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► **To cite this version:**

F Bustamante-Castañeda, Jean-Guy G Caputo, G Cruz-Pacheco, A Knippel, F Mouatamide. Epidemic model on a network: analysis and applications to COVID-19. 2020. hal-02558195

HAL Id: hal-02558195

<https://hal.science/hal-02558195>

Preprint submitted on 29 Apr 2020

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Epidemic model on a network: analysis and applications to COVID-19

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Abstract

We analyze an epidemic model on a network consisting of susceptible-infected-recovered equations at the nodes coupled by diffusion using a graph Laplacian. We introduce an epidemic criterion and examine different vaccination/containment strategies: we prove that it is most effective to vaccinate a node of highest degree. The model is also useful to evaluate deconfinement scenarios and prevent a so-called second wave. The model has few parameters enabling fitting to the data and the essential ingredient of importation of infected; these features are particularly important for the current COVID-19 epidemic.

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1 Introduction

Many models of the propagation of an epidemic such as the current COVID-19 [1] involve a network. This can be a contact network between individuals. Then, the network is oriented and is used to understand how a given individual can infect others at the very early stages. The models are typically probabilistic, see [2] for example. Once the epidemic is established, the geographical network becomes important. There, nodes represent locations and edges the means of communication; for COVID-19 these are the airline routes [3]. Such a network is non oriented and the important nodes are the ones that are most connected.

One of simplest models of a disease is the Kermack-McKendrick system of equations [4] involving three populations of susceptible, infected and recovered individuals (S, I, R) . Using this model together with a probability transition matrix [5] for the geographic coupling, Brockman and Helbling [6] performed a remarkable study of the propagation of well-known epidemics like SARS or H1N1 due to airline travel. They emphasized that the fluxes between the nodes govern the propagation of the epidemic.

In this article, we consider (S, I, R) Kermack-McKendrick equations coupled to a network through a graph Laplacian matrix [7]. The combination of the simple SIR dynamics with the diffusion yields the essential ingredients to model and understand an epidemic, such as the COVID-19. In particular,

- there are few parameters so that fitting to data can be successful,
- it contains the essential ingredient of importation of infected subjects from country to country.

The epidemic front is controlled by the availability of susceptibles. If susceptibles are large enough, the front cannot be stopped. The number of susceptibles varies from node to node. Reducing this number at a given location can be done through vaccination. This is expensive and the whole network cannot be vaccinated. It is therefore important to address the question: what nodes are more useful to vaccinate to mitigate the epidemic?

Using this model together with the detailed data available [10] [11], we predicted the onset of the COVID-19 epidemic in Mexico [3]. The present article is devoted to the detailed analysis of the model. We first prove that it is well-posed and that solutions remain positive. We introduce an epidemic criterion that generalizes the well-known R_0 of the scalar case. For small diffusion, nodes are almost decoupled and an outbreak occurs at a node if the local R_0 is larger than one. When the diffusion is moderate, the epidemic criterion depends on the network and when there is an outbreak, it starts synchronously on the network. Using this criterion, we define a vaccination or isolation policy. We find that it is most useful to vaccinate the high connectivity nodes and not efficient

to vaccinate neighbors. For the particular case of the COVID-19 we discuss the effect of deconfining; the model shows that allowing circulation between heavily and weakly infected areas will prolong the outbreak in the latter.

The article is organized as follows. In section 2, we introduce the model, discuss its main features and present the epidemic criterion. Section 3 shows a simple six node network based on the country of Mexico; there the effect of vaccination is discussed. The COVID-19 disease is studied in section 4 and we show the estimation of the time of outbreak in Mexico. The important issue of deconfinement is studied in section 5. We conclude in section 6.

2 The model and epidemic criterion

One of the main models to describe the time evolution of the outbreak of an epidemic is the Kermack-McKendrick model [4]

$$\begin{cases} \dot{S} = -\alpha SI, \\ \dot{I} = \alpha SI - \beta I \\ \dot{R} = \beta I \end{cases} \quad (1)$$

where the dynamics of transmission depends of the frequency and intensity of the interactions between (healthy) susceptible S and infected individuals I and produce recovered individuals R . The parameters α and β are the infection rate and the recovery rate. The model conserves $N = S + I + R$ the total number of individuals. Note that R is essentially the integral of I and therefore plays no role in the dynamics. We will omit it below and only discuss S and I .

An epidemic occurs if $\alpha S - \beta > 0$ [4]. At $t = 0$, $S = 1$ so that an infection occurs if the infection factor defined as

$$R_0 \equiv \frac{\alpha}{\beta}, \quad (2)$$

is greater than one. An important moment in the time evolution of S and I is when the number of infected is maximum. The corresponding values (S^*, I^*) can be calculated easily; we give the derivation in the Appendix. The expressions are

$$S^* = \frac{1}{R_0}, \quad (3)$$

$$I^* = I_0 + S_0 - \frac{1}{R_0}(1 + \log(R_0 S_0)) \quad (4)$$

Note that I^* and S^* depend strongly on R_0 . Take for example $\beta = 0.625$ and different values of α .

α	R_0	S^*	I^*
2.5	4	0.25	0.403
1.5	2.4	0.417	0.218
1.1	1.76	0.568	0.111

The value of I^* depends also on the initial number of susceptibles S_0 which is smaller than the total number N . Generally, a large N gives a large S_0 and I^* .

