Influence of human behaviors on the spread of an epidemic

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MOVI 2024 – Colloque sur l'épidémiologie comportementale

Rennes, 31 mai 2024

Outline

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- Context: "*an epidemic of epidemics*"

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- Spatial heterogeneity and human mobilities:

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  joint work with Cristiana J. Silva

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- Influence of human behaviors:
  - $\rightsquigarrow$ coupling with a discrete-probabilistic process
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  - ⇝ complex networks of epidemic models

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- Influence of human behaviors:
  - ⇝ coupling with a discrete-probabilistic process

    joint work with Cristiana J. Silva and Arnaud Banos
- On-going work:
  - ⇝ continuous domains
  - ⇝ abstraction and verification of hybrid dynamical systems

Context: “*an epidemic of epidemics*”

Emergent diseases

"A major change happened in the 1960s: the emergence of a globalized epidemiological environment specific to the Anthropocene, the new geological era that began with the industrial revolution.
Today, new plagues are appearing. Are we witnessing the last outbreak of plagues with the emergence of the Ebola or Zika?"

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SERGE MORAND

L'homme, la faune sauvage et la peste

fayard

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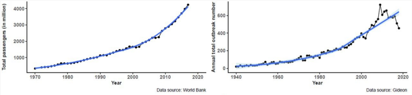
Multiple suspected causes

- Air traffic



Data source: World Bank

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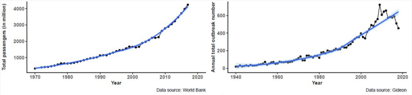

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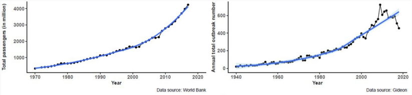

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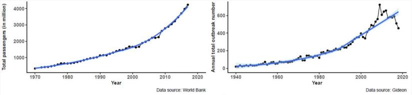

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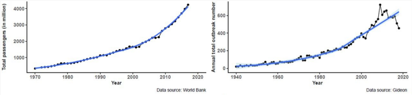

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- Human behaviors

[Epstein *et al.* (2008). *Coupled contagion dynamics of fear and disease : mathematical and computational explorations*. PLoS One.]

A huge literature...

⇝ Numerous books, thousands of papers...

Wei et al. *Advances in Difference Equations* (2018) 2018:60
https://doi.org/10.1186/s13662-018-1501-6

RESEARCH

Advances in Difference Equations
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Global stability of an SIS epidemic model with feedback mechanism on networks

Xiaodan Wei[1,2]*, Gaochao Xu[1] and Wenshu Zhou[3]

Hindawi Publishing Corporation
Computational and Mathematical Methods in Medicine
Volume 2014, Article ID 680743, 10 pages
http://dx.doi.org/10.1155/2014/680743

Research Article

An SIRS Epidemic Model Incorporating Media Coverage with Time Delay

Huitao Zhao,[1,2] Yiping Lin,[1] and Yunxian Dai[1]

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Received 24 December 2013; Accepted 17 January 2014; Published 3 March 2014

Academic Editor: Chengjun Sun

Research Article

Statistics in Medicine

Received 3 June 2016, Accepted 12 May 2017, Published online in Wiley Online Library

(wileyonlinelibrary.com) DOI: 10.1002/sim.7364

Bayesian epidemic models for spatially aggregated count data

Chrisovalantis Malesios,[a*†] Nikolaos Demi…, Konstantinos Kalogeropoulos[b]

J. Math. Biol. (2013) 67:411–432
DOI 10.1007/s00285-012-0555-4

Mathematical Biology

Outbreak analysis of an SIS epidemic model with rewiring

David Juher · Jordi Ripoll · Joan Saldaña

Received: 16 February 2012 / Revised: 18 May 2012 / Published online: 12 June 2012
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A nonlinear SEIR epidemic model with feedback vaccination control

Raul Nistal, Manuel de la Sen, Santiago Alonso-Quesada, Asier Ibeas

Hindawi Publishing Corporation
Abstract and Applied Analysis
Volume 2014, Article ID 742730, 7 pages
http://dx.doi.org/10.1155/2014/742730

Hindawi

Research Article

The Behavior of an SVIR Epidemic Model with Stochastic Perturbation

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Received 18 October 2013; Revised 4 May 2014; Accepted 6 May 2014; Published 24 June 2014

Academic Editor: Cristina Pignotti

Applied Mathematics, 2016, 7, 1082-1086
Published Online June 2016 in SciRes. http://www.scirp.org/journal/am
http://dx.doi.org/10.4236/am.2016.710096

Scientific Research Publishing

Stability Analysis of SIQS Epidemic Model with Saturated Incidence Rate

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Received 10 May 2015; accepted 29 July 2015; published 22 June 2016

