

# numerical computation of $R_0$

Dimitri Breda



CDLab – Computational Dynamics Laboratory

Department of Mathematics, Computer Science and Physics – University of Udine

calcolo scientifico e modelli matematici

April 7, 2022 @ Rome

## [3, 4, 5] joint works with

- Simone De Reggi, Rossana Vermiglio @ CDLab
- Francesco Florian @ Zurich/CDLab
- Jordi Ripoll @ Girona
- Toshikazu Kuniya @ Kobe
- Francesca Scarabel @ Manchester/CDLab
- Jianhong Wu @ York

---

[3] B., De Reggi, Scarabel, Vermiglio, Wu – Comput. Math. Appl. 2021

[4] B., Florian, Ripoll, Vermiglio – J. Comput. Appl. Math. 2021

[5] B., Kuniya, Ripoll, Vermiglio – J. Sci. Comput. 2020

# outline

- historical perspective
- theoretical background
- abstract discretization
- bivariate collocation
- convergence

## timeline [7]

- demography: *expected number of newborns*
  - 1886: first ever estimate from fertility table [Böckh]
  - 1925: fully developed concept in demography [Dublin, Lotka]
- epidemiology: *expected number of secondary cases*
  - 1927: celebrated threshold theorem [Kermack, McKendrick]
  - ... incomplete surveys, re-discovering ...
  - 1975: current definition and notation  $R_0$  [Dietz]
  - 1990: full mathematical development [Diekmann, Heesterbeek, Metz]
  - 1991: influential book on infectious diseases [Anderson, May]
- numerics:
  - 2007: rectangles rule [1]
  - 2017: Euler scheme [8]

---

[1] Bacaër, Guernaoui – J. Math. Biol. 2006

[7] Heesterbeek – Acta Biother. 2002

[8] Kuniya – Appl. Math. Lett. 2017

## demography vs epidemiology [7]

- demography – each individual of a population of density  $P$  produces on average  $\mathcal{B}P$  offspring per unit of time for an average of  $1/\gamma$  time units:

$$R_0 = \mathcal{B}P \cdot \frac{1}{\gamma}$$

- $R_0 > 1$  growth,  $R_0 < 1$  extinction
- epidemiology – interpretation in terms of critical population density:

$$\frac{\mathcal{B}P}{\gamma} \geq 1 \quad \Rightarrow \quad P \geq P_c := \frac{\gamma}{\mathcal{B}}$$

## modern account for heterogeneous populations [6]

$R_0$ : expected number of secondary cases produced in a completely susceptible population by a typical infected individual during its entire period of infectiousness

- $\xi \in \Omega$ : *structure*, one or more traits characterizing individuals (age, size...)
- $S(\xi)$ : density of susceptibles in absence of disease
- $A(\tau, \xi, \eta)$ : infectivity towards a susceptible with structure  $\xi$ , of an individual infected  $\tau$  units of time ago while having structure  $\eta$
- density of newly infected in  $S$  caused by density of infected  $\phi$

$$(K(S)\phi)(\xi) := S(\xi) \int_{\Omega} \int_0^{\infty} A(\tau, \xi, \eta) d\tau \phi(\eta) d\eta \quad \text{next-generation operator}$$

- long run per-generation growth factor:

$$R_0 = \lim_{q \rightarrow \infty} \|K(S)^q\|^{1/q} \quad \text{spectral radius } \rho(K(S))$$

## unstructured single species [2]

- balance of birth ( $\beta$ ) and “death” ( $\mu$ ):

$$x' = \beta x - \mu x \quad (\text{in } \mathbb{R})$$

- asymptotic dynamics ruled by the *malthusian* parameter  $\beta - \mu \geq 0$
- alternatively, for the birth rate  $b(t) := \beta x(t)$ , variation of constants gives

$$b(t) = \beta e^{-\mu t} x(0) + \beta \int_0^t e^{-\mu(t-s)} b(s) ds$$

- taking  $x(0) = 0$ ,  $b \equiv 1$  and  $t \rightarrow +\infty$  gives  $R_0$  as

$$\beta \int_0^{\infty} e^{-\mu \sigma} d\sigma = \beta \cdot \frac{1}{\mu} \geq 1$$

- note that  $e^{-\mu t}$ 
  - is the solution semigroup of  $x' = -\mu x$  (absence of birth)
  - gives the survival probability ( $= x(t)/x(0)$ ), hence  $1/\mu$  is the life expectancy