2.1 SIR on a network

We consider a geographic network of cities connected by roads or communications and obtain the model and introduce a geographical component so that (S, I) become vectors and we drop R . This is similar to Murray's model where he introduces spatial dispersion using a continuous Laplacian term [9]. The evolution at a node j in a network of n nodes reads

$$\dot{S}_j = -\alpha \frac{S_j}{N_j} I_j + \epsilon \sum_{k \sim j} (S_k - S_j), \quad (5)$$

$$\dot{I}_j = \alpha \frac{S_j}{N_j} I_j - \beta I_j + \epsilon \sum_{k \sim j} (I_k - I_j), \quad (6)$$

where N_j is the population at node j , the $\sum_{k \sim j}$ is the exchange with the neighboring nodes k of j and where ϵ is a constant. The main difference with the model of [6] is that we assume symmetry in the exchanges.

These equations can be written concisely as

$$\begin{cases} \dot{S} = \epsilon \Delta S - \alpha S I, \\ \dot{I} = \epsilon \Delta I + \alpha S I - \beta I. \end{cases} \quad (7)$$

where $S = (S_1, S_2, \dots, S_n)^T$, $I = (I_1, I_2, \dots, I_n)^T$, $\alpha \equiv (\alpha/N_1, \alpha/N_2, \dots, \alpha/N_n)^T$, Δ is the graph Laplacian matrix [7] and we denote by SI the vector $(S_1 I_1, S_2 I_2, \dots, S_n I_n)^T$. The infection rate α can vary from one geographical site to another while the recovery rate β depends only on the disease. The diffusion ϵ should be small so that the populations involved in that process remain much smaller than the node populations N_j . Another point is that the diffusion could act only on the infected population. We chose to put the diffusion on both S and I for symmetry reasons.

The graph Laplacian Δ is the real symmetric negative semi-definite matrix, defined as

$$\Delta_{kl} = 1 \text{ if } kl \text{ connected, } 0 \text{ otherwise; } \Delta_{kk} = - \sum_{l \neq k} w_{kl}. \quad (8)$$

The graph Laplacian has important properties, see ref. [7], in particular it is a finite difference approximation of the continuous Laplacian [8]. The eigenvalues of Δ are the n non positive real numbers ordered and denoted as follows:

$$0 = -\omega_1^2 \geq -\omega_2^2 \geq \dots \geq -\omega_n^2. \quad (9)$$

The eigenvectors $\{v^1, \dots, v^n\}$ satisfy

$$\Delta v^j = -\omega_j^2 v^j. \quad (10)$$

and can be chosen to be orthonormal with respect to the scalar product in \mathbb{R}^n , i.e. $v^i \cdot v^j = \delta_{i,j}$ where $\delta_{i,j}$ is the Kronecker symbol.

2.2 Well posedness and positivity

The model (7) is well posed in the sense that the solution remains bounded. We show this in the Appendix using standard techniques.

The biological domain of the system is

$$\Omega = \{(S, I) : S \geq 0; I \geq 0\}.$$

Let us show that Ω is an invariant set for (7) so that the model makes sense in biology. Consider the different axes $S_j = 0$ and $I_j = 0$, $j = 1, \dots, n$. First assume $I_j = 0$, $j = 1, \dots, n$, then equation (7) reduces to

$$\dot{S} = \epsilon \Delta S$$

which conserves the positivity of S . Similarly when $S = 0$, we get

$$\dot{I} = \epsilon \Delta I - \beta I$$

and again the positivity of I is preserved.

2.3 Epidemic criterion

Here we extend the 1D epidemic criterion of Kermack-McKendrick [4] to our graph model. Initially, the vector I will follow the second equation of (7)

$$\dot{I} = (\epsilon \Delta - \beta)I + \alpha SI. \quad (11)$$

Equation (11) describes the onset of the epidemic on the network. It can be written

$$\dot{I} = AI$$

where A is the symmetric matrix

$$A = \epsilon\Delta - \beta Id_n + \text{diag}(\alpha_1 S_1, \alpha_2 S_2, \dots, \alpha_n S_n). \quad (12)$$

The eigenvalues of A $\sigma_1, \dots, \sigma_n$ are real. If one of them is positive, then the solution $I(t)$ increases exponentially and the epidemic occurs. We can then write

Epidemic criterion : there is an onset of the epidemic if one eigenvalue σ_i of A is positive.

Two situations occur, depending whether the diffusion is small or moderate. For small diffusion, the contribution of Δ to A can be neglected. Then each node will develop independently from the others. We will have outbreaks in some and not in others.

When the diffusion is moderate, the Laplacian contributes to A . Since A is symmetric the eigenvalues of A remain in the same order as the ones of Δ . This is the interlacing property [7]. Then σ_1 will tend to 0 for $\beta, \alpha \rightarrow 0$. Note also that since $\|S\|$ decreases with time, the estimate given by the eigenvalues of A indicates the size of the epidemic i.e. $\max \|I\|$. Then, the eigenvector of A for the eigenvalue σ_1 will be almost constant and the epidemic will start synchronously on the network.