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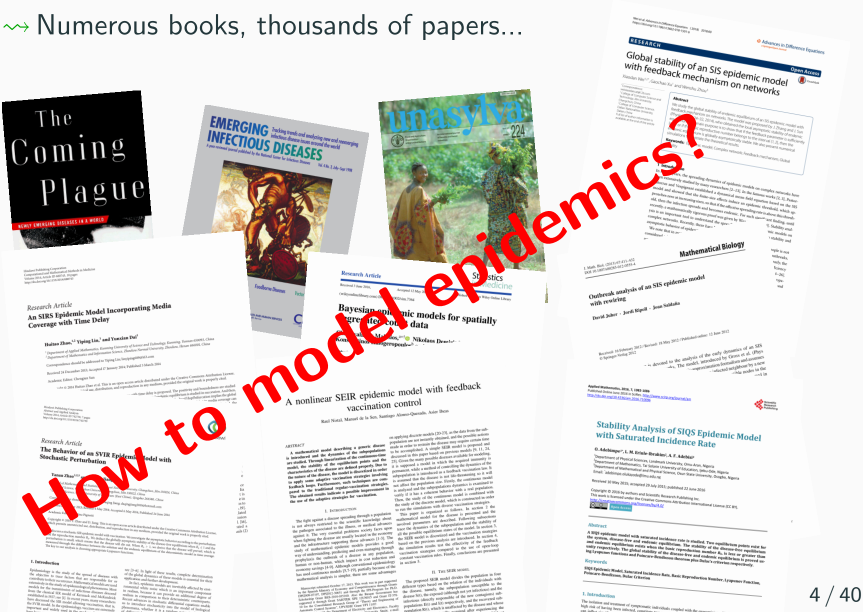

The Coming Plague

NEWLY EMERGING DISEASES IN A WORLD

EMERGING INFECTIOUS DISEASES

Tracking trends and analyzing new and reemerging infectious disease issues around the world

A peer-reviewed journal published by the National Center for Infectious Diseases

Vol. 4 No. 3, July–Sept 1998

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How to model epidemics?

Differential equations

- The SIR model (S: susceptible, I: infected, R: recovered):

$$\begin{cases} \dfrac{dS}{dt} = -\dfrac{\beta IS}{N}, \\ \dfrac{dI}{dt} = +\dfrac{\beta IS}{N} - \gamma I, \\ \dfrac{dR}{dt} = +\gamma I. \end{cases}$$

Important hypotheses:

⇝ the transmission of the disease is much faster than the dynamics of birth and death,

⇝ large population.

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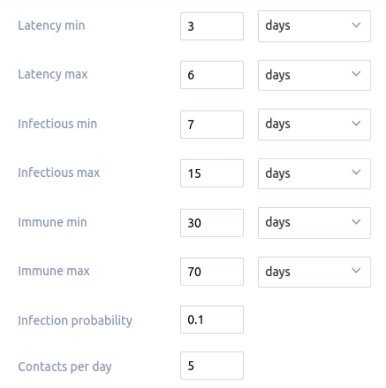
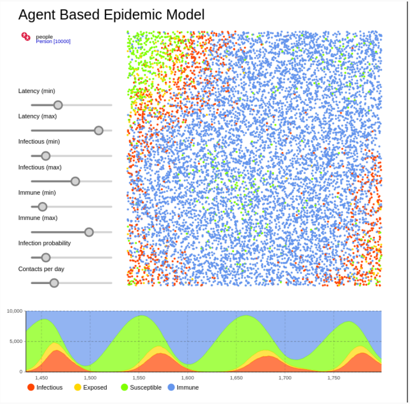
- Multiple variants: additional compartments, reaction-diffusion, fractional diffusion, time delays, age structure...

Individual-based models

- Agent-based models, cellular automata, transition systems...

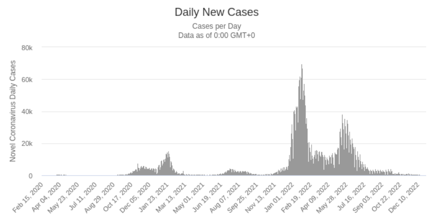


Latency min	3	days
Latency max	6	days
Infectious min	7	days
Infectious max	15	days
Immune min	30	days
Immune max	70	days
Infection probability	0.1	
Contacts per day	5	



Source: https://cloud.anylogic.com/models

Challenge: explain multiple epidemic waves



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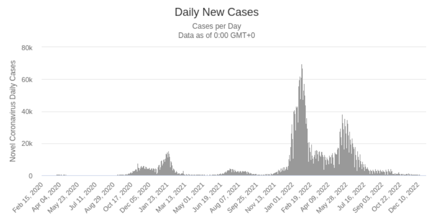

- Existence of irregular oscillations

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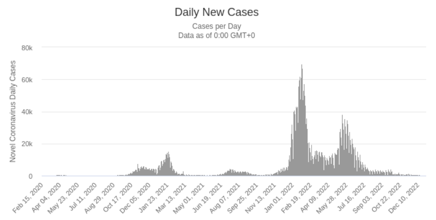
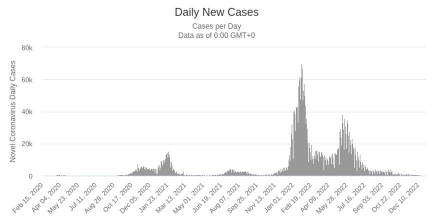


