B}$ in the complex plane for $\beta_0 = (1 - k)/k$ (left), $\beta_0 = 1/k$ (center) and $\beta_0 = (1 + k)/k$ (right), with k as in (6.5.4), corresponding respectively to $R_0 < 1$, $R_0 = 1$ and $R_0 > 1$, computed with $N = M = 30$ (×) and with $N = M = 50$ (•).

where

$$\Gamma(\tau) := e^{-\int_0^\tau \gamma(\xi) d\xi}$$

is the probability of still being infectious at infection age $\tau \in [0, a^\dagger]$. Hence we expect the DFE to undergo a bifurcation at $R_0 = 1$ and specifically we expect a real eigenvalue crossing the imaginary axis from left to right.

For the numerical simulations, we consider $a^\dagger = 100$ (yr), $\tau^\dagger = 2$ (weeks), $\mu(a) = (a^\dagger - a)^{-1}$, $\gamma(\tau) = (\tau^\dagger - \tau)^{-1}$ and we vary $\beta(\tau) = \beta_0 > 0$. These are simplified parameters but broadly consistent with a short infection like COVID-19. For this choice of parameters, from (6.5.2)–(6.5.3) we get $R_0 = \beta_0 k$, where k is a constant given by

$$k := \int_0^{a^\dagger} \int_0^{\min\{a^\dagger - a, \tau^\dagger\}} \Gamma(\tau) w_0(a + \tau) d\tau da = \frac{40549601}{81120000}. \quad (6.5.4)$$

Since discretizing a large interval causes slower convergence of interpolation methods, and to properly deal with the unbounded terms μ and γ , for the purpose of the numerical experiments we rescale a and τ to the interval $[0, 1]$ considering new variables $x := a/a^\dagger$ and $y := \tau/\tau^\dagger$ and $u(t, x, y) := i(t, a^\dagger x, \tau^\dagger y) (\Pi(a^\dagger x) \Gamma(\tau^\dagger y))^{-1}$. The resulting model for u reads

$$\begin{cases} \tilde{\mathcal{D}}u(t, x, y) = 0, & t \geq 0, \quad (x, y) \in [0, 1]^2, \\ u(t, x, 0) = \int_0^1 \int_0^\xi \beta(\tau^\dagger y) \Pi(a^\dagger \xi) \Gamma(\tau^\dagger y) u(t, \xi, y) a^\dagger \tau^\dagger dy d\xi & t \geq 0, \quad x \in [0, 1], \\ u(t, 0, y) = 0 & t \geq 0, \quad y \in [0, 1], \end{cases} \quad (6.5.5)$$

where

$$\tilde{\mathcal{D}}u(t, x, y) := \partial_t u(t, x, y) + \frac{1}{a^\dagger} \partial_x u(t, x, y) + \frac{1}{\tau^\dagger} \partial_y u(t, x, y).^3$$

In view of asymptotic stability, (6.5.1) and (6.5.5) are equivalent since $\Pi(a)\Gamma(\tau)$ is bounded for $(a, \tau) \in \Omega$.

Figure 6.5.2 shows the rightmost part of the spectrum of $\mathcal{B}$ for values of R_0 around the bifurcation at $R_0 = 1$. As anticipated, the rightmost eigenvalue is real and crosses the imaginary axis. The figure shows the eigenvalues of $\mathcal{B}_{N,M}$ for two different values of $N = M$. The comparison suggests that some of the eigenvalues are spurious, more precisely the ones seemingly not lying on the emerging exponential-like curves (excluding, of course, the spectral bound).

³Note that here the velocities of the variables are not equal to one as in (6.1.1). However, it is not difficult to see that the proposed method can be easily adapted to account also for this case.

7

Conclusions

In this thesis, we developed numerical methods for different classes of models from population and infectious disease dynamics. For each of them, we considered the approximation of threshold parameters that determine the stability of invariants. The methods developed in this thesis rely on (pseudo)spectral discretizations, which allow to obtain accurate approximations with relatively small dimension of the discretization space. Moreover, we extensively discussed applications of our methods to models from epidemiology. We hope that the methods here developed may be useful in the future to obtain new insights on the dynamics of populations and infectious diseases.

An important aspect to highlight is that, for the classes of models considered in this thesis, the eigenvalues of interest are typically simple and isolated. This is of great advantage for the methods here developed, as it allows us to tackle their computation with standard tools and without the need to resort to particular alternative strategies (which instead may be required in the presence of, e.g., clusters or multiple eigenvalues).