The analysis of the moderate diffusion case can be extended when α is constant. Expanding I on an orthonormal basis of eigenvectors (v^k) of Δ

$$I = \sum_{k=1}^n \gamma_k v^k, \quad (13)$$

we get

$$\dot{\gamma}_k = (-\omega_k^2 - \beta)\gamma_k + \langle \alpha SI | v^k \rangle. \quad (14)$$

Assume that the susceptible population is constant on the network. Then $\text{diag}(S_1, S_2, \dots, S_n) = S Id_n$ so that equation (16) reduces to

$$\dot{\gamma}_k = (-\omega_k^2 - \beta + \alpha S)\gamma_k. \quad (15)$$

The epidemic starts if $-\beta + \alpha S > 0$ which is a simple generalization of the criterion in the scalar case.

When the population of susceptibles is inhomogeneous and α is homogeneous, equation (14) becomes

$$\dot{\gamma}_k = (-\omega_k^2 - \beta)\gamma_k + \alpha \sum_{l=1}^n \gamma_l \left(\sum_{j=1}^n S_j v_j^l v_j^k \right). \quad (16)$$

Then the eigenvectors and the geometry of the network play a role.

3 A simple example

We illustrate the results given above on a 6 node network inspired from the geographical map of Mexico, see Fig. 1. A node represents a city and an edge is a road link between two cities. For simplicity here we assume that the weights on all the branches are equal to 1.

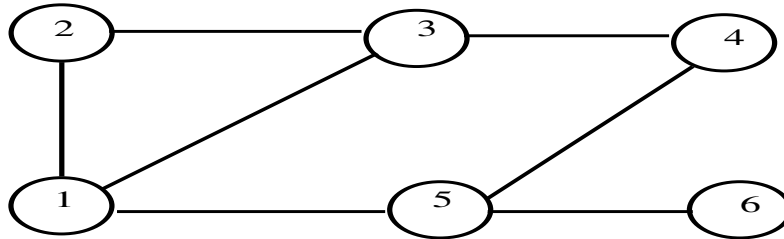


Figure 1: Graph of the six main cities in Mexico numbered from 1 to 6: Guadalajara, Zacatecas, Queretaro, Pachuca, Mexico City, Puebla. The links represent the main roads connecting these cities.

The graph Laplacian is

$$\Delta = \begin{bmatrix} -3 & 1 & 1 & 0 & 1 & 0 \\ 1 & -2 & 1 & 0 & 0 & 0 \\ 1 & 1 & -4 & 1 & 1 & 0 \\ 0 & 0 & 1 & -2 & 1 & 0 \\ 1 & 0 & 1 & 1 & -4 & 1 \\ 0 & 0 & 0 & 0 & 1 & -1 \end{bmatrix}.$$

The eigenvalues of this graph laplacian are

0	-0.885	-1.70	-3.25	-4.86	-5.31
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The corresponding eigenvectors are

-0.4082	-0.2410	-0.2307	-0.6432	0.5275	0.1735
-0.4082	-0.4011	-0.5313	0.5802	0.0502	-0.2261
-0.4082	-0.2061	0.0699	-0.0844	-0.6711	0.5731
-0.4082	-0.0975	0.7620	0.3323	0.3607	0.0525
-0.4082	0.0975	0.1609	-0.3323	-0.3607	-0.7466
-0.4082	0.8483	-0.2307	0.1474	0.0934	0.1735

3.1 Influence of the diffusion

The variable ϵ measures the intensity of the diffusion of S and I on the network. When $\epsilon \ll 1$ the diffusion is very weak and the evolution at each node can be decoupled from the one of its neighbors. For larger ϵ , the diffusion and reaction occur on similar time periods and need to be analyzed together. To see the influence of the diffusion, we plot in Fig. 2 the evolution of $I_k(t)$, $k = 1, \dots, 6$ for $\epsilon = 0.1$ (left panel) and $\epsilon = 10^{-7}$ (right panel).

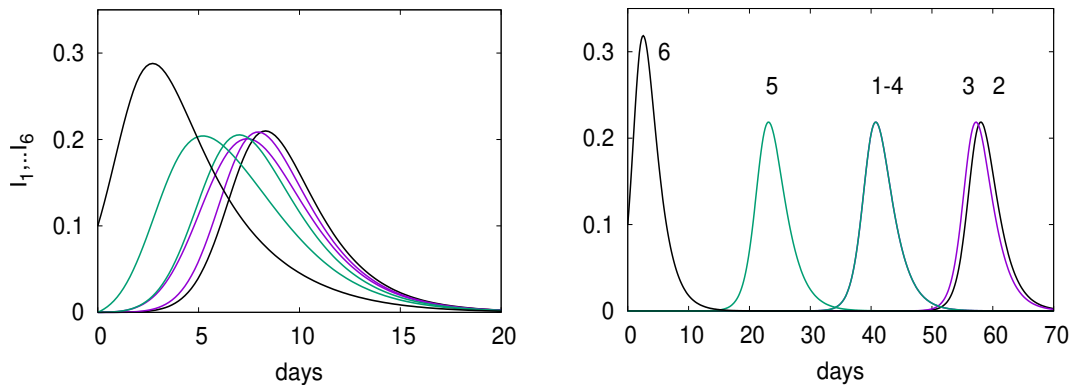


Figure 2: Time evolution $I_k(t)$, $k = 1, \dots, 6$ for an outbreak at node 6 for $\epsilon = 0.1$ (left panel) and 10^{-7} (right panel). The other parameters are $\alpha = 1.5$ and $\beta = 0.625$.