## structured populations [2]

- let  $X = X(\Omega)$  be a Banach lattice of functions  $\Omega \subseteq \mathbb{R}^s \rightarrow \mathbb{R}$  ( $s = 1, 2$ )
- *abstract* ODE

$$x' = Bx - Mx \quad (\text{in } X)$$

- birth  $B : X \rightarrow X$  linear and bounded
- “death”  $M : \text{dom}(M) \subset X \rightarrow X$  linear and such that  $-M$  generates a  $C_0$ -semigroup  $\{T(t)\}_{t \geq 0}$  with spectral abscissa  $s(-M) < 0$
- asymptotic dynamics ruled by the malthusian parameter  $s(B - M) \geq 0$
- or, equivalently, by the **next-generation operator**

$$B \int_0^\infty T(\sigma) d\sigma = BM^{-1}$$

through its **spectral radius**  $R_0 = \rho(BM^{-1}) \geq 1$

- $BM^{-1}$  is in general linear, bounded and positive



# Malthus vs $R_0$

- sign relation [9]:

$$\text{sign } s(B - M) = \text{sign } [\rho(BM^{-1}) - 1]$$

- pros/cons [2]:

- $\text{rank}(B) \leq \text{rank}(B - M)$

- B finite rank:  $BM^{-1}$  is compact, whereas  $B - M$  is not in general

- splitting in birth/“death” not unique (\*)

- assumption:  $BM^{-1}$  compact, implying  $R_0 = \rho(BM^{-1}) \geq 0$  dominant eigenvalue

---

[2] Barril, Calsina, Ripoll – Bull. Math. Biol. 2017

[9] Thieme – SIAM J. Appl. Math. 2009

(\*) e.g., cell proliferation:  $\beta - \mu = 2\beta - (\beta + \mu)$

# standard vs generalized eigenvalue problems

- $BM^{-1} : X \rightarrow X$  is linear, bounded, positive and compact
- yet infinite-dimensional  $\Rightarrow$  infinitely-many eigenvalues
- discretize

$$BM^{-1}\psi = \lambda\psi$$

with a finite-dimensional SEP

- $M^{-1}$  unknown in general, so consider equivalently the GEP

$$B\phi = \lambda M\phi, \quad \phi \in \text{dom}(M)$$

- $\text{dom}(M) \subset X$  more regular than  $X$ , plus additional constraints  $C\phi = 0$  for some  $C : \text{dom}(M) \subset X \rightarrow \bar{X}$  with  $\bar{X} := X(\bar{\Omega})$  and  $\bar{\Omega}$  a boundary of  $\Omega$ , hence consider

$$\begin{cases} B\phi = \lambda M\phi \\ 0 = \lambda C\phi \end{cases}$$



# abstract discretization – 1

- let  $X_N \subset X$  be a finite-dimensional approximation space, isomorphous to  $\mathbb{R}^N$
- define
  - restriction  $R_N : X \rightarrow \mathbb{R}^N$
  - prolongation  $P_N : \mathbb{R}^N \rightarrow X_N$such that  $R_N P_N = I_N$  (hence  $L_N := P_N R_N : X \rightarrow X_N$  is a projection)
- act similarly for  $\bar{N} < N$  on
  - $\bar{X}$  with  $\bar{X}_{\bar{N}}$ ,  $\bar{R}_{\bar{N}}$ ,  $\bar{P}_{\bar{N}}$  and  $\bar{L}_{\bar{N}}$
  - $X^\circ := X(\Omega \setminus \bar{\Omega})$  with  $X_{N-\bar{N}}^\circ$ ,  $R_{N-\bar{N}}^\circ$ ,  $P_{N-\bar{N}}^\circ$  and  $L_{N-\bar{N}}^\circ$

## abstract discretization – 2

- discretize

$$\begin{cases} B\phi = \lambda M\phi \\ 0 = \lambda C\phi \end{cases} \quad (\text{in } X)$$

with

$$B_N \Phi = \lambda M_N \Phi \quad (\text{in } \mathbb{R}^N)$$

for

$$B_N := \begin{pmatrix} R_{N-\bar{N}}^\circ B P_N \\ 0_{\bar{N},N} \end{pmatrix}, \quad M_N := \begin{pmatrix} R_{N-\bar{N}}^\circ M P_N \\ \bar{R}_{\bar{N}} C P_N \end{pmatrix}$$

