Seminar Report about Mathematical Modeling and Complex Network of a SAIRP Model

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Covid-19 caused by coronavirus SARS-COV-2 is a recent infectious disease firstly appeared during november 2019 in Wuhan, in China. The Covid-19 pandemic still not tamed needs to be better understood and one of the biggest issue is the modeling of its evolution. These researches have been conducted to find a model and parameters fitting the real data in order to find an optimal control permitting to take up the resulting challenges of the pandemic. This is a report of some important points of Mathematics and Applications Research and Development Center's work carried out by Cristina Silva. In this document, will be exposed the SAIRP model considered to study the disease evolution in Portugal on the period of time: from March 2, 2020 until February 11, 2021. The choice of piecewise constant parameters will be discussed before exposing the consideration of Portugal regions as a complex network.

1 Introduction to the model

The following problem is considered. We subdivided the total population N in five different classes: S the susceptible (people not infected and not immuned), A the infected but asymptomatic people, I the infected and symptomatic people, R the recovered and dead from the disease and P the protected ones.

$$(\mathcal{P}_{SAIRP}) \begin{cases} \dot{S}(t) = \Lambda - \beta(1-p)\frac{\theta A(t)+I(t)}{N(t)}S(t) - \phi p S(t) + \omega P(t) - \mu S(t) \\ \dot{A}(t) = \beta(1-p)\frac{\theta A(t)+I(t)}{N(t)}S(t) - \nu A(t) - \mu A(t) \\ \dot{I}(t) = \nu A(t) - \delta I(t) - \mu I(t) \\ \dot{R}(t) = -\delta I(t) - \mu R(t) \\ \dot{P}(t) = -\phi p S(t) - \omega P(t) - \mu P(t) \end{cases}$$

defined for $t \in [0, T]$, $T > 0$ representing the time in days, Λ the recruitment rate of total population and μ the natural death rate. These are the different parameters:

Parameter	Description	Parameter	Description
β	Infection transmission rate	p	Fraction of susceptible S transfered
θ	Modification parameter		to protected class P
δ	Transition rate from active infected I	ϕ	Transition rate from susceptible S
	to removed R		to protected class P
$\omega = wm$		$\nu = vq$	
w	Transition rate from protected P	v	Transition rate from asymptomatic A
	to susceptible S		to active infected I
m	Fraction of protected P transfered	q	Fraction of asymptomatic A transfered
	to susceptible S		to active infected individuals I

2 Choice of piecewise constant parameters

In this model, piecewise constant parameters are taken into account to better describe the real situation. Indeed, the parameters change according to governmental decisions or people's behavior. For example, if there is a sanitary confinement, they are not the same as they are with no sanitary confinement: in this case there is a larger protected person rate (P is greater in this situation). So, the time line is subdivided into a finite number n of intervals and these parameters vary in accordance with the interval considered. This subdivision of the time line is relevant to better fit the real data on the period studied. Then, considering n Cauchy problems defined on each interval of time permits to lead to the existence and unicity of a solution for each Cauchy problem in $\Omega = \{x = (S, A, I, R, P)^T \in (\mathbb{R}^+)^5, \, 0 < S + A + I + R + P \leq \frac{\Lambda}{\mu}\}$. It is interesting to specify that choosing piecewise constant parameters may lead to pseudo-periodic solutions. This means for example, the curve of the solution may be the same on each interval of time taking into account a sanitary confinement. Then, the parameters considered have been taken from real data given by DGS about COVID-19. To find the parameters β, p, m giving a solution which matches with the data, the least squared method has been used. Finally, taking $n = 10$ and the subdivision considered for the time line gave the best results, it permitted to fit the data. All of this led to a model describing well the evolution of active infected population I during the period studied as we can see below
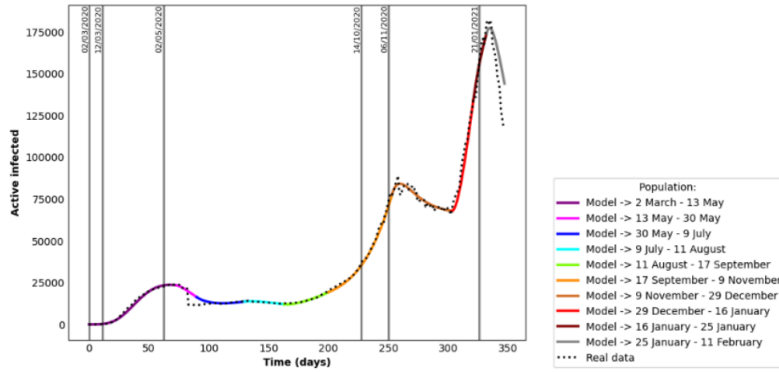

Figure 1: Active Infected (I) evolution with 10 subdivisions of the period studied and parameters $\beta \in [0.100, 1.531]$, $p \in [0.290, 0.675]$, $m \in [0.090, 0.379]$