Note the times of arrival of the infection, first in node 5 the neighbor of node 6, then nodes 1 and 4 and finally nodes 3 and 2. For the large diffusion (left panel of Fig. 2) the peaks are very close and there is a strong influence between the nodes. On the other hand for a small diffusion, the peaks are well separated and the nodes are decoupled. The maximum of I_k is given by the estimate (4).

Infesting node 2 changes the time of arrival of the outbreak as shown in Fig. 3. It reaches first nodes 1 and 3, then nodes 4 and 5 and finally node 6.

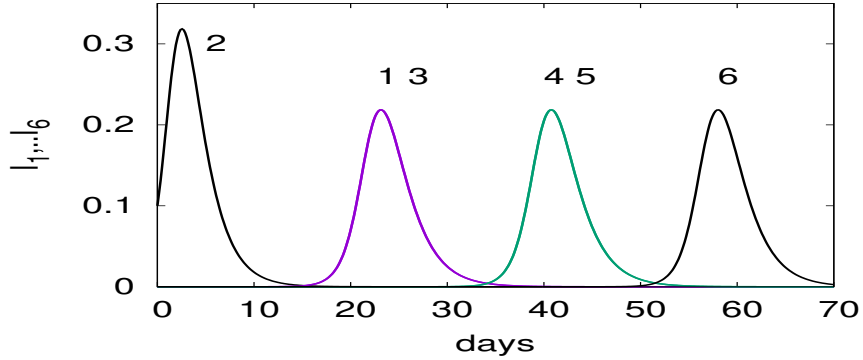


Figure 3: Time evolution $I_k(t)$, $k = 1, \dots, 6$ for an outbreak at node 2. The parameters are as in Fig. 2 (right panel).

3.2 Vaccination or isolation policies for large diffusion

We first consider that the diffusion and the nonlinear terms have similar orders of magnitude. We will address the case of weak diffusion in the next section.

When the diffusion is large, one should consider the epidemic on the network as a whole and use the topology of the network to reduce the strength of the outbreak. From the amplitude equations (16), one can devise a strategy of vaccination. By this we mean choosing $S_j = 0$ at some well chosen indices j so that the maximal eigenvalue of A from the epidemic criterion is minimum. Another public policy is isolation which consists in reducing α_j so that again the maximal eigenvalue of A is minimum. Vaccination is usually implemented a priori, see for example the case of flu shots. Isolation, on the other hand is a measure implemented when the epidemic is present. Both vaccination and isolation act similarly on the matrix A , we will therefore refer to vaccination only.

We choose $\epsilon = 0.1$. Table 1 shows the eigenvalues $\sigma_1, \dots, \sigma_n$ of A from (12) when vaccinating a node of the network, i.e. setting $S_j = 0$ at a specific node j and keeping the other nodes the same. We chose $S = 0.29 \times (1, 1, 1, 1, 1, 1)^T$.

j	degree	σ_3	σ_2	σ_1
6	1	$-2.17 \cdot 10^{-1}$	$-6.38 \cdot 10^{-2}$	$8.56 \cdot 10^{-2}$
2	2	$-1.42 \cdot 10^{-1}$	$-1.29 \cdot 10^{-2}$	$7.63 \cdot 10^{-2}$
4	2	$-1.92 \cdot 10^{-1}$	$1.02 \cdot 10^{-2}$	$7.33 \cdot 10^{-2}$
1	3	$-8.38 \cdot 10^{-2}$	$-5.96 \cdot 10^{-3}$	$6.62 \cdot 10^{-2}$
3	3	$-7.18 \cdot 10^{-2}$	$-1.02 \cdot 10^{-2}$	$5.86 \cdot 10^{-2}$
5	3	$-7.81 \cdot 10^{-2}$	$6.77 \cdot 10^{-3}$	$5.43 \cdot 10^{-2}$

Table 1: Vaccinated node I and associated eigenvalues of A

The table shows that it is most effective to vaccinate nodes 1,3 and 5. These nodes have the highest degree of the network.

We now vaccinate two cities in the network. The results are presented in table 3. We chose $S = 0.28(1, 1, 1, 1, 1, 1)^T$.