- Existence of irregular oscillations
- The environment is not necessarily periodic

Challenge: explain multiple epidemic waves



▶ Existence of irregular oscillations

▶ The environment is not necessarily periodic

⇝ First step: provide an heterogeneous spatial structure

→ geographical network

⇝ Second step: integrate the impacts of human behaviors

→ hybrid dynamical system

Spatial heterogeneity and human mobilities: complex networks of epidemic models

Setting of the problem: the SICA model

We consider a population affected by a HIV/AIDS epidemic. The SICA model [Silva & Torres (2017)] is given by

$$\begin{cases} \dot{S} = \Lambda - \beta \left(I + \eta_C C + \eta_A A \right) S - \mu S, \\ \dot{I} = \beta \left(I + \eta_C C + \eta_A A \right) S - \left(\rho + \phi + \mu \right) I + \omega C + \alpha A, \\ \dot{C} = \phi I - (\omega + \mu) C, \\ \dot{A} = \rho \, I - (\alpha + \mu + d) A. \end{cases}$$

S: number of susceptible individuals;

I: HIV-infected individuals with no clinical symptoms of AIDS;

C: HIV-infected individuals under ART treatment;

A: HIV-infected individuals with AIDS clinical symptoms;

N: total population.

Parameters of the SICA model

Λ	Recruitment rate
μ	Natural death rate
β	HIV transmission rate
η_C	Modification parameter
η_A	Modification parameter
ϕ	HIV treatment rate for I individuals
ρ	Default treatment rate for I individuals
α	AIDS treatment rate
ω	Default treatment rate for C individuals
d	AIDS induced death rate

Dynamics of the SICA model

- The SICA model admits a disease-free equilibrium (DFE) given by $\Sigma_0 = \left(\frac{\Lambda}{\mu}, 0, 0, 0\right)$.

- Its basic reproduction number R_0 (expected average number of new infections produced by a single infected individual) is given by

$$R_0 = \frac{S^0 \beta \, [\xi_2 (\xi_1 + \rho \eta_A) + \eta_C \phi \xi_1]}{\mu [\xi_2 (\rho + \xi_1) + \phi \xi_1 + \rho d] + \rho \omega d}.$$

- The disease free equilibrium Σ_0 is globally asymptotically stable if $R_0 < 1$.

- The SICA model admits an endemic equilibrium Σ_+, which is globally asymptotically stable if $R_0 > 1$.

- The SICA model can be rewritten:

$$\dot{x} = f(x, p), \quad x = (S, I, C, A)^T, \quad p = (\Lambda, \beta, \ldots, \alpha, d).$$

Case study: Cape Verde archipelago

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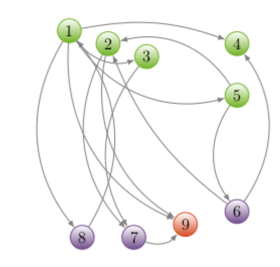

- Ideas:

⇝ we can model the archipelago by a graph,

⇝ we can couple each vertex of the graph with an instance of the SICA model.

Complex network of SICA models

- We consider a graph $\mathscr{G}$ with n vertices.
- We divide the vertices into two subsets $\mathscr{V}_1$, $\mathscr{V}_2$.
- We couple:

$\rightsquigarrow$ the vertices of $\mathscr{V}_1$ with an instance of the SICA model for which $R_0 < 1$,

$\rightsquigarrow$ the vertices of $\mathscr{V}_2$ with an instance of the SICA model for which $R_0 > 1$.

Complex network of SICA models

- The complex network is determined by:

$$\dot{X} = F(X,\, P) + LHX,$$

where

$$\begin{aligned} X &= (x_1,\, \dots,\, x_n)^T \in \left(\mathbb{R}^4\right)^n, \\ HX &= (Hx_1,\, \dots,\, Hx_n)^T \in \left(\mathbb{R}^4\right)^n, \\ P &= (p_1,\, \dots,\, p_n) \in \left(\mathbb{R}^{10}\right)^n, \end{aligned}$$

and F determines the internal dynamic of each vertex:

$$F(X,\, P) = \big(f(x_1,\, p_1),\, \dots,\, f(x_n,\, p_n)\big)^T.$$

Complex network of SICA models

- Explicit equations of the complex network:

$$\begin{cases} \dot{S}_j = \Lambda_j - \beta_j\big(I_j + \eta_{C,j}\, C_j + \eta_{A,j} A_j\big) S_j - \mu_j S_j + \varepsilon_S \displaystyle\sum_{k=1}^{n} L_{j,k} S_k, \\ \dot{I}_j = \beta_j\big(I_j + \eta_{C,j}\, C_j + \eta_{A,j} A_j\big) S_j - (\rho_j + \phi_j + \mu_j)\, I_j \\ \qquad +\omega_j C_j + \alpha_j A_j + \varepsilon_I \displaystyle\sum_{k=1}^{n} L_{j,k} I_k, \\ \dot{C}_j = \phi_j I_j - (\omega_j + \mu_j) C_j + \varepsilon_C \displaystyle\sum_{k=1}^{n} L_{j,k} C_k, \\ \dot{A}_j = \rho_j\, I_j - (\alpha_j + \mu_j + d_j) A_j + \varepsilon_A \displaystyle\sum_{k=1}^{n} L_{j,k} A_k. \end{cases}$$