Note that in this thesis we did not discuss procedures and methods to determine values of the discretization parameters (in this thesis denoted by N and M) necessary to obtain a prefixed accuracy of the approximation(s). For instance, for finite-order methods like finite-differences and Runge-Kutta methods, one can derive a relation between the convergence order s of the approximation(s) and the discretization parameter $h > 0$, of the form $O(h^s)$. Then, one can exploit this information to derive algorithms based on the Richardson's extrapolation procedure to obtain a prefixed accuracy of the approximation(s), see for instance [33, Section 6.4]. However, for (pseudo)spectral methods, in the presence of infinite convergence order, the error formulae are typically given by nonlinear and nonpolynomial functions of the discretization parameter(s), which makes it difficult to determine appropriate discretization indexes a priori, see for instance [34, Section 3]. Nevertheless, one can take advantage of the (relatively) small dimension of the matrices resulting from the discretization to re-run the program for a few iterations in order to reach the required accuracy. Indeed, experimental evidence shows that in general high accuracy is reached with matrix approximations of dimension around the order of tenths.

Of course, this line of research opens many perspectives for future developments. As an example, in this thesis we restricted to models with finite age span. Although this assumption may be acceptable in certain context, other situations may require to deal with unbounded variables. Yet, models with unbounded structuring variables require much more attention in the development of numerical methods. We plan in the future to extend these techniques also to this family of models. Another future perspective is that of extending the method for the computation of reproduction numbers in time periodic environments to more complicated models, for instance with delay, as they play an important role in the modeling of, for instance, vector-transmitted diseases. To conclude, another important extension that we plan to tackle is that of extending our methods to the analysis of nonlinear models in view of possible bifurcation analyses through suitable softwares.

A

Modeling details

In this appendix, we collect some further modeling and computational details regarding the models considered throughout this thesis, including the original formulation of the models in their nonlinear form. We use capital letters ($S, I, R, \dots$) to denote the age-densities (or numbers depending on the context), and small letters to denote the densities divided by either the total size or the age-density of the host population (e.g., $s(t, a) = S(t, a)/P(t, a)$).

A.1 An SAIR model structured by disease and infection age

Model (2.5.1) is obtained by partitioning the population into four classes: susceptibles, asymptomatic, symptomatic and removed individuals. In the model, the asymptomatic individuals are structured by the infection age (time elapsed since infection) and the symptomatic individuals are structured by the disease age (time elapsed since the onset of symptoms), see for example [90]. Let $S(t)$ and $R(t)$ denote the number of susceptible and removed individuals, respectively, at time $t \geq 0$, $A(t, a)$ denote the density of asymptomatic infectious individuals at time $t \geq 0$ and disease age $a \in [0, a^+]$, and $I(t, a)$ denote the density of infectious individuals which are symptomatic at time $t \geq 0$ and infection age $a \in [0, a^+]$. We assume that the total population

$$P := S(t) + \int_0^{a^+} (A(t, a) + I(t, a)) da + R(t)$$

is constant (no demographic turnover). The variables and model structure are shown in Figure A.1.1.

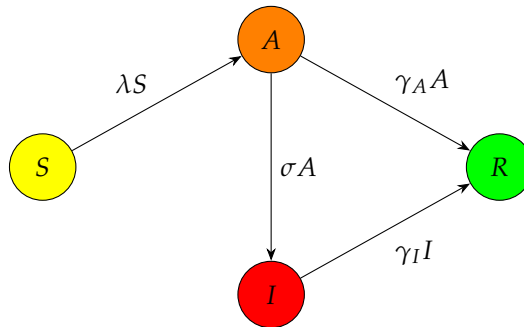


Figure A.1.1: Flow chart for the SAIR model (A.1.1).

The model reads as follows:

$$\left\{ \begin{array}{l} S'(t) = -\lambda(t)S(t), \\ \mathcal{D}A(t,a) = -(\sigma(a) + \gamma_A(a))A(t,a), \\ \mathcal{D}I(t,a) = -\gamma_I(a)I(t,a), \\ A(t,0) = \lambda(t)S(t), \\ I(t,0) = \int_0^{a^\dagger} \sigma(a)A(t,a) da, \\ R'(t) = \int_0^{a^\dagger} (\gamma_A(a)A(t,a) + \gamma_I(a)I(t,a)) da, \end{array} \right. \quad (\text{A.1.1})$$

where $\mathcal{D}$ is defined as in (I.2.6) and

$$\lambda(t) := \int_0^{a^\dagger} \frac{b_A(a)A(t,a) + b_I I(t,a)}{P} da, \quad t \geq 0,$$

is the force of infection. Linearizing the equations for the infected individuals around the disease-free equilibrium

$$(S^*, A^*(a), I^*(a), R^*) = (P, 0, 0, 0),$$

we obtain system (2.5.1), to which we refer for the parameters interpretation.

