

Complex networks and hybrid models applied to epidemics

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Université de Nantes, 7 April, 2022

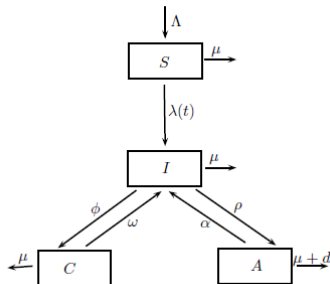
Joint work with Guillaume Cantin

5th International Conference on Complex Dynamical Systems
in Life Sciences: Modeling and Analysis (5thICDS'2018)



Mathematical HIV/AIDS model


 C. J. Silva and D. F. M. Torres, *A SICA compartmental model in epidemiology with application to HIV/AIDS in Cape Verde*, *Ecological Complexity* 30 (2017) 70-75.
 DOI: 10.1016/j.ecocom.2016.12.001
<https://arxiv.org/abs/1612.00732v1>



Mathematical model for HIV/AIDS - SICA model

Divide the total population N in:

↗ **S**: susceptible;

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

→ **C**: HIV-infected individuals under treatment for HIV infection;

↘ **A**: HIV-infected individuals with AIDS clinical symptoms.

$$\begin{cases} \dot{S}(t) = \Lambda - \lambda(t)S(t) - \mu S(t), \\ \dot{I}(t) = \lambda(t)S(t) - (\rho + \phi + \mu)I(t) + \alpha A(t) + \omega C(t), \\ \dot{C}(t) = \phi I(t) - (\omega + \mu)C(t), \\ \dot{A}(t) = \rho I(t) - (\alpha + \mu + d)A(t), \end{cases}$$

where

$$N(t) = S(t) + I(t) + A(t) + C(t)$$

and

$$\lambda(t) = \frac{\beta}{N(t)} (I(t) + \eta_C C(t) + \eta_A A(t)).$$

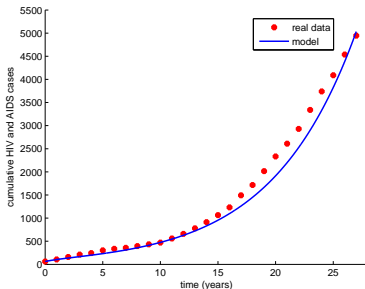
HIV/AIDS: case study for Cape Verde

- Assume: $(\eta_C, \eta_A) = (0.015, 1.3)$; estimated $\beta = 0.752$;

Symbol	Description	Value	References
N	Total population	variable	
$N(0)$	Initial population	323972	World Bank
Λ	Recruitment rate	10724	World Bank
μ	Natural death rate	1/69.54	World Bank
ϕ	HIV treatment rate for I_H individuals	1	Silva & Torres (2015)
ρ	Rate at which individuals leave I_H class to A	0.1	Silva & Torres (2015)
α	AIDS treatment rate	0.33	Silva & Torres (2015)
ω	Rate at which individuals leave C_H class	0.09	Silva & Torres (2015)
d	AIDS induced death rate	1	UNAIDS

Note: data from World Bank was considered the average from 1987 to 2014.

HIV/AIDS: case study for Cape Verde



$$(\beta, \eta_C, \eta_A) = (0.752, 0.015, 1.3), R_0 = 4.0983$$

Remark: The parameter β was estimated. The l_2 norm of the difference between the real data and the cumulative cases of infection by HIV/AIDS given by model (1) gives, in both cases, an error of 0.03% of individuals per year with respect to the total population of Cape Verde in 2014.

Complex network of HIV-AIDS epidemic models: main goals

- Geographical heterogeneity, represents a key factor in understanding the spreading of infectious diseases, can be studied through the *complex networks* approach, which combines dynamical systems with graph theory, in order to propose refined mathematical models.



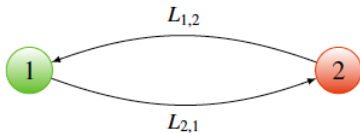
- Propose a complex network model for the HIV/AIDS epidemic problem in an heterogeneous geographical area.