i	j	degrees	neighbors?	σ_3	σ_2	σ_1
1	2	3 2	yes	$-3.01 \cdot 10^{-1}$	$-4.99 \cdot 10^{-2}$	$3.33 \cdot 10^{-2}$
4	6	2 1	no	$-3.47 \cdot 10^{-1}$	$-1.96 \cdot 10^{-1}$	$3.09 \cdot 10^{-2}$
5	6	3 1	yes	$-2.73 \cdot 10^{-1}$	$-1.02 \cdot 10^{-1}$	$2.65 \cdot 10^{-2}$
2	3	2 3	yes	$-1.77 \cdot 10^{-1}$	$-7.19 \cdot 10^{-2}$	$2.64 \cdot 10^{-2}$
2	4	2 2	no	$-3.52 \cdot 10^{-1}$	$-8.05 \cdot 10^{-2}$	$2.43 \cdot 10^{-2}$
2	6	2 1	no	$-3.87 \cdot 10^{-1}$	$-1.66 \cdot 10^{-1}$	$2.08 \cdot 10^{-2}$
3	4	3 2	yes	$-2.30 \cdot 10^{-1}$	$-3.86 \cdot 10^{-2}$	$2.00 \cdot 10^{-2}$
1	3	3 3	yes	$-1.10 \cdot 10^{-1}$	$-7.27 \cdot 10^{-2}$	$1.97 \cdot 10^{-2}$
1	4	3 2	no	$-2.44 \cdot 10^{-1}$	$-5.43 \cdot 10^{-2}$	$1.64 \cdot 10^{-2}$
1	6	3 1	no	$-3.13 \cdot 10^{-1}$	$-1.05 \cdot 10^{-1}$	$1.19 \cdot 10^{-2}$
4	5	2 3	yes	$-2.65 \cdot 10^{-1}$	$-1.84 \cdot 10^{-2}$	$1.18 \cdot 10^{-2}$
3	6	3 1	no	$-2.42 \cdot 10^{-1}$	$-8.92 \cdot 10^{-2}$	$-2.75 \cdot 10^{-3}$
2	5	2 3	no	$-1.70 \cdot 10^{-1}$	$-4.50 \cdot 10^{-2}$	$-6.25 \cdot 10^{-3}$
1	5	3 3	yes	$-1.15 \cdot 10^{-1}$	$-3.19 \cdot 10^{-2}$	$-6.28 \cdot 10^{-3}$
3	5	3 3	no	$-1.09 \cdot 10^{-1}$	$-3.67 \cdot 10^{-2}$	$-9.78 \cdot 10^{-3}$

Table 2: Vaccinated nodes i, j and associated eigenvalues of A .

Again the high degree nodes 1,3 and 5 are the ones that reduce σ_1 the most and are therefore the most effective when applying vaccination. It is also not effective to vaccinate neighboring nodes.

The results shown in tables 1 and 3 can be explained from the properties of the matrix A and the graph Laplacian Δ . The maximal eigenvalue σ_1 of A verifies [7]

$$\sigma_1 = \sup_{\|X\|=1} \langle X|AX \rangle. \quad (17)$$

We can find inequalities for σ_1 by choosing

$$X = (1, 0 \dots 0)^T, X = (0, 1, 0 \dots 0)^T, \dots$$

Denoting d_i the degree of node i , we get

$$\sigma_1 \geq -d_1 + \alpha s - \beta, \tag{18}$$

$$\sigma_1 \geq -d_2 + \alpha s - \beta, \tag{19}$$

$$\dots \tag{20}$$

$$\sigma_1 \geq -d_n + \alpha s - \beta, \tag{21}$$

so that

$$\sigma_1 \geq -\min_k d_k + \alpha s - \beta. \tag{22}$$

This relation shows that vaccinating a node that has not smallest degree does not change the estimate. Conversely, if there is a unique node of minimal degree and we vaccinate it, then the bound changes.

Using similar arguments, it can be shown that vaccinating two neighboring nodes, say 1 and 2 will be less effective than vaccinating two non neighboring nodes.

Now we look at what happens if we cut a link, which corresponds to condemning a road for example. Let Δ' be the Laplacian of the new graph obtained by deleting a link. Without loss of generality we can assume this link to be between vertices 1 and 2. Then $\Delta' = \Delta - M$ where

$$M = \begin{pmatrix} -1 & 1 & 0 & \dots & 0 \\ 1 & -1 & 0 & \dots & 0 \\ 0 & \dots & \dots & & 0 \end{pmatrix}$$

M has all eigenvalues equal to 0 except one which has value -2 . Applying the Courant-Weyl inequalities, see for example [7], we get the following result for the maximum eigenvalue of Δ'

$$\sigma'_1 \leq \sigma_1.$$

Note that equality is possible: when S is homogeneous, the maximum eigenvalue of A will always be $-\beta + \alpha S$. In such a case, cutting a link is ineffective.

3.3 Small diffusion and vaccination policies

When diffusion is low, the nodes evolve almost independently so that the simple dynamics of the scalar SIR model apply. Then some nodes can be vaccinated and the epidemic is not seen there. Fig. 4 shows such a situation. We choose

$$\alpha = 1.98, \quad \beta = 0.5, \quad \epsilon = 10^{-3}$$

and the initial conditions are given in the table below. The local R_0 is also computed and one sees that an outbreak will occur at nodes 1,3 and 5 and not

at nodes 2,4 and 6. Fig. 4 shows the peaks for I_3 and I_5 and the maxima of I_3 and I_5 are close to the ones predicted by the SIR formulas (4).

node j	1	2	3	4	5	6
$S_j(t=0)$	0.26	0.14	0.55	0.16	0.5	0.18
$I_j(t=0)$	0	0	0.01	0	0	0
$R_0 = \alpha \frac{S_{j0}}{\beta}$	1.0296	0.5544	2.1780	0.6336	1.9800	0.7128
I^*	0.0001	0.0364	0.1109	0.0227	0.0750	0.0130

Table 3: Initial conditions and local R_0 for the plots of Fig. 4.