A.2 A model for the spread of Rubella with vertical transmission

Here we refer to [54] and we consider a model inspired by [2]. Let $M(t,a)$, $S(t,a)$, $E(t,a)$, $I(t,a)$ and $R(t,a)$ denote the density of individuals who are protected by maternal antibodies, susceptible, infected but not infectious, infectious, and immune (acquired naturally or via vaccination), respectively, at time $t \geq 0$ and demographic age $a \in [0, a^\dagger]$. The variables and model structure are shown in Figure A.2.1. The model reads as follows

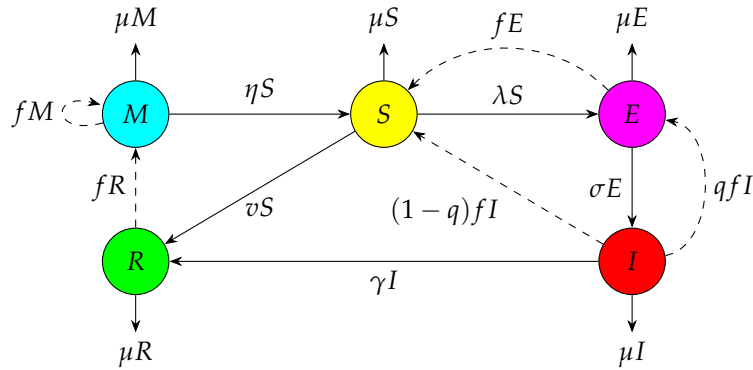


Figure A.2.1: Flow chart for the MSEIR model for the spread of Rubella with vertical transmission (A.2.1). The solid lines describe the horizontal dynamics, while the dashed lines describe the vertical dynamics.

$$\begin{cases} \mathcal{D}M(t, a) = -(\mu(a) + \eta)M(t, a), \\ \mathcal{D}S(t, a) = \eta M(t, a) - (\mu(a) + \lambda(t, a) + v(a))S(t, a), \\ \mathcal{D}E(t, a) = \lambda(t, a)S(t, a) - (\mu(a) + \sigma)E(t, a), \\ \mathcal{D}I(t, a) = \sigma E(t, a) - (\mu(a) + \gamma)I(t, a), \\ \mathcal{D}R(t, a) = \gamma I(t, a) + v(a)S(t, a) - \mu(a)R(t, a), \end{cases} \quad (\text{A.2.1})$$

with the following boundary conditions

$$\begin{aligned} M(t, 0) &= \int_0^{a^+} f(a)(M(t, a) + R(t, a)) \, da, \\ S(t, 0) &= \int_0^{a^+} f(a)[S(t, a) + E(t, a) + (1 - q)I(t, a)] \, da, \\ E(t, 0) &= q \int_0^{a^+} f(a)I(t, a) \, da, \\ I(t, 0) &= R(t, 0) = 0, \end{aligned}$$

where $\mathcal{D}$ is defined as in (I.2.6),

$$\lambda(t, a) := \int_0^{a^+} \hat{k}(a, \alpha) I(t, \alpha) \, d\alpha$$

is the force of infection, with $\hat{k}(a, \zeta)$ the transmission rate between one individual of age a and one individual of age ζ , and $\mu(a)$ is the age-specific mortality rate. We refer to Section 2.5 for the interpretation of the other parameters. Note that an individual is assumed to have permanent immunity once infected.

We assume that f and Π satisfy (I.2.15), where Π is the survival probability defined in (I.2.3), and that the age-density of the host population $P(t, a) := M(t, a) + S(t, a) + E(t, a) + I(t, a) + R(t, a)$ has already attained the stationary age-density $P(t, a) = P^*(a) = P_0 w_0$, for some $P_0 > 0$, where w_0 is defined as in (I.2.11), see (I.2.16). For convenience, we define the standardized transmission rate as follows:

$$k(a, \alpha) := \frac{P_0 \hat{k}(a, \alpha)}{\int_0^{a^+} \Pi(\zeta) \, d\zeta}.$$