- examples:

- pseudospectral collocation in  $L^1$
- Fourier expansion in  $L^2$



## age-immunity model [3]

- individuals characterized by age  $\alpha \in [0, \bar{\alpha}]$  and immunity level  $w \in [0, 1]$  waning as  $w' = -g(w)$  for some positive  $g$
- susceptibles  $s = s(t, \alpha, w)$  and infected  $i = i(t, \alpha, w)$  at time  $t$ , age  $\alpha$  and immunity  $w$  ruled by

$$\begin{cases} \partial_t s + \partial_\alpha s - \partial_w [g(w)s] = -[\mu(\alpha) + \lambda(i, w) + \eta(i, w)]s \\ \partial_t i + \partial_\alpha i = \lambda(i, w)s - [\mu(\alpha) + \gamma]i \\ g(1)s(t, \alpha, 1) = \gamma \int_0^1 i \, dw + \int_0^1 \eta(i, w)s \, dw, \quad i(t, \alpha, 1) = 0 \\ s(t, 0, w) = \mathcal{B}(w), \quad i(t, 0, w) = 0 \end{cases}$$

with

- force of infection  $\lambda(i, w) := \beta(w)p(i)$
- force of boosting  $\eta(i, w) := [1 - \beta(w)]p(i)$
- probability  $\beta(w)$  of infection upon contact
- infection pressure  $p(i) := \int_0^1 \nu(w) \int_0^{\bar{\alpha}} i(t, \alpha, w) \, d\alpha \, dw$  (infectivity  $\nu$ )

# linearization, $B$ and $M$

- disease-free equilibrium  $\bar{s}(\mathbf{a}, \mathbf{w}) > 0$ ,  $\bar{i}(\mathbf{a}, \mathbf{w}) = 0$  by integration along characteristics
- the linearized equation for the infected reads

$$\begin{cases} \partial_t x + \partial_{\mathbf{a}} x = \lambda(x, \mathbf{w}) \bar{s}(\mathbf{a}, \mathbf{w}) - [\mu(\mathbf{a}) + \gamma] x \\ x(t, \mathbf{a}, 1) = 0 \\ x(t, 0, \mathbf{w}) = 0 \end{cases} \quad (\text{in } \mathbb{R})$$

- equivalently,

$$x' = Bx - Mx \quad (\text{in } X := L^1([0, \bar{a}] \times [0, 1]))$$

for

- $x(t) : (\mathbf{a}, \mathbf{w}) \mapsto x(t, \mathbf{a}, \mathbf{w})$
- $(B\phi)(\mathbf{a}, \mathbf{w}) := \beta(\mathbf{w}) \left( \int_0^1 \nu(\omega) \int_0^{\bar{a}} \phi(\xi, \omega) d\xi d\omega \right) \bar{s}(\mathbf{a}, \mathbf{w})$
- $(M\phi)(\mathbf{a}, \mathbf{w}) := \partial_{\mathbf{a}} \phi(\mathbf{a}, \mathbf{w}) + [\mu(\mathbf{a}) + \gamma] \phi(\mathbf{a}, \mathbf{w})$
- $\text{dom}(M) := \{\phi \in X : \partial_{\mathbf{a}} \phi \in X \text{ and } \phi(0, \mathbf{w}) = \phi(\mathbf{a}, 1) = 0\}$

# tensorial bivariate collocation

- recall:

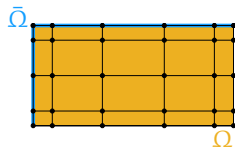
$$\begin{cases} B\phi = \lambda M\phi \\ 0 = \lambda C\phi \end{cases} \text{ in } X = L^1([0, \bar{a}] \times [0, 1]) \text{ discretized by } B_N\Phi = \lambda M_N\Phi \text{ in } \mathbb{R}^N$$

with

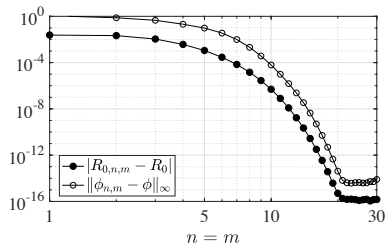
$$B_N := \begin{pmatrix} R_{N-\bar{N}}^\circ B P_N \\ 0_{\bar{N}, N} \end{pmatrix}, \quad M_N := \begin{pmatrix} R_{N-\bar{N}}^\circ M P_N \\ \bar{R}_{\bar{N}} C P_N \end{pmatrix}$$