Connections

▶ L is the matrix of connectivity: for each edge $(k,\, j) \in \mathscr{E}$, $k \neq j$, we have $L_{j,k} > 0$. If $(k,\, j) \notin \mathscr{E}$, $k \neq j$, we set $L_{j,k} = 0$. The diagonal coefficients satisfy

$$L_{j,j} = -\sum_{\substack{k=1 \\ k\neq j}}^{n} L_{k,j}.$$

▶ Finally, H is the matrix of the coupling strengths and it is given by

$$H = \begin{bmatrix} \varepsilon_S & 0 & 0 & 0 \\ 0 & \varepsilon_I & 0 & 0 \\ 0 & 0 & \varepsilon_C & 0 \\ 0 & 0 & 0 & \varepsilon_A \end{bmatrix},$$

with non negative coefficients ε_S, ε_I, ε_C and ε_A.

Disease-Free Equilibrium of the complex network

▶ **Theorem (Cantin & Silva 2019)**

The complex network of SICA models admits a unique disease-free equilibrium Σ_0*, which is globally asymptotically stable in the region* Ω *defined by*

$$\Omega = \left\{ (x_j)_{1 \leq j \leq 4n} \in \left(\mathbb{R}^+\right)^{4n} \; ; \; \sum_{j=1}^{4n} x_j \leq \frac{\sum \Lambda_j}{\min \mu_j} \right\}.$$

provided

$$\frac{\Lambda_0}{\mu_0} \frac{\mathcal{N}_i}{\mathcal{D}_i} < 1,$$

for all $i \in \{1, \ldots, n\}$*, with known constants* $\mathcal{N}_i$*,* $\mathcal{D}_i$*.*

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for all $i \in \{1, \ldots, n\}$, *with known constants* $\mathcal{N}_i$, $\mathcal{D}_i$.

$\rightsquigarrow$ Local basic reproduction number: $R_{0,i} = \dfrac{\Lambda_i}{\mu_i} \dfrac{\mathcal{N}_i}{\mathcal{D}_i}$.

Example: simple two-nodes network

Two-nodes network. Green node: $R_{0,1} < 1$. *Red node:* $R_{0,2} > 1$.

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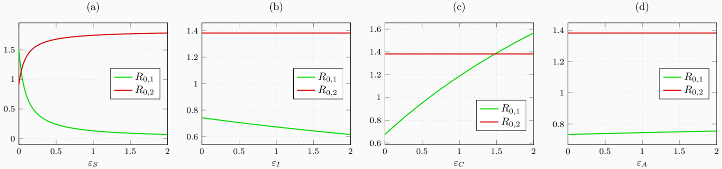
Two-nodes network. Green node: $R_{0,1} < 1$. *Red node:* $R_{0,2} > 1$.



Influence of the coupling strengths ε_S, ε_I, ε_C *and* ε_A *on the basic reproduction numbers* $R_{0,1}$ *and* $R_{0,2}$.

Randomly generated topologies

- We introduce the final level of infected individuals:

$$L_f = \sum_{j=1}^{n} \left[I_j(T) + C_j(T) + A_j(T) \right].$$

- Question: *can we find a network topology that minimizes L_f?*

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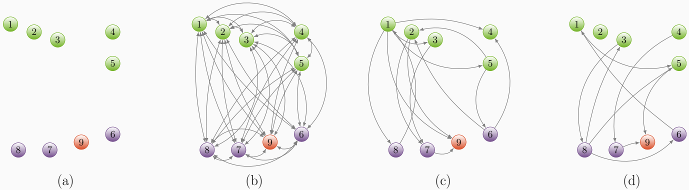
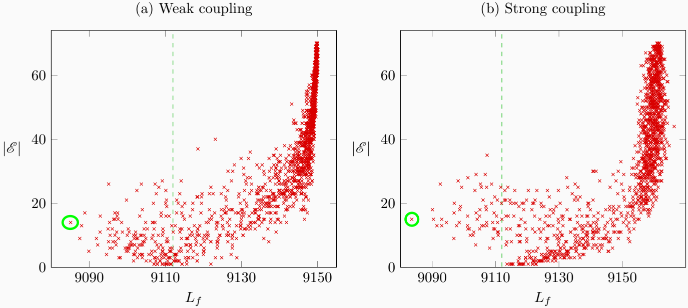
- Question: *can we find a network topology that minimizes L_f?*

- Idea: we generate a sample of randomly generated topologies, by choosing a random number of edges $1 \leq |\mathscr{E}| \leq 72$, and a random subset of $|\mathscr{E}|$ edges.