Assumptions of the complex network of HIV-AIDS epidemic model

- Take into account the situation where a part of the population is not concerned with the migrations.
- The displacements can be different in some places of the network.
- Migrations are instantaneous.
- Individuals are not subject to an evolution from one compartment to another during migration from one node to another.

Construction of the complex network of HIV-AIDS epidemic model

- Usually, a complex network is built by considering a graph, given by a set of vertices and a set of edges, and by coupling each vertex with an instance of a given dynamical system, which can be determined by a set of differential equations.
- We consider a graph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$, where the set of vertices \mathcal{V} models the zones of high population concentration, and the set of edges \mathcal{E} corresponds to human displacements among those separated zones.

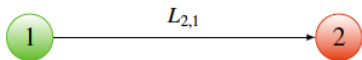


Symmetric two-nodes network.

Construction of the complex network of HIV-AIDS epidemic model

Split the set of vertices of the graph \mathcal{G} into at least two subsets:

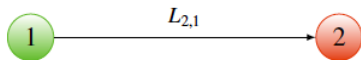
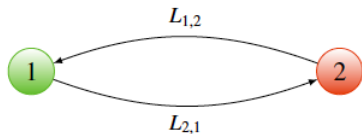
- first subset being coupled with instances of the HIV model for which the basic reproduction number satisfies $R_0 < 1$, thus admitting a unique equilibrium which is a DFE;
- second subset being coupled with instances of the HIV model for which $R_0 > 1$, thus presenting the coexistence of a DFE and an EE.



Asymmetric two-nodes network, built with two nonidentical instances of the SICA system. The green node (1) is associated with an instance of system SICA for which the basic reproduction number R_0 satisfies $R_0 < 1$, whereas the red node (2) is coupled with an instance of system SICA for which $R_0 > 1$.

Questions

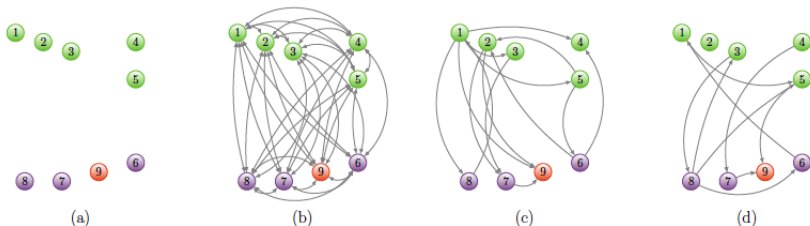
- *Does the coupling between the two subsets of vertices create new equilibrium points?*
- *Is it possible to eliminate the endemic equilibriums with a suitable disposition of the couplings?*
- *If not, is it possible to minimize the propagation of the epidemic in the network by searching an optimal topology?*



A case study: Cape Verde archipelago

The network is divided into 3 groups of nodes:

- group 1 (nodes 1, 2, 3, 4, 5);
- group 2 (nodes 6, 7, 8);
- group 3 (single node 9 - Santiago island).



Cape Verde archipelago: four distinct topology sets. (a) Empty topology corresponding to a network without couplings. (b) Complete graph topology. (c) and (d) Weakly dense topologies.

Initial population

Island	Node	$N(0)$	$S(0)$	$I(0)$	$C(0)$	$A(0)$	R_0
Santo Antão	1	40500*	40388	10*	93	9	0.914
São Vicente	2	81000*	80763	32*	186	19	0.914
Sau Nicolau	3	12420*	12381	7*	29	3	0.914
Sal	4	33750*	33642	22*	78	8	0.914
Bõa Vista	5	14450*	14404	10*	33	3	0.914
Maio	6	6980*	6957	5*	16	2	1.371
Fogo	7	35840*	35735	15*	82	8	1.371
Brava	8	5700*	5681	5*	13	1	1.371
Santiago	9	394130*	293084	303*	676	67	7.312

Official 2015 data are marked with a star. The values of $C_j(0)$ and $A_j(0)$ have been assumed, so that the corresponding subpopulations are in proportionality with the total population.