- concretely:

- $[0, \bar{a}]$  discretized by  $0 =: \mathbf{a}_0 < \mathbf{a}_1 < \dots < \mathbf{a}_n := \bar{a}$
- $[0, 1]$  discretized by  $0 =: \mathbf{w}_0 < \mathbf{w}_1 < \dots < \mathbf{w}_m := 1$
- $\Phi = \text{vec}(\Phi_{i,j})_{i=0,\dots,n,j=0,\dots,m}$
- $P_N\Phi = \phi_{n,m}$  bivariate polynomial interpolant
- $R_{N-\bar{N}}^\circ$ : evaluation at grid points  $(\mathbf{a}_i, \mathbf{w}_j)_{i=1,\dots,n,j=0,\dots,m-1}$
- $\bar{R}_{\bar{N}}$ : evaluation at grid points  $(\mathbf{a}_0, \mathbf{w}_j)_{j=0,\dots,m}$  and  $(\mathbf{a}_i, \mathbf{w}_m)_{i=1,\dots,n}$
- $N = (n+1)(m+1)$ ,  $\bar{N} = n+m+1$

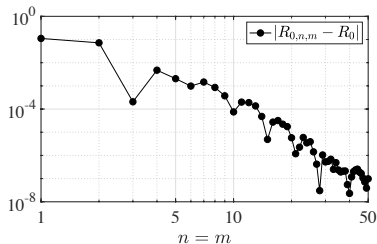


# results



$$g(w) = \beta(w) = \nu(w) = 1 - w$$
$$\mathcal{B}(w) = (1 - w)^2$$
$$\mu \equiv \gamma = 1, \bar{a} = 2$$

$R_0$  and  $\phi$  known exactly  
 $\bar{s}$  analytic



$$g(w) = w, \beta(w) = \nu(w) = 1 - w$$
$$\mathcal{B}(w) = (1 - w)^2$$
$$\mu(a) = 1/(\bar{a} - a)^2, \gamma = 1, \bar{a} = 2$$

$R_0$  and  $\phi$  unknown  
 $\bar{s}$  only  $C^1$



## convergence: one structure, $\Omega \subset \mathbb{R}$ [5]

$$\|\phi_N - \phi\|_X = \begin{cases} O(N^{-s} \log N) & \text{for coefficients of class } C^s \\ O(k^{-N} \log N), k > 1 & \text{for analytic coefficients} \end{cases}$$

$$|\lambda_N - \lambda| = O(\|\phi_N - \phi\|_X^{1/\alpha}), \quad \alpha \text{ algebraic multiplicity of } \lambda$$

- steps of the proof:
  - the eigenvalue problem leads basically to an ODE or to a Volterra integro-differential equation
  - bound the relevant collocation error  $\|\phi_N - \phi\|_X$
  - consolidated tools as variation of constants or resolvent theory leads to a characteristic equation for the eigenvalues
  - compare with the discrete version from collocation and apply Rouché's Theorem to bound  $|\lambda_N - \lambda|$

## convergence: two structures, $\Omega \subset \mathbb{R}^2$

- work in progress
- apparently no trivial extension from  $\Omega \subset \mathbb{R}$ :
  - the eigenvalue problem leads to a PDE
  - no easy tool to get a characteristic equation
  - integration along characteristics only for “simple” models

## convergence: two structures, $\Omega \subset \mathbb{R}^2$

- work in progress
- apparently no trivial extension from  $\Omega \subset \mathbb{R}$ :
  - the eigenvalue problem leads to a PDE
  - no easy tool to get a characteristic equation
  - integration along characteristics only for “simple” models
- promising alternative through an abstract approach:

(SEP)

$$\boxed{BM^{-1}\psi = \lambda\psi}$$

## convergence: two structures, $\Omega \subset \mathbb{R}^2$

- work in progress
- apparently no trivial extension from  $\Omega \subset \mathbb{R}$ :
  - the eigenvalue problem leads to a PDE
  - no easy tool to get a characteristic equation
  - integration along characteristics only for “simple” models
- promising alternative through an abstract approach:

(SEP)

$$\boxed{BM^{-1}\psi = \lambda\psi}$$



(GEP)

$$\boxed{\begin{cases} B\phi = \lambda M\phi \\ 0 = \lambda C\phi \end{cases}}$$

# convergence: two structures, $\Omega \subset \mathbb{R}^2$

- work in progress
- apparently no trivial extension from  $\Omega \subset \mathbb{R}$ :
  - the eigenvalue problem leads to a PDE
  - no easy tool to get a characteristic equation
  - integration along characteristics only for “simple” models
- promising alternative through an abstract approach:

(SEP)

$$\boxed{BM^{-1}\psi = \lambda\psi}$$



(GEP)

$$\boxed{\begin{cases} B\phi = \lambda M\phi \\ 0 = \lambda C\phi \end{cases}}$$

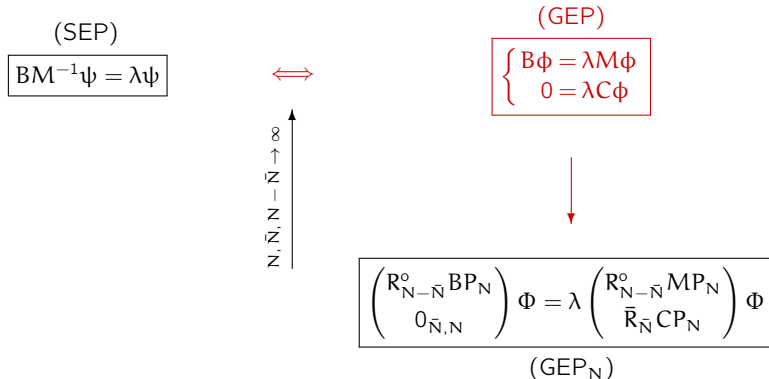


$$\boxed{\begin{pmatrix} R_{N-\bar{N}}^o & BP_N \\ 0_{\bar{N},N} \end{pmatrix} \Phi = \lambda \begin{pmatrix} R_{N-\bar{N}}^o & MP_N \\ \bar{R}_{\bar{N}} & CP_N \end{pmatrix} \Phi}$$

(GEP<sub>N</sub>)

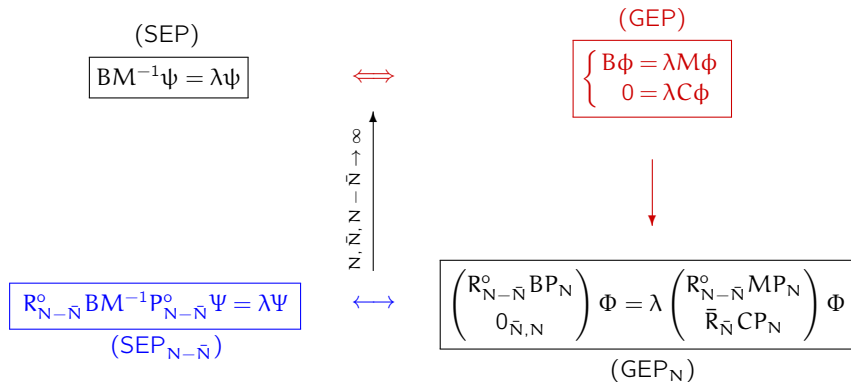
# convergence: two structures, $\Omega \subset \mathbb{R}^2$

- work in progress
- apparently no trivial extension from  $\Omega \subset \mathbb{R}$ :
  - the eigenvalue problem leads to a PDE
  - no easy tool to get a characteristic equation
  - integration along characteristics only for “simple” models
- promising alternative through an abstract approach:



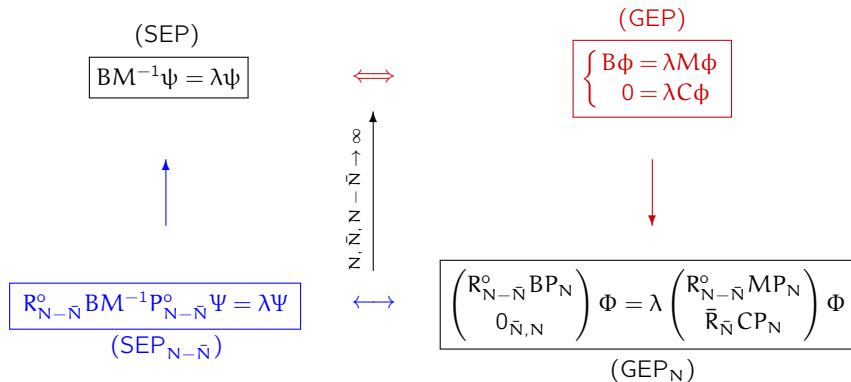
# convergence: two structures, $\Omega \subset \mathbb{R}^2$