Optimal topologies



Numerical results for two samples of 1400 *randomly generated topologies. Green dotted vertical line: level of infected individuals without coupling. Optimal topology: green circle.*

Time series of an optimal topology

- A near-optimal topology detected by the random simulation:

$$\begin{aligned}\mathscr{E} = \Big\{&[1,3],[2,9],[5,6],[3,7],[7,9],[2,7],[1,9],\\ &[6,2],[6,4],[2,8],[5,2],[8,1],[1,5],[1,4]\Big\}.\end{aligned}$$

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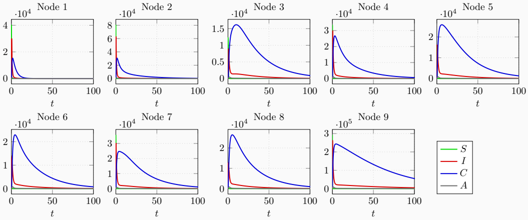

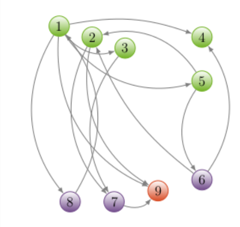

Influence of human behaviors: hybrid dynamical systems

Construction of a class of abstract hybrid models

▶ Assume a population of individuals is subject to a complex evolution process which cannot be described at a single scale.

▶ We construct a hybrid model by coupling a system of ordinary differential equations and a discrete process, which can be derived from an agent-based model.

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- We construct a hybrid model by coupling a system of ordinary differential equations and a discrete process, which can be derived from an agent-based model.
- The population is divided into several disjoint groups

$$X = (x_1, \dots, x_n).$$

- We consider a discrete sequence of times (t_s).

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$$X = (x_1, \dots, x_n).$$

▶ We consider a discrete sequence of times (t_s).

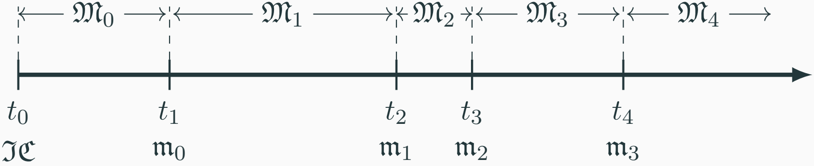
▶ We introduce, for $s \geq 0$, the abstract hybrid problem

$$\begin{cases} (\mathfrak{IC}) & X(t_0) = X_0, \quad \lambda_0 \in J, \\ (\mathfrak{M}_s) & \dot{X}(t) = F\big(X(t), \lambda_s\big), \quad t_s < t \leq t_{s+1}, \\ (\mathfrak{m}_s) & \lambda_{s+1} = G\big(X(t_{s+1}), \lambda_s\big). \end{cases}$$

Construction of a class of abstract hybrid models

- F is a function defined in $E \times J$ with values in $\mathbb{R}^n$, where E is an open subset of $\mathbb{R}^n$ and J is an open subset of $\mathbb{R}^d$.
- G is a function defined in $E \times J$ with values in J.
- $(\mathfrak{IC})$ determines the initial condition $(X_0, \lambda_0) \in E \times J$.
- $(\mathfrak{M}_s)$ is an ordinary differential equation which determines the macroscopic part of the hybrid problem.
- $(\mathfrak{m}_s)$ is a discrete mapping which determines the microscopic part of the hybrid problem.

Timeline of the hybrid model



Timeline of the hybrid model. At $t = t_0$*, the initial condition* $(\mathfrak{IC})$ *gives* $(X_0, \lambda_0) \in E \times J$*. On each interval* $[t_s, t_{s+1}]$*, the macroscopic part* $(\mathfrak{M}_s)$ *is determined by an ordinary differential equation. At each time step* $t = t_s$*, the microscopic part* $(\mathfrak{m}_s)$ *follows from a discrete mapping which is derived from an agent-based model.*

Well-posedness of the hybrid model: assumptions

▶ **Assumption 1.** The function F involved in the macroscopic part $(\mathfrak{M}_s)$ of the hybrid problem is $\mathscr{C}^1(E \times J)$.

▶ **Assumption 2.** There exists a compact set $K \subset E$ such that, for all $(X_0, \lambda_0) \in K \times J$, each local solution $X(t, X_0)$ of the Cauchy problem

$$X(t_0) = X_0, \quad \dot{X}(t) = F\big(X(t), \lambda_0\big)$$

defined on $[t_0, t_0 + T]$ with $T > 0$ satisfies

$$X(t, X_0) \in K,$$

for all $t \in [t_0, t_0 + T]$.

▶ **Assumption 3.** The function G involved in the microscopic part $(\mathfrak{m}_s)$ of the hybrid problem is continuous in $E \times J$.