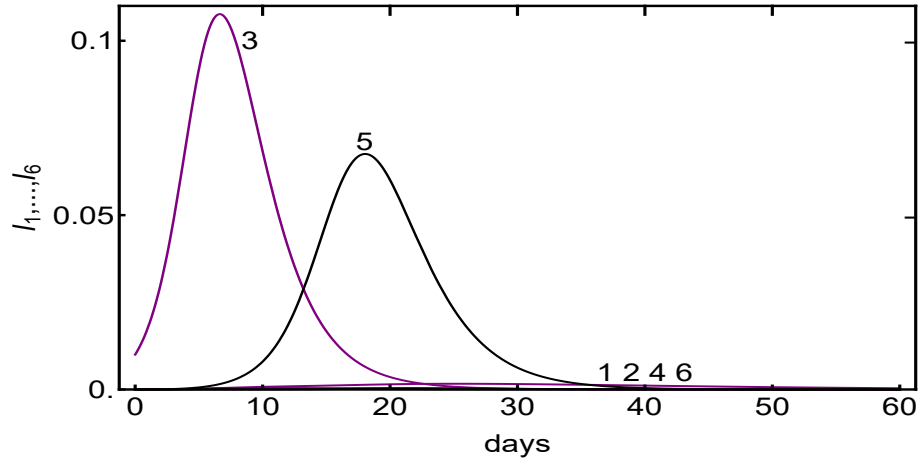


Figure 4: Time evolution of the infected for different initial susceptibles at the nodes.

4 Propagation of Corona virus COVID-19

We consider the propagation of the Corona virus COVID-19 on a network consisting of a complete graph of 7 nodes with an additional link to an 8th node, see top left panel of Fig. 5.

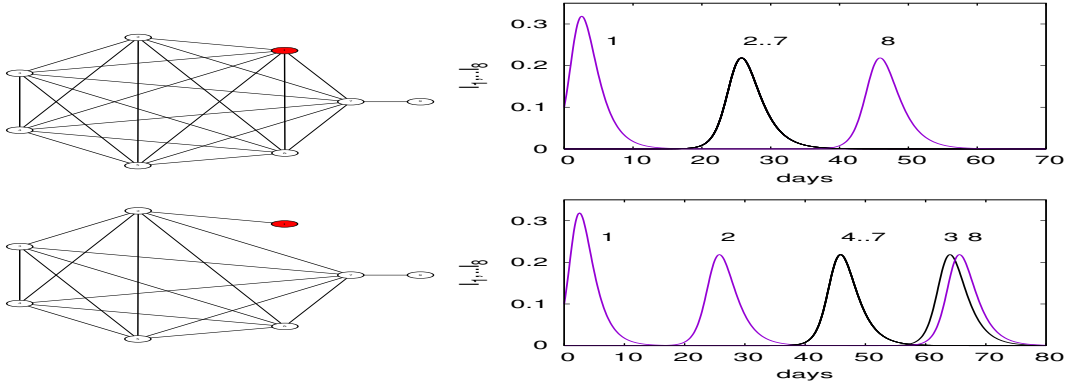


Figure 5: Graph of the 7 nodes forming a complete graph (top left) and the time evolution of the infected per node (top right). In the bottom panel, node 1 has been isolated from all nodes except 2 (bottom left). The corresponding time evolution of the infected is shown in the bottom right.

The 7 nodes correspond to the following cities or regions, Hubei, Beijing, Shanghai, Japan, western Europe, eastern USA and western USA and the 8th node is Mexico. We assume a complete graph because the airline routes connect any two of these regions.

The parameters chosen are $\alpha = 0.5, \beta = 0.2$ and $\epsilon = 10^{-6} \text{days}^{-2}$. These were suggested by very early estimations of the outbreak in Wuhan. Using the data from the John Hopkins website [10] and our model, we estimated the starting time of the outbreak in Mexico to be from March 20 to March 30 2020 [3]. These results were shared with the Ministry of health of Mexico at the end of February 2020 so that preparations could be made.

The top right panel of Fig. 5 shows the time evolution in days of the infected in the different nodes. The simulation is started at node 1 (Hubei in red in Fig. 5) with $I_1 = 0.1$ and the other nodes are set at 0. The susceptibles are set to 1 everywhere. As expected the maximum $I_1^* = 0.32$ and the subsequent maxima $I_j^* = 0.21, j = 2, \dots, 8$. Notice how the nodes 2-7 start simultaneously while node 8 is delayed. Communications with the province of Hubei were restricted at the end of December 2019. To model this, we now consider that node 1 is only connected to node 2 which forms a complete graph with nodes 3-7, see bottom left panel of Fig. 5. The infected are shown in the bottom right panel; as expected the epidemic first arrives in node 2 then synchronously in nodes 3-7 and then in node 8.

To test the effect of having different α s at each node we increased α_3 , reduced α_4 and kept the other α s the same. Then the epidemic arrives sooner at node 3 and later at node 4. As expected from the formulas (4) $I_3^* > I_j^* > I_4^*$ for $j = 5, 6, 7$, see [3].

5 Confinement and deconfinement

Since there is no vaccine for COVID-19 disease and the mortality is relatively high, many countries put in place a confinement or measures to reduce the movement of the population. China confined the Hubei region around January 22, Italy confined its population on March 9, France on March 17, ... In the middle of the epidemic, Spain and France reached a situation like the one shown in Fig. 6 (data obtained from the website [12]) where some regions are highly infected while others have fewer cases.