Then, if we consider new variables

$$m(t, a) := \frac{M(t, a)}{P^*(a)}, \quad s(t, a) := \frac{S(t, a)}{P^*(a)}, \quad e(t, a) := \frac{E(t, a)}{P^*(a)}, \quad i(t, a) := \frac{I(t, a)}{P^*(a)}, \quad r(t, a) := \frac{R(t, a)}{P^*(a)},$$

we can reduce to the following model

$$\begin{cases} \mathcal{D}m(t, a) = -\eta m(t, a), \\ \mathcal{D}s(t, a) = \eta m(t, a) - (\lambda(t, a) + v(a))s(t, a), \\ \mathcal{D}e(t, a) = \lambda(t, a)s(t, a) - \sigma e(t, a), \\ \mathcal{D}i(t, a) = \sigma e(t, a) - \gamma i(t, a), \\ \mathcal{D}r(t, a) = \gamma i(t, a) + v(a)s(t, a), \end{cases}$$

with the following boundary conditions:

$$\begin{aligned} m(t, 0) &= \int_0^{a^+} f(a) \Pi(a) (m(t, a) + r(t, a)) \, da, \\ s(t, 0) &= \int_0^{a^+} f(a) \Pi(a) [s(t, a) + e(t, a) + (1 - q)i(t, a)] \, da, \\ e(t, 0) &= q \int_0^{a^+} f(a) \Pi(a) i(t, a) \, da, \\ i(t, 0) &= r(t, 0) = 0, \end{aligned}$$

where the force of infection can be expressed as follows:

$$\lambda(t, a) = \int_0^{a^+} k(a, \alpha) \Pi(a) i(t, \alpha) \, d\alpha.$$

The disease-free equilibrium $E^* := (m^*(a), s^*(a), e^*(a), i^*(a), r^*(a))$ explicitly reads as follows

$$\begin{aligned} m^*(a) &= (1 - s^*(0)) e^{-\eta a}, \\ s^*(a) &= s^*(0) e^{-\int_0^a v(\xi) \, d\xi} + \eta \int_0^a e^{-\int_\xi^a v(\theta) \, d\theta} m^*(\xi) \, d\xi, \\ r^*(a) &= \int_0^a v(\xi) s^*(\xi) \, d\xi, \\ e^*(a) &= i^*(a) = 0, \end{aligned}$$

where

$$s^*(0) = \frac{\eta \int_0^{a^+} f(a) \Pi(a) \int_0^a e^{-\int_\xi^a v(\theta) \, d\theta} e^{-\eta \xi} \, d\xi \, da}{1 - \int_0^{a^+} f(a) \Pi(a) e^{-\int_0^a v(\theta) \, d\theta} \, da + \eta \int_0^{a^+} f(a) \Pi(a) \int_0^a e^{-\int_\xi^a v(\theta) \, d\theta} e^{-\eta \xi} \, d\xi \, da}.$$

Assuming a constant vaccination rate $v(a) \equiv v$ and $\eta > v$, the density of susceptible population reads as follows:

$$s^*(a) = s^*(0) \left[e^{-va} - \frac{\eta}{v - \eta} (e^{-\eta a} - e^{-va}) \right] + \frac{\eta}{v - \eta} (e^{-\eta a} - e^{-va}),$$

where

$$s^*(0) = \frac{\eta (v - \eta)^{-1} \int_0^{a^+} f(a) \Pi(a) (e^{-\eta a} - e^{-va}) \, da}{1 - \int_0^{a^+} f(a) \Pi(a) (e^{-va} - \eta (v - \eta)^{-1} (e^{-\eta a} - e^{-va})) \, da}.$$

Observe that we have $s^*(a) \equiv 1$ for $v \equiv 0$. The linearization around the DFE is given in (2.5).

We estimate k using real-world prevalence data taken from [2, Table 2], which are collected in Table A.2.1. To do this, we assume that k is piecewise constant in the six age groups defined in Table A.2.1, i.e.,

$$k(a, \xi) \equiv k_{ij} \quad \text{for } (a, \hat{a}) \in [\bar{a}_{i-1}, \bar{a}_i) \times [\bar{a}_{j-1}, \bar{a}_j), \quad i, j = 1, \dots, 6.$$

In particular, we assume the form for the WAIFW matrix $(k_{ij})_{i,j=1,\dots,6}$ illustrated in Section 2.5.

In Table A.2.1, we list the values of k_i , $i = 1, \dots, 6$, obtained from the corresponding values of λ_i , $i = 1, \dots, 6$ using the procedure described below.