Well-posedness of the hybrid model: statement

▶ **Theorem (Cantin Silva Banos, 2022)**

Let the assumptions 1, 2 hold. Then for all $(X_0, \lambda_0) \in K \times J$*, the hybrid problem admits a unique global solution* $X(t, X_0, \lambda_0)$ *defined on* $[t_0, +\infty)$*.*

If moreover assumption 3 holds, then each global solution $X(t, X_0, \lambda_0)$ *of the hybrid problem is continuous at* (X_0, λ_0)*, uniformly on each finite time interval* $[t_0, t_0 + T]$ *with* $T > 0$*, that is, for each* $T > 0$ *and each* $\varepsilon > 0$*, there exists* $\delta > 0$ *such that*

$$\|X(t, X_0 + h, \lambda_0 + k) - X(t, X_0, \lambda_0)\|_{\mathbb{R}^n} < \varepsilon,$$

for all $t \in [t_0, t_0 + T]$*, provided that* $\|(h, k)\|_{\mathbb{R}^n \times \mathbb{R}^d} < \delta$*.*

Well-posedness of the hybrid model: statement

▶ **Theorem (Cantin Silva Banos, 2022)**

Let the assumptions 1, 2 hold. Then for all $(X_0, \lambda_0) \in K \times J$, *the hybrid problem admits a unique global solution* $X(t, X_0, \lambda_0)$ *defined on* $[t_0, +\infty)$.

If moreover assumption 3 holds, then each global solution $X(t, X_0, \lambda_0)$ *of the hybrid problem is continuous at* (X_0, λ_0), *uniformly on each finite time interval* $[t_0, t_0 + T]$ *with* $T > 0$, *that is, for each* $T > 0$ *and each* $\varepsilon > 0$, *there exists* $\delta > 0$ *such that*

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for all $t \in [t_0, t_0 + T]$, *provided that* $\|(h, k)\|_{\mathbb{R}^n \times \mathbb{R}^d} < \delta$.

▶ What if G is discontinuous? $\rightsquigarrow$ High sensitivity of the model.

Irregular oscillations

- We suppose that there exist two distinct parameters sets $\Lambda_1 \subset J$ and $\Lambda_2 \subset J$ with $\Lambda_1 \cap \Lambda_2 = \varnothing$.
- Assume Σ_1 is an equilibrium point of the equation

$$\dot{X} = F(X, \lambda_1),$$

for each $\lambda_1 \in \Lambda_1$, and Σ_2 is an equilibrium point of the equation

$$\dot{X} = F(X, \lambda_2),$$

for each $\lambda_2 \in \Lambda_2$.

- We introduce the minimum step of the timeline $\{t_s\}$:

$$\tau = \min_{s \geq 0} \left| t_s - t_{s+1} \right| .$$

Irregular oscillations

▶ Theorem

Suppose that assumptions 1, 2 hold. Assume that Σ_1 *is globally asymptotically stable in* $W_1 \subset K$ *for each* $\lambda_1 \in \Lambda_1$, Σ_2 *is globally asymptotically stable in* $W_2 \subset K$ *for each* $\lambda_2 \in \Lambda_2$*. Assume moreover that* $\Sigma_1 \in W_2$, $\Sigma_2 \in W_1$ *and* $G(Y, \lambda) \in \Lambda_2$ *if* Y *is near* Σ_1 *and* $\lambda \in \Lambda_1$, $G(Y, \lambda) \in \Lambda_1$ *if* Y *is near* Σ_2 *and* $\lambda \in \Lambda_2$*.*

Then every solution $X(t, X_0, \lambda_0)$ *of the hybrid problem starting from* $(X_0, \lambda_0) \in W_1 \times \Lambda_1$ *admits irregular oscillations, that is, oscillations between a neighborhood* $\mathcal{N}_1$ *of* Σ_1 *and a neighborhood* $\mathcal{N}_2$ *of* Σ_2*, provided the minimum step* τ *of the timeline is sufficiently large.*

Hybrid model applied to COVID-19

- We consider the $SAIRP$ model with refractory behaviors [Silva *et al.* 2021]:

$$\begin{cases}\dot{S} = \Lambda - \beta\big(1-p(1-u)\big)\frac{(\theta A+I)}{N}S - \phi p(1-u)S + \omega P - \mu S,\\ \dot{A} = \beta\big(1-p(1-u)\big)\frac{(\theta A+I)}{N}S - \nu A - \mu A,\\ \dot{I} = \nu A - \delta I - \mu I,\\ \dot{R} = \delta I - \mu R,\\ \dot{P} = \phi p(1-u)S - \omega P - \mu P.\end{cases}$$

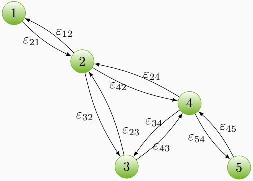
- S: susceptible individuals, A: asymptomatic infected individuals, I: active infected individuals, R: removed (including recovered and COVID-19 induced deaths); P: protected individuals.

Parameters of the SAIRP model

Λ	Recruitment rate
μ	Natural death rate
θ	Infectiousness of the asymptomatic infected individuals
v	Transfer rate from A to I
q	Fraction of A individuals that are confirmed to be infected
ϕ	Transfer rate from S to P
δ	Transfer rate from I to R
ω	Transfer rate from P to S
p	Fraction of protected individuals
u	Refractory or opposition behaviors to the protection strategy

Geographical network modeling the spatial distribution

▶ We assume that the individuals are spatially distributed into a finite number of regions $D_1, \ldots, D_m$ with $m \geq 1$; some of these regions are interconnected and individuals present a spatial mobility from one region to another.