Parameters values and coupling strengths

Parameter	Nodes 1, 2, 3, 4, 5	Nodes 6, 7, 8	Node 9
Λ_i	2	2	2
β_i	0.001	0.0015	0.008
$\eta_{C,i}$	0.04	0.04	0.04
$\eta_{A,i}$	1.3	1.3	1.3
μ_i	1/70	1/70	1/70
ρ_i	0.1	0.1	0.1
ϕ_i	1	1	1
ω_i	0.09	0.09	0.09
α_i	0.33	0.33	0.33
d_i	1	1	1

- Coupling strengths for weak coupling:

$$\varepsilon_S = 0.02, \quad \varepsilon_I = 0.01, \quad \varepsilon_C = 0.01, \quad \varepsilon_A = 0.01,$$

- Coupling strengths for strong coupling:

$$\varepsilon_S = 0.2, \quad \varepsilon_I = 0.3, \quad \varepsilon_C = 0.1, \quad \varepsilon_A = 0.3.$$

Randomly generated topologies

The numerical integration on a finite time interval $[0, 200]$.
The final level of infected individuals, is given by

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

- In absence of coupling: $L_f \simeq 9112.77$.
- For the complete graph topology : $L_f \simeq 9161.02$.

The total number of possible topologies is given by the sum of binomial coefficients

$$\sum_{k=1}^{72} \binom{72}{k} \simeq 4.72 \cdot 10^{21}.$$

It is not reasonable to explore the total set of topologies.

Randomly generated topologies

GOAL: determine a near-optimal topology minimizing the level of infection L_f .

Assume that there are no loops nor parallel edges, then

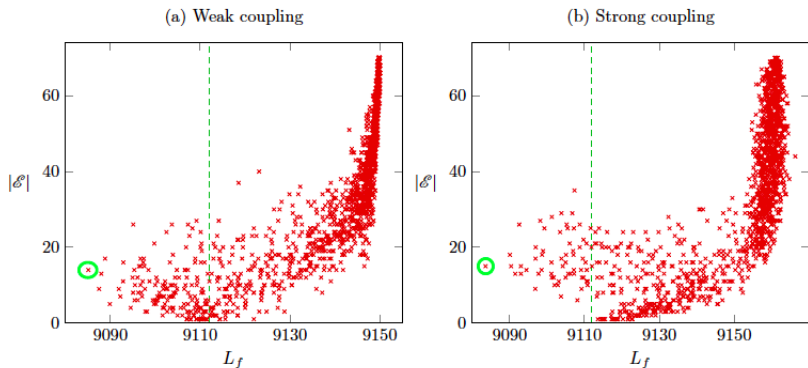
- a 9 nodes network can admit at most 72 edges

We propose to investigate a sample of randomly generated topologies, by choosing a random number of edges

$$1 \leq |\mathcal{E}| \leq 72.$$

We have computed the final level L_f of infected individuals for a sample of 1400 randomly generated topologies.

Randomly generated topologies: numerical simulations



The green dotted vertical line of equation $x = 9113$ shows the level of infected individuals without coupling. The optimal topology is marked with a green circle. (a) Weak coupling: $\varepsilon_S = 0.02$, $\varepsilon_I = \varepsilon_C = \varepsilon_A = 0.01$. (b) Strong coupling: $\varepsilon_S = 0.2$, $\varepsilon_I = \varepsilon_A = 0.3$, $\varepsilon_C = 0.1$.

Some conclusions and future work

- It seems delicate to identify the characteristic features of such a near-optimal topology, since weakly dense topologies can produce a high level of infection as well as limit the infection at a low level.
- In a future work, we aim to deepen this subtle question, which could lead to establishing a necessary and sufficient condition of synchronization in the network.



Guillaume Cantin, Cristiana J. Silva, *Influence of the topology on the dynamics of a complex network of HIV/AIDS epidemic models*, AIMS Mathematics, 2019, 4(4): 1145-1169.
doi: [10.3934/math.2019.4.1145](https://doi.org/10.3934/math.2019.4.1145).