Age class (years)	0 – 4	5 – 9	10 – 14	15 – 19	20 – 29	30 – 75
λ_i (case a)	0.081	0.115	0.115	0.083	0.091	0.067
k_i (case a)	2.205	5.905	3.932	2.644	2.940	2.132
λ_i (case b)	0.089	0.134	0.151	0.148	0.126	0.126
k_i (case b)	1.938	6.502	4.866	4.753	4.000	4.000

Table A.2.1: Age-specific forces of infection λ_i 's (yr^{-1}) and relevant values of k_i (yr^{-1}), $i = 1, \dots, 6$ in case a and case b for (2.5.2). Data are taken from [2, Table 2] according to their comments at page 324.

A.2.1 Estimation of age-dependent transmission rates

Here, we recall the procedure described in [4, Appendix A] to estimate the age-dependent transmission rate k under the hypothesis that it is piecewise constant among different age groups, i.e.,

$$k(a, \xi) \equiv k_{ij} \quad \text{for } (a, \xi) \in [\bar{a}_{i-1}, \bar{a}_i] \times [\bar{a}_{j-1}, \bar{a}_j], \quad i, j = 1, \dots, n,$$

for given $0 = \bar{a}_0 < \bar{a}_1 < \dots < \bar{a}_n = a^\dagger$. We assume that the age-specific mortality rate μ has the following form:

$$\mu(a) = \begin{cases} 0, & \text{if } a \leq a^\dagger, \\ +\infty & \text{otherwise,} \end{cases}$$

so that $\int_0^{a^\dagger} \Pi(a) da = a^\dagger$, and that the age-specific force of infection

$$\lambda(a) \equiv \lambda_i, \quad \text{for } a \in [\bar{a}_{i-1}, \bar{a}_i], \quad i = 1, \dots, n, \quad (\text{A.2.2})$$

is known.

Then, the following algorithm can be applied:

- (i) define $\psi_0 := 0$ and $\psi_i := \sum_{j=1}^i \lambda_j (\bar{a}_j - \bar{a}_{j-1})$ for $i = 1, \dots, n$;
- (ii) define $\Psi_i := \exp(-\psi_{i-1}) - \exp(-\psi_i)$ for $i = 1, \dots, n$;
- (iii) solve the linear problem $\lambda_i = \frac{1}{\gamma} \sum_{j=1}^n k_{ij} \Psi_j$ for $i = 1, \dots, n$.

Observe that the linear system in (iii) is over-determined; thus some hypotheses on the structure of the WAIFW matrix $(k_{ij})_{i,j=1,\dots,n}$ are needed. We refer the reader to [4] for some possible choices.

A.3 A multigroup SIR model with seasonality in contact rates

We consider the spread of an infectious disease in a population which is divided into $d \geq 1$ groups with seasonality in the contact rates. Let $S_j(t)$, $I_j(t)$ and $R_j(t)$ denote the number of susceptible, infectious and removed individuals, respectively, at time $t \geq 0$, and let $P_j(t) = S_j(t) + I_j(t) + R_j(t)$, $j = 1 \dots d$, denote the size of each group of the population, see [82, Section 8.8 and Section 8.9]. In the model, we include demography and we assume that there is no disease-induced mortality. The variables and model structure are shown in Figure A.3.1. The model reads

$$\begin{cases} S'_j(t) = \Lambda_j - S_j(t) \sum_{k=1}^d \beta_{jk}(t) \frac{I_k(t)}{P_k} - \mu_j S_j(t), \\ I'_j(t) = S_j(t) \sum_{k=1}^d \beta_{jk}(t) \frac{I_k(t)}{P_k} - (\mu_j + \gamma) I_j(t), \\ R'_j(t) = \gamma I_j(t), \end{cases} \quad (\text{A.3.1})$$

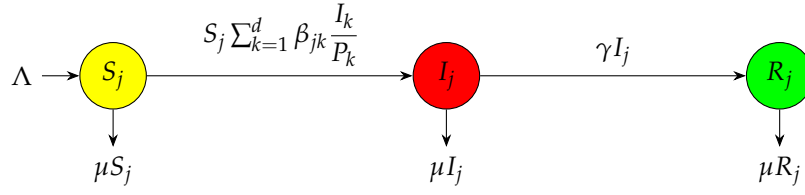


Figure A.3.1: Flow chart for the multigroup SIR model (A.3.1).

with

$$\beta_{jk}(t) = b_0 c_j(t) \frac{c_k(t) P_k}{\sum_{h=1}^d c_h(t) P_h} \geq 0, \quad j, k = 1, \dots, d,$$

where b_0 is the infectiousness probability per contact, $c_j(t)$ is the τ -periodic contact rate of individuals of group j , $\mu_j > 0$ is the natural mortality rate of group j , $\gamma \geq 0$ is recovery rate and Λ_j is the influx of new individuals in group j . We assume that $\Lambda_j = \mu_j P_j$, $j = 1, \dots, d$, so that the population size of each group, P_j , is constant.