▶ The dynamics of the epidemic is modeled at the macroscopic scale by a complex network of ordinary differential equations:

$$\frac{dx_{i,j}}{dt} = f_j(x_i, \alpha_i) + \sigma_j \sum_{k=1}^{n} L_{i,k} x_{j,k}, 1 \leq j \leq 5, 1 \leq i \leq m, t \geq 0.$$

Transition from the ODE to an agent-based model

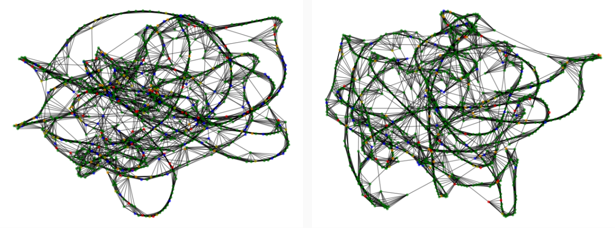
▶ We cannot follow the trajectory of a single individual during the macroscopic process.

Transition from the ODE to an agent-based model

▶ We cannot follow the trajectory of a single individual during the macroscopic process.

▶ Assume $X(t, X_s, \lambda_s)$ solves $(\mathfrak{M}_s)$ on $[t_s, t_{s+1}]$. For each sub-population x_{ij} of type j in each region D_i, we evaluate $x_{ij}(t_{s+1})$ and we compute $N_{ij}(t_{s+1}) = \lfloor x_{ij}(t_{s+1}) \rfloor$. We then introduce the agents: $\mathfrak{A}_{ij} = \{\mathfrak{a}_{ij}^1, \mathfrak{a}_{ij}^2, \dots, \mathfrak{a}_{ij}^{N_{ij}}\}$.

▶ We generate a social network over the groups $(\mathfrak{A}_{ij})_{1 \leq j \leq 5}$ of each region D_i by running a graph generation algorithm.



Collective behaviors in response to the epidemic

We assume that agents model citizens or decision makers and focus on two types of actions.

▶ *Action 1*. In each region D_i, $1 \leq i \leq m$, decision makers evaluate the rate $\rho_I(D_i, t_{s+1})$ of infected individuals.

- If the rate $\rho_I(D_i, t_{s+1})$ overcomes a given threshold $\mathcal{T}_1$, that is $\rho_I(D_i, t_{s+1}) > \mathcal{T}_1$, then decision makers decide to increase the fraction p_i of individuals.
- Else, the fraction of protected individuals is maintained.
- If at least one of the rates $\rho_I(D_i, t_{s+1})$, $1 \leq i \leq m$, overcomes a second threshold $\mathcal{T}_2 > \mathcal{T}_1$, then decision makers decide to confine the individuals in their region.
- Else, then decision makers reestablish the mobilities.

Collective behaviors in response to the epidemic

▶ *Action 2.* In each region D_i, agents $\mathfrak{a}_{ij}^{g}$ observe the types of their neighbors. Among these neighbors, each agent $\mathfrak{a}$ evaluates the number $\mathfrak{N}(I, \mathfrak{a}, t_{s+1})$ of infected neighbors.

- If the rate of infected neighbors overcomes a given threshold $\mathcal{T}_3$, then citizens decide to be in opposition with the protection strategy.
- Else, then citizens accept to decrease their level of opposition.

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- If the rate of infected neighbors overcomes a given threshold $\mathcal{T}_3$, then citizens decide to be in opposition with the protection strategy.
- Else, then citizens accept to decrease their level of opposition.

▶ The two-actions protocol defines a discrete mapping

$$\lambda_{s+1} = G\big(X(t_{s+1}), \lambda_s\big),$$

which determines the microscopic part $(\mathfrak{m}_s)$ of a hybrid model.

Analysis of the hybrid model

▶ **Theorem (Cantin Silva Banos, 2022)**

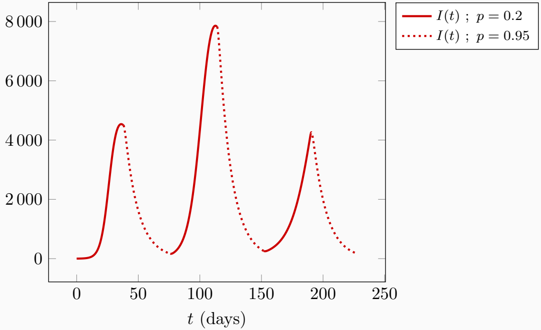
(1) For any $X_0 \in (\mathbb{R}^+)^{5m}$ *and any* $\lambda_0 \in J$*, the hybrid model admits a unique solution denoted by* $X(t,\, X_0,\, \lambda_0)$*, defined on* $[0,\, \infty)$*, whose components are non-negative.*

(2) Furthermore, the hybrid model admits a compact and positively invariant region K*.*

(3) The hybrid model admits solutions exhibiting irregular solutions between two equilibrium points (DFE and EE).

Irregular oscillations

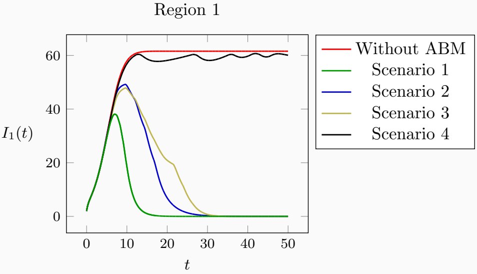
- Solutions exhibiting irregular solutions can easily be generated by forcing a variation of the parameter p.