Application to Tuberculosis model

Math.Comput.Sci. (2021) 15:107–120
<https://doi.org/10.1007/s11786-020-00472-2>

Mathematics in Computer Science



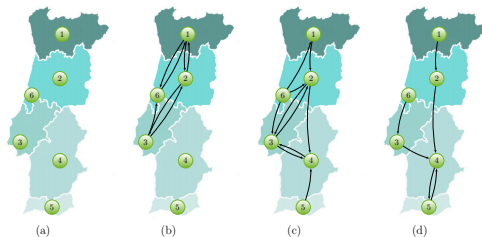
Synchronization and Self-organization in Complex Networks for a Tuberculosis Model

Cristiana J. Silva · Guillaume Cantin

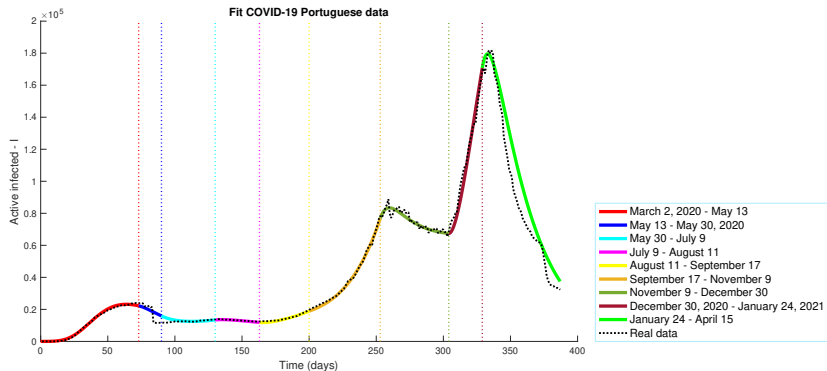
Received: 7 July 2019 / Revised: 31 December 2019 / Accepted: 2 March 2020 / Published online: 31 March 2020
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Abstract In this work, we propose and analyze the dynamics of a complex network built with non identical instances of a tuberculosis (TB) epidemiological model, for which we prove the existence of non-negative and bounded global solutions. A two nodes network is analyzed where the nodes represent the TB epidemiological situation of the countries Angola and Portugal. We analyze the effect of different coupling and intensity of migratory movements between the two countries and explore the effect of seasonal migrations. For a random complex network setting, we show that it is possible to reach a synchronization state by increasing the coupling strength and test the influence of the topology in the dynamics of the complex network. All the results are analyzed through numerical simulations where the given algorithms are implemented with the python 3.5 language, in a Debian/GNU-Linux environment.

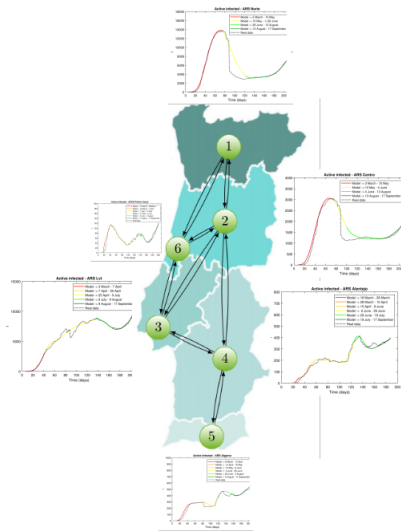
Complex network: application COVID-19



SAIRP model - fitting active infected individuals with COVID-19 in Portugal - 02 March, 2020 - 15 April, 2021



Model with piecewise constant parameters: fit COVID-19 data in 6 Portuguese regions



Dynamics of a complex network of non-identical SAIRP models

- Mobilities play an important role on the dynamics of epidemics.

Goal:

- study the propagation of the COVID-19 outbreak in Portugal by modeling this country by a complex network in which the six regions studied previously for the calibration of the SAIRP model with piecewise constant parameters.