For simplicity, we take $\mu_i \equiv \mu > 0$ and $P_j \equiv P > 0$, $j = 1, \dots, d$. Moreover, we take

$$c_j(t) = \bar{c}_j f(t), \quad j = 1, \dots, d,$$

where $c_j > 0$, $j = 1, \dots, d$, and f is a nonnegative τ -periodic function. Then, the linearized equation for the infected individuals around the DFE $S_j^* = P$, $I_j^* = 0$, $R_j^* = 0$ reads as in (3.5.1).

A.4 A vector-host model with seasonal fluctuations in the vector population

Inspired by [11, 132] and with reference to [1, 68, 75, 118], in this section we consider a simple vector-host model for dengue fever. Let $S_H(t)$, $I_H(t)$ denote the number of susceptible and infected humans, respectively, at time $t \in \mathbb{R}$, and let $S_V(t)$, $I_V(t)$ denote the number of susceptible and infected mosquitoes, respectively, at time $t \in \mathbb{R}$. The variables and model structure are shown in Appendix A.4.

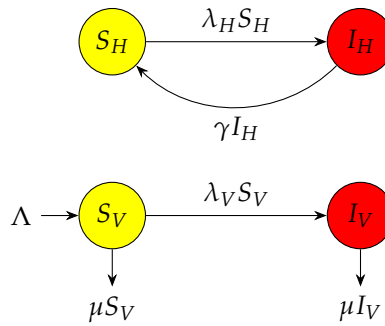


Figure A.4.1: Flow chart for the vector-host model (A.4.1).

The model reads

$$\begin{cases} S_H'(t) = \gamma I_H(t) - \lambda_H(t) S_H(t), \\ I_H'(t) = \lambda_H(t) S_H(t) - \gamma I_H(t), \\ S_V'(t) = \Lambda(t) - \lambda_V(t) S_V(t) - \mu S_V(t), \\ I_V'(t) = \lambda_V(t) S_V(t) - \mu I_V(t), \end{cases} \quad (\text{A.4.1})$$

where

$$\lambda_H(t) := \beta \frac{I_V(t)}{P_V(t)}, \quad \lambda_V(t) := \alpha \frac{I_H(t)}{P_H}, \quad t \geq 0,$$

denote the force of infection for the host and the vector population, respectively, with $P_H := S_H + I_H = \text{const}$, $P_V := S_V + I_V$ and

$$\Lambda(t) = (1 + \varepsilon \cos(2\pi t)) \mu P_V(t), \quad \varepsilon \in (0, 1).$$

We refer to Section 3.5 for the interpretation of the model parameters. Note that P_V satisfies the equation

$$P_V'(t) = \Lambda(t) - \mu P_V,$$

which admits for every $p_0 = P_V(0)$ the unique 1-periodic solution $P_V(t) = p_0 f(t)$, $t \in \mathbb{R}$, where

$$f(t) := e^{\delta \sin(2\pi t)}, \quad t \in \mathbb{R},$$

and $\delta := \varepsilon \mu / (2\pi)$. Hence, given $p_0 := P_V(0)$, system (A.4.1) admits the disease-free periodic solution

$$S_H^*(t) = P_H, \quad I_H^*(t) = 0, \quad S_V^*(t) = P_V(t), \quad I_V^*(t) = 0.$$

Linearizing the equations for the infected individuals around the the disease-free periodic solution, we get

$$\begin{cases} I_H'(t) = \beta \frac{P_H}{P_V(t)} I_V(t) - \gamma I_H(t), \\ I_V'(t) = \alpha \frac{P_V(t)}{P_H} I_H(t) - \mu I_V(t). \end{cases} \quad (\text{A.4.2})$$

In (3.5.3), we argue in terms of the variables $i_H := I_H / P_H$ and $i_V := I_V / p_0$.

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*"E non ricordo manco più come si fa a parlare
con te era bello volar via
dalla noia di questa città
o forse insieme si pensava solo a noi
e non a quel che ci fa male"*

"Requiem for a Gin", Storia di Anonima Controtendenza, No Good (2020).