- work in progress
- apparently no trivial extension from  $\Omega \subset \mathbb{R}$ :
  - the eigenvalue problem leads to a PDE
  - no easy tool to get a characteristic equation
  - integration along characteristics only for “simple” models
- promising alternative through an abstract approach:



# convergence: two structures, $\Omega \subset \mathbb{R}^2$

- work in progress
- apparently no trivial extension from  $\Omega \subset \mathbb{R}$ :
  - the eigenvalue problem leads to a PDE
  - no easy tool to get a characteristic equation
  - integration along characteristics only for “simple” models
- promising alternative through an abstract approach:





## so far

- $M$  does not regularize, whereas  $M^{-1}$  does
- let  $\sigma^*$  denotes nontrivial eigenvalues, with multiplicities and relevant eigenvectors
- if  $BM^{-1}X \subseteq Y \subset X$  and  $\|L_{N-\bar{N}}^0 - I_X\|_{X \leftarrow Y} \rightarrow 0$  as  $N, \bar{N}, N - \bar{N} \rightarrow \infty$ , then

$$\lim_{N, \bar{N}, N - \bar{N} \rightarrow \infty} \sigma^*(\text{SEP}_{N-\bar{N}}) = \sigma^*(\text{SEP})$$

- the following standard property seems crucial to understand the relation between  $\sigma^*(\text{SEP}_{N-\bar{N}})$  and  $\sigma^*(\text{GEP}_N)$ :

$$\|(\lambda I_d - A)^{-1}\| \geq \frac{1}{\text{dist}(\lambda, \sigma(A))}, \quad \lambda \notin \sigma(A), \quad A \in \mathbb{R}^{d \times d}$$

- need for careful extensions to pencils  $\lambda B - A : \mathcal{U} \rightarrow \mathcal{V}$  (possibly with  $\dim \mathcal{U} < \dim \mathcal{V} \leq \infty$  or vice versa)

## open

- abstract convergence proof (linear operator pencils)
- lack of compactness
- more structures (Padua points)
- user-friendly tool (codes @ <http://cdlab.uniud.it/software>)

# open

- abstract convergence proof (linear operator pencils)
- lack of compactness
- more structures (Padua points)
- user-friendly tool (codes @ <http://cdlab.uniud.it/software>)

---

thank you all for the attention

# References I

- [1] N. Bacaër and S. Gernaoui, The epidemic threshold of vector-borne diseases with seasonality – The case of cutaneous leishmaniasis in Chichaoua, Morocco, *J. Math. Biol.*, 53:421–436, 2006
- [2] C. Barril, A. Calsina, and J. Ripoll, On the reproduction number of a gut microbiota model, *Bull. Math. Biol.*, 79:2727–2746, 2017
- [3] D. Breda, S. De Reggi, F. Scarabel, R. Vermiglio and J. Wu, Bivariate collocation for computing  $R_0$  in epidemic models with two structures, *Comput. Math. Appl.*, 2021, DOI:10.1016/j.camwa.2021.10.026
- [4] D. Breda, F. Florian, J. Ripoll and R. Vermiglio, Efficient numerical computation of the basic reproduction number for structured populations, *J. Comput. Appl. Math.*, 384:113165, 2021
- [5] D. Breda, T. Kuniya, J. Ripoll and R. Vermiglio, Collocation of next-generation operators for computing the basic reproduction number of structured populations, *J. Sci. Comput.* 85(40), 2020

## References II

- [6] O. Diekmann, J. A. P. Heesterbeek, and J. A. J. Metz, On the definition and the computation of the basic reproduction number  $R_0$  in models for infectious diseases in heterogeneous populations, *J. Math. Biol.*, 28:365–382, 1990
- [7] J. A. P. Heesterbeek, A brief history of  $R_0$  and a recipe for its calculation, *Acta Biother.*, 50:189–204, 2002
- [8] T. Kuniya, Numerical approximation of the basic reproduction number for a class of age-structured epidemic models, *Appl. Math. Lett.*, 73:106–112, 2017.
- [9] H. R. Thieme, Spectral bound and reproduction number for infinite-dimensional population structure and time heterogeneity, *SIAM J. Appl. Math.*, 70:188–211, 2009