Construction of the complex network

- Consider the six regions of Portugal: *Norte* (1), *Centro* (2), *Lisboa e Vale do Tejo* (3), *Alentejo* (4), *Algarve* (5), *Pinhal Litoral* (6).
- Those six regions are connected by a finite number of links that define a graph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ made of a set \mathcal{V} of 6 vertices, which correspond to the six regions, and of a set \mathcal{E} of edges, which model the main connections between those 6 regions.
- Couple each vertex of the graph with one instance of the SAIRP model.
- Since each region has its own specificity, we consider that the multiple instances of the model are non-identical, which means that the values of the parameters can differ from one region to another.

Complex network model: numerical simulations for COVID-19 in Portugal

Goal:

- investigate the effect of the topology on the dynamics of the epidemics;
- analyze the existence of a topology which minimizes the average number of active infected individuals, during a fixed time interval;
- analyze if other topologies are likely to worsen the level of infection.

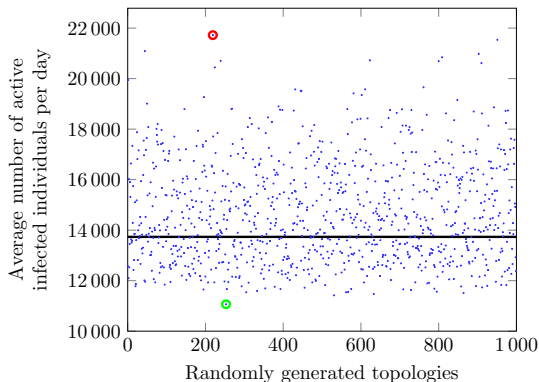


Figure: Average number of active infected individuals, per day, f or a sample of 1000 randomly generated topologies. The black line shows the level of infection for the empty topology. The green circle shows the optimum topology which minimizes the level of infection, whereas the red circle shows the topology which leads to the highest level of infection.

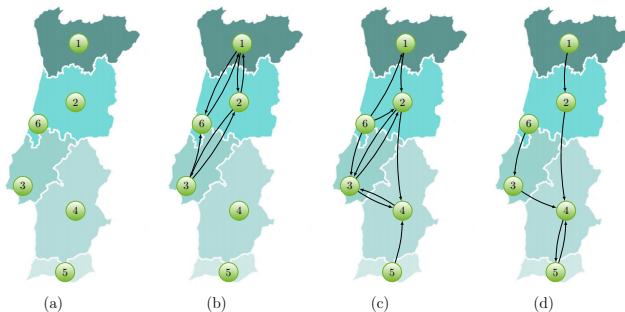
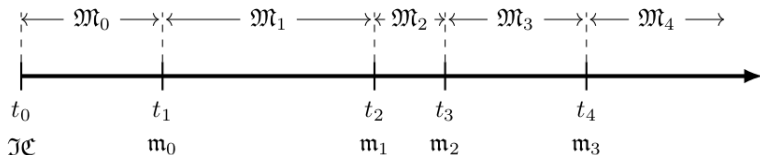


Figure: Four remarkable topologies. (a) Empty topology, which corresponds to the situation where individuals do not migrate from one region to another. (b) Topology that minimizes the level of infection. (c) Topology that leads to a level of infection greater than the level of the empty topology for only a weak coupling strength. (d) Topology that permanently overcomes the level of the empty topology.



C. J. Silva, G. Cantin, C. Cruz, R. Fonseca-Pinto, R. Fonseca, E. S. Santos, D. F. M. Torres, *Complex network model for COVID-19: human behavior, pseudo-periodic solutions and multiple epidemic waves*, Journal of Mathematical Analysis and Applications, 125171 (2021).

Hybrid model: impacts of individual behaviors on the spreading of an epidemic



Guillaume Cantin, Cristiana J. Silva, Arnaud Banos, *Mathematical analysis of a hybrid model: Impacts of individual behaviors on the spreading of an epidemic*, Networks & Heterogeneous Media, 2022.

doi: 10.3934/nhm.2022010

Construction of hybrid models

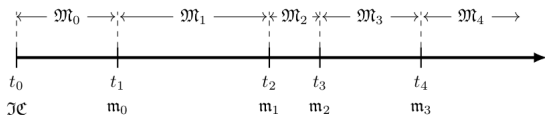
- Construction of hybrid problems: couple a system of ordinary differential equations with a discrete process (which can be derived from an agent-based model) along a common timeline.