$\rightsquigarrow$ Roughly: $p = 0.95 \Leftrightarrow$ confinement, $p = 0.2 \Leftrightarrow$ end of confinement.

Testing scenarios *ad lib*

Scenario 1: infection under control with fast confinement decision
Sc. 2: postponed extinction of the disease by slowness in the decision process
Sc. 3: postponed extinction of the disease by opposition behaviors
Sc. 4: emergence of multiple pandemic waves due to risk negation



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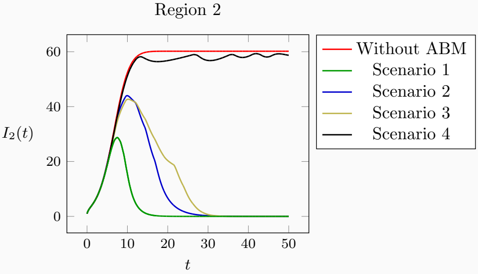

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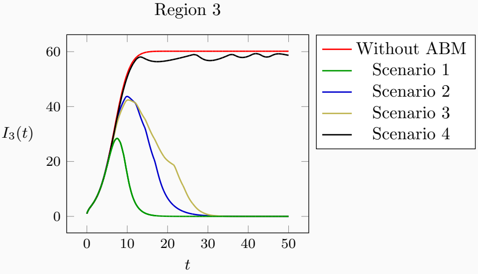

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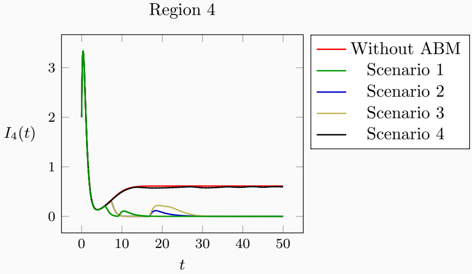

On going work

Hybrid dynamical system with continuous domains

- We consider a reaction-diffusion epidemic model

$$\begin{cases} \partial_t S = d_1 \Delta S + \mu N - \mu S - \beta S I, & x \in \Omega, \quad t > 0, \\ \partial_t I = d_2 \Delta I - (\mu + \nu) I + \beta S I, & x \in \Omega, \quad t > 0, \end{cases}$$

in a bounded domain Ω, coupled with a discrete-probabilistic process along a timeline of step $\tau > 0$.

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- well-posedness of the hybrid model?
- stability of the equilibrium points?
- bifurcation of cycles w.r.t τ?
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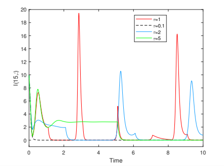
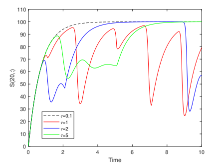




Abstraction and verification of hybrid dynamical systems

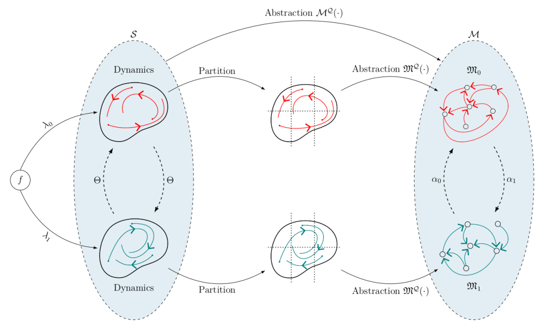
▶ We consider a continuous dynamical system $S_\lambda(t)$ depending on a parameter λ, with uniform phase space Φ, coupled with a discrete probabilistic process Θ along a timeline of step $\tau > 0$.

▶ How to verify dynamical properties of the hybrid system $(\mathcal{S})$ resulting from the coupling?

$\rightsquigarrow$ We can abstract the dynamics of the hybrid system as a Markov decision process $(\mathcal{M})$ and verify relevant properties directly on $(\mathcal{M})$, with *Model Checking* algorithmic techniques of theoretical computer science.

▶ The abstraction requires to consider a discretization of the hybrid model $(\mathcal{S})$.

Abstraction and verification of piecewise deterministic Markov processes



- How to abstract a property of $(\mathcal{S})$ as a property of $(\mathcal{M})$?
- Is the abstraction a "surjective" mapping?
- Can we "inverse" the verification‘ of $(\mathcal{M})$?

Conclusion

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- It is difficult to model human behaviors and their influence on the spread of an epidemic.
- It is important to couple multiple formalisms and multiple scales.
- A hybrid model can reproduce complex epidemic waves.

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⇝ Joint work with Cristiana J. Silva, Arnaud Banos

[*Mathematical analysis of a hybrid model: Impacts of individual behaviors on the spreading of an epidemic*, Networks and Heterogeneous Media (2022)]

- and also: A. Tajani, B. Delahaye, G. Ardourel, D. Julien.

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Thank you for your attention!