3 Consideration of regions described by complex network

Furthermore, as the previous model fitted the data when studied on a national scale and on a regional scale, the migration between different regions issue had raised. So, it was proposed to study different population dynamics between the six regions in Portugal: Norte (1), Centro (2), Lisboa e Vale do Tejo (3), Alentejo (4), Algarve (5), Pinhal Litoral (6). A focus has been made on 4 different migration models, the no migration model is part of it and is relatively easy to consider. The strategy is to consider the country as a complex network where the different edges are the different regions and the oriented vertices represent the different displacements from a region to another one. Here is considered a finite number of displacements. Each region has its own specificities, so the parameters can differ from one region to another one. Each model will be adapted using a "connectivity" matrix $(L_{i,j})_{1 \leq i,j \leq 6}$ where $L_{i,j}$ is a displacement rate from region i to region j if $i \neq j$ and $L_{i,j} = -\sum_{k=1, k \neq i}^{6} L_{k,i}$ otherwise. So, let x_i be $(S_i, A_i, I_i, R_i, P_i) \in \mathbb{R}^5$ for i in $\{1, 2, 3, 4, 5, 6\}$ the problem for each region i is

$$
(\mathcal{P}_i)
\begin{cases}
\dot{S}_i\,(t) = \Lambda_i - \beta_i(1-p_i)\frac{\theta_i A_i(t)+I_i(t)}{N_i(t)}S_i(t) - \phi_i p_i S_i(t) + \omega_i P_i(t) - \mu_i S_i(t) + \sigma_S \displaystyle\sum_{k=1,k\neq i}^{6} L_{i,k}S_k(t) \\[2ex]
\dot{A}_i\,(t) = \beta_i(1-p_i)\frac{\theta_i A_i(t)+I_i(t)}{N_i(t)}S_i(t) - \nu_i A_i(t) - \mu_i A_i(t) + \sigma_A \displaystyle\sum_{k=1,k\neq i}^{6} L_{i,k}A_k(t) \\[2ex]
\dot{I}_i\,(t) = \nu_i A_i(t) - \delta_i I_i(t) - \mu_i I_i(t) + \sigma_I \displaystyle\sum_{k=1,k\neq i}^{6} L_{i,k}I_k(t) \\[2ex]
\dot{R}_i\,(t) = -\delta_i I_i(t) - \mu_i R_i(t) + \sigma_R \displaystyle\sum_{k=1,k\neq i}^{6} L_{i,k}R_k(t) \\[2ex]
\dot{P}_i\,(t) = -\phi_i p_i S_i(t) + \omega_i P_i(t) - \mu_i P_i(t) + \sigma_P \displaystyle\sum_{k=1,k\neq i}^{6} L_{i,k}P_k(t)
\end{cases}
$$

where σ_i for $i \in \{S, A, I, R, P\}$ is the rate of people in the state i that migrates to another region.

This new problem admits a unique solution on $\Theta = \{(x_i)_{1\leq i\leq 30} \in (\mathbb{R}^+)^{30}, \sum_{i=1}^{30} x_i \leq \frac{\Lambda_0}{\mu_0}\}$ where $\mu_0 = \min_{1\leq i\leq 6}\mu_i$ is the minimum mortality rate and $\Lambda_0 = \sum_{i=1}^{6}\Lambda_i$. As done previously, the parameters are fixed by real data, some are the same from a region to another one and some differ. Constant piecewise parameters are estimated by the least squared method. However, it is important to specify that the time line has been subdivided differently in accordance with the different regions. Once again, it permitted to fit the real data for the solution of $(\mathcal{P}_i)$ for each region i and each complex network considered with $\sigma_S > 0$, $\sigma_A > 0$ and $\sigma_I = \sigma_P = 0$. Then, was naturally aimed the existence of a complex network which minimizes the active infected average number. Simulations have been done with one thousand different topologies among all topologies existing. The following parameters have been chosen: $\sigma_S = \sigma_A \in [0.01, 0.1]$ and $\sigma_I = \sigma_R = \sigma_P = 0$, which seem to be pretty good conditions because considering that there is no displacement of people under protective measures, infected and isolated and dead from covid-19 is a consistent choice. For $\sigma_S = \sigma_A = 0.01$, the following complex network minimizes the level of infection among the one thousand randomly generated. It is then compared to the one with no migration between regions.
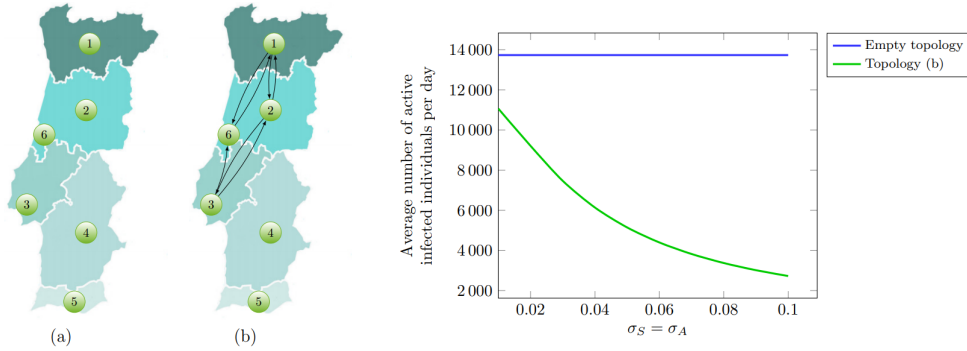

Figure 2: The model with no migration called empty topology (a) and the topology minimizing the level of infection (b) among the one thousand networks randomly generated

The SAIRP model considered permitted to distinguish people by classifying them according to their state in front of the disease. To better adapt the model, piecewise constant parameters have been chosen and some have been estimated by the least squared method in order for the solution to fit the real data. To go further, regions were considered as a complex network to integrate into the model the migration dynamics which is essential for this type of modeling. Thereby, the next goal is to apply optimal control onto the system. This step is the continuation of this work, it is to find a control allowing to restore the economy while minimizing the hospitalized number and include it into the equations.

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