Assume that the population can be divided into several disjoint groups x_1, \dots, x_n ($n \geq 1$). Let $X = (x_1, \dots, x_n)^T$.

Consider a discrete sequence of times

$$t_0 < t_1 < \dots < t_s < t_{s+1} < \dots, \quad (2)$$

which tends to infinity.



Construction of abstract hybrid problem (AHP)

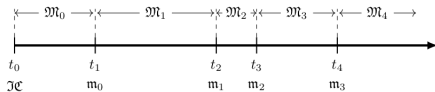
$$\left\{ \begin{array}{l} (\mathcal{I}\mathcal{C}) \quad X(t_0) = X_0, \quad \lambda_0 \in J, \\ (\mathfrak{M}_s) \quad \dot{X}(t) = F(X(t), \lambda_s), \quad t_s < t \leq t_{s+1}, \\ (\mathfrak{m}_s) \quad \lambda_{s+1} = G(X(t_{s+1}), \lambda_s), \quad s \geq 0. \end{array} \right. \quad (AHP)$$

- $F : E \times J \rightarrow \mathbf{R}^n$ is a function; E, J open subsets of \mathbf{R}^n and \mathbf{R}^d , respect.; $G : E \times J \rightarrow J$ is a function.

($\mathcal{I}\mathcal{C}$): initial condition - $(X_0, \lambda_0) \in E \times J$;

(\mathfrak{M}_s): macroscopic part - ordinary differential system;

(\mathfrak{m}_s): microscopic part - discrete mapping.



Mathematical analysis of an abstract hybrid problem

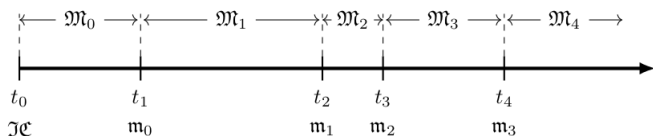
- Well-posedness of the hybrid model (AHP) (Theorem 2.3., Cantin et al. NHM, 2022).
- Existence of particular solutions of (AHP) exhibiting irregular oscillations (Theorem 2.4., Cantin et al. NHM, 2022).



Guillaume Cantin, Cristiana J. Silva, Arnaud Banos, *Mathematical analysis of a hybrid model: Impacts of individual behaviors on the spreading of an epidemic*, Networks & Heterogeneous Media, 2022.
doi: [10.3934/nhm.2022010](https://doi.org/10.3934/nhm.2022010)

Hybrid model applied to COVID-19

- (\mathfrak{M}_s) : macroscopic part - deterministic compartmental *S AIRP* model for the transmission of SARS-CoV-2 with opposition behaviors;
- (\mathfrak{m}_s) : microscopic part - follows from an agent-based model.
- Both microscopic and macroscopic parts of the problem are supported by a complex network structure.



Hybrid model applied to COVID-19

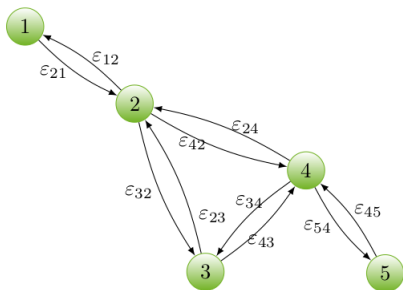
- (\mathfrak{M}_s) : macroscopic part: *SAIRP* model for the transmission of SARS-CoV-2 with opposition behaviors:

$$\left\{ \begin{array}{l} \dot{S}(t) = \Lambda - \beta(1 - p(1 - u)) \frac{(\theta A(t) + I(t))}{N(t)} S(t) - \phi p(1 - u) S(t) + \omega P(t) - \mu S(t), \\ \dot{A}(t) = \beta(1 - p(1 - u)) \frac{(\theta A(t) + I(t))}{N(t)} S(t) - \nu A(t) - \mu A(t), \\ \dot{I}(t) = \nu A(t) - \delta I(t) - \mu I(t), \\ \dot{R}(t) = \delta I(t) - \mu R(t), \\ \dot{P}(t) = \phi p(1 - u) S(t) - \omega P(t) - \mu P(t). \end{array} \right. \quad (3)$$