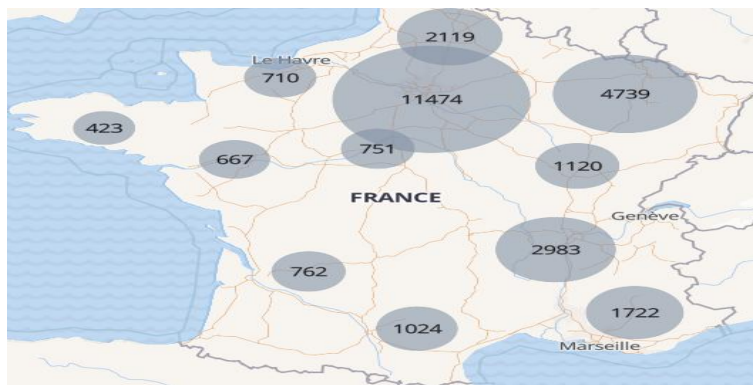


Figure 6: Map of the number of hospital admissions due to COVID-19 in France per region on April 5 2020.

The graph to be studied now is a graph containing the main cities like the one for Mexico 1. The confinement can be modeled by

- (i) reducing the capacity N_j of each node j and therefore α_j
- (ii) reducing the diffusion ϵ , ie the travel between nodes

An important issue when deconfining the population once the peak of the epidemic has passed is to avoid a so-called second wave. This happens in particular when the epidemic affected a small fraction of the total number N . Then, relaxing α or equivalently increasing N causes a number of new susceptibles to enter the reaction and therefore produce a second peak of infection. This is what happens in Fig. 7. Only one node is involved. The computation is started at $t = 0$ with $S_0 = 1$, $I_0 = 0.01$ the parameters are $\alpha = 0.33$, $\beta = 0.13$. At $t = 30$, we continue the evolution with a new $\alpha = 0.5$. One can see the new peak in I .

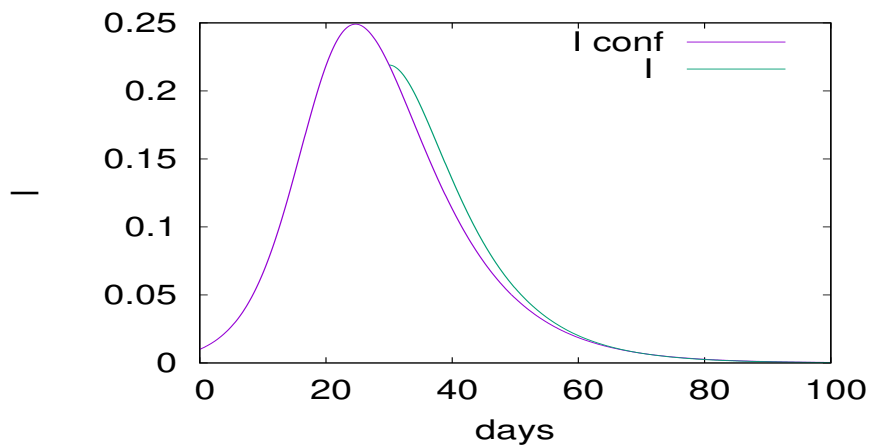


Figure 7: *Deconfinement by increasing α at a single node.*

Another issue with deconfining is the increase of the diffusion which can bring infected from large centers to small centers. In the example shown in Fig. 6, this corresponds to allowing travel from Paris to Rouen in Normandy. To understand this effect, consider a very simple two node graph where $N_1 = 20$ millions and $N_2 = 1$ million. Fig. 8 shows two scenarios corresponding to an increase of diffusion at $t = 15$ before the peak (left panel) and $t = 22$ after the peak (right panel). We see that in both cases, the number of infected in the smaller node I_2 increases significantly.

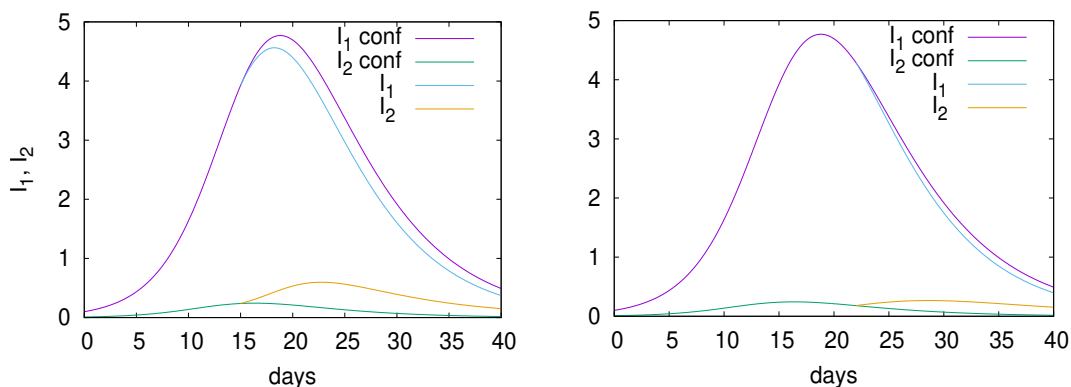


Figure 8: *Time evolution of the infected when ϵ is increased from 10^{-6} to 10^{-2} , at $t = 15$ before the epidemic peak (left panel) and at $t = 22$ (right panel) after the epidemic peak .*

6 Conclusion

We analyzed a model of an epidemic on a network where susceptible-infected equations at the nodes are coupled by a geographic diffusion term. It also contains the essential ingredient of importation of infected subjects from country to country. We have kept the number of parameters to a minimum so that fitting to the data can be successful. This is particularly important for the present epidemic of COVID-19.