Hybrid model applied to COVID-19

- geographical network modeling the spatial distribution of the population.

In order to take into account the geographical distribution of the population which is affected by the epidemic, we propose to embed the latter *S AIRP* model into a complex network structure. Thus we assume that the individuals are spatially distributed into a finite number of regions D_1, \dots, D_m with $m \geq 1$; some of these regions are interconnected and individuals present a spatial mobility from one region to another.



Hybrid model applied to COVID-19

- microscopic part (m_s): transition from a system of ordinary differential equations towards an agent-based model.

Agent-based process in which agents are determined by *non-integer* individuals.

- 1 Assume we have solved the previous SAIRP system on a finite time interval $[t_s, t_{s+1}]$, with $s \geq 0$, and denote by $X(t, X_s, \lambda_s)$ the corresponding orbit.
- 2 For each sub-population x_{ij} of type j , $1 \leq j \leq 5$, in each region D_i , $1 \leq i \leq m$, we evaluate $x_{ij}(t_{s+1})$ and we compute the floor value $N_{ij}(t_{s+1}) = \lfloor x_{ij}(t_{s+1}) \rfloor$.
- 3 Consider a finite set

$$\mathfrak{A}_{ij} = \{a_{ij}^1, a_{ij}^2, \dots, a_{ij}^{N_{ij}}\},$$

and we call its elements *non-integer individuals* or simply *agents*.

Hybrid model applied to COVID-19

- The set \mathfrak{A}_{ij} admits N_{ij} agents, which model the individuals of the sub-population x_{ij} ($1 \leq i \leq m$, $1 \leq j \leq 5$).
- The size of the population at time $t = t_{s+1}$ is stored in the vector $X_{s+1} = X(t_{s+1}, X_s, \lambda_s)$, which is the initial condition for the next instance of the macroscopic part (\mathfrak{M}_s) on the time interval $[t_{s+1}, t_{s+2}]$.
- The set \mathfrak{A}_{ij} is called the *group of agents* \mathfrak{a}_{ij}^g *in the sub-population of type* j *in region* D_i , $1 \leq g \leq N_{ij}$.

Generate a social network over the groups $(\mathfrak{A}_{ij})_{1 \leq j \leq 5}$ of each region D_i , $1 \leq i \leq m$, by running a graph generation algorithm of edges over the finite set

$$\mathfrak{A}_i = \bigcup_{1 \leq j \leq 5} \mathfrak{A}_{ij}. \quad (4)$$

Choose to generate a Newman–Watts–Strogatz small-world graph, since it is well recognized to reproduce important aspects of the structure of social interactions.

Hybrid model applied to COVID-19

Agent-based model approach for integrating the collective behaviors in response to the epidemic.

- The microscopic part (m_s) of the hybrid model (AHP) is finally determined by a decision protocol. → Assume that agents model citizens or decision makers and focus on two types of actions (see Section 3.4. in Cantin et al. NHM, 2022.).



Guillaume Cantin, Cristiana J. Silva, Arnaud Banos, *Mathematical analysis of a hybrid model: Impacts of individual behaviors on the spreading of an epidemic*, Networks & Heterogeneous Media, 2022.
doi: 10.3934/nhm.2022010

Merci!

Acknowledgments

This research is partially supported by the Portuguese Foundation for Science and Technology (FCT) within project UIDB/04106/2020 (CIDMA). Silva is also supported by FCT via the FCT Researcher Program CEEC Individual 2018 with reference CEECIND/00564/2018.