We generalize the well-known epidemic criterion of Kermack-McKendrick. For small diffusion, outbreaks occur at different times as the disease advances through the network. A larger diffusion will cause the outbreak to occur synchronously on the network. Using this criterion, we designed a vaccination or isolation policy: we find it best to vaccinate high degree nodes and not efficient to vaccinate neighbors.

Finally we discuss the important aspect of deconfining a region after the outbreak. Circulation between highly infected regions and less impacted areas should be reduced to prevent the spread of infected to the latter.

Acknowledgements

This work is part of the XTerM project, co-financed by the European Union with the European regional development fund (ERDF) and by the Normandie Regional Council.

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A Analysis of SIR model

From $I_t = 0$ we obtain

$$S^* = \frac{\beta}{\alpha} = \frac{1}{R_0}. \quad (23)$$

Dividing the second equation of (1) by the first, we get

$$\frac{dI}{dS} = -1 + \frac{\beta}{\alpha S},$$

which can be integrated to yield

$$I = I_0 + S_0 - S + \frac{\beta}{\alpha} \log \frac{S}{S_0}, \quad (24)$$

where we assumed $S(t=0) = S_0$ and $I(t=0) = I_0$. Then one can compute I^*

$$I^* = I_0 + S_0 - S^* + \frac{\beta}{\alpha} \log \frac{S^*}{S_0}. \quad (25)$$

Assuming $S_0 = 1$, equations (23,25) can be written in terms of R_0 as

$$S^* = \frac{1}{R_0}, \quad (26)$$

$$I^* = I_0 + S_0 - \frac{1}{R_0}(1 + \log(R_0 S_0)) \quad (27)$$

The time t^* corresponding to S^*, I^* can be calculated in the following way. From the second equation of (1) one can write

$$\frac{dt}{dS} = -\frac{1}{\alpha} \frac{1}{SI} = -\frac{1}{\alpha} \frac{1}{S(1 + I_0 - S + \frac{1}{R_0} \log S)}$$

Integrating this expression from S^* to 1 yields the value t^*

$$t^* = \frac{1}{\alpha} \int_{S^*}^1 \frac{dS}{S(1 + I_0 - S + \frac{1}{R_0} \log S)}. \quad (28)$$

This integral diverges as expected when $I_0 \rightarrow 0$. It corresponds to a homoclinic orbit [13].

B Well-posedness of the model

To prove the well-posedness, we rewrite the system (7) as the following abstract differential equation:

$$\begin{cases} x'(t) = Ax(t) + f(x(t)) \\ x(0) = x_0 \in R^n \end{cases} \quad (29)$$

where $x := \begin{pmatrix} s \\ i \end{pmatrix}$, A is the matrix given by

$$A := \begin{pmatrix} \Delta & 0 \\ 0 & \Delta \end{pmatrix}$$

and $f : R^n \times R^n \rightarrow R^{2n}$ defined by

$$f(x) := \begin{pmatrix} -\alpha si \\ \alpha si - \beta i \end{pmatrix}$$

and $x_0 := \begin{pmatrix} S_0 \\ I_0 \end{pmatrix}$.

It is clear that, the function f is L_f -lipschitzian with L_f depends only on α and β . Now, we formulate the well-posedness theorem, which is the main theorem of this section:

Theorem B.1 *Given $x_0 \in R^n$. Then, the equation (29) has a unique solution satisfying the following formula:*

$$x(t) = e^{tA}x_0 + \int_0^t e^{(t-s)A}f(x(s))ds, \quad t \geq 0. \quad (30)$$

proof

Let $x_0 \in R^n$ and $T > 0$. Consider the mapping $\Gamma : C \rightarrow C$ given by

$$\Gamma u(t) = e^{tA}x_0 + \int_0^t e^{(t-s)A}f(u(s))ds$$

where $C := C([0, T], R^n)$. Let us prove that Γ is a contraction. Indeed, let $u, v \in C$, then

$$\begin{aligned} \|\Gamma(u(t)) - \Gamma(v(t))\| &\leq \int_0^t e^{(t-s)\|A\|} \|f(u(s)) - f(v(s))\| ds \\ &\leq L_f \int_0^t e^{(t-s)\|A\|} \|u(s) - v(s)\| ds \\ &\leq L_f e^{T\|A\|} \int_0^t \|u(s) - v(s)\| ds \\ &\leq L_f e^{T\|A\|} t \|u - v\|_\infty. \end{aligned}$$

On the other hand

$$\begin{aligned} \|\Gamma^2(u(t)) - \Gamma^2(v(t))\| &= \|\Gamma(\Gamma u(t)) - \Gamma(\Gamma v(t))\| \\ &\leq L_f e^{T\|A\|} \int_0^t s \|\Gamma(u(s)) - \Gamma(v(s))\| ds \\ &\leq \frac{(L_f e^{T\|A\|} t)^2}{2} \|u - v\|_\infty. \end{aligned}$$

Hence, by iterating for $n \geq 1$, we conclude that

$$\|\Gamma^n(u(t)) - \Gamma^n(v(t))\| \leq \frac{(L_f e^{T\|A\|} T)^n}{n!} \|u - v\|_\infty.$$

Now, for n large enough,

$$\frac{(L_f e^{T\|A\|} T)^n}{n!} < 1.$$

The mapping Γ^n is a contraction. Therefore, by using the iterating fixed point theorem Γ is also a contraction. Consequently, the system (13) has a unique solution which is given by (14). **end proof**