An adaptive nonlinear SIR epidemic model for CoviD-19 disease spreading and forecasting

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Abstract

A various mathematical models of the COVID-19 coronavirus has been proposed. We develop here a model describing this epidemic, focused on the impact of moroccan government imposed public policies designed to contain this epidemic. The proposed model is a general form SIR and SIER epidemic in [3]. We identfy a constant transmission rate ...

Keywords: ..., ...

1. Introduction

?⟨sec:intro⟩?

The worldwide spread of the new coronavirus that causes severe acute respiratory syndrome has led more than 180 countries. This virus has affected more than 5 million and caused the death of 350.000 people at 20th May and which also affects the world economy. The World Health Organization (WHO) named the pneumonia caused by the new coronavirus COVID-19. The International Committee on Taxonomy of Viruses named it SARS-CoV-2. SARS-CoV-2 is a coronavirus similar to SARS-CoV and MERS-CoV. SARS-CoV first occurred from November 2002 to June 2003 in Guangdong, China, and spread to many parts of the world. MERS-CoV was found in 2012 in Saudi Arabia. In the fight against this virus and the absence of a treating vaccine, the international community has more interest in putting in place tools which illustrate the principle of its virality and which aim to understand and consequently to control the spread of the virus and / or to mitigate it. This global health crisis of Covid-19 has brought to light the primordial role of the development of research and scientific evolution. In particular, the role of mathematical modeling in understanding the spread of the disease over time. In front of this situation of invasion of covid19 on an international scale, access is now facilitated to much more data and even to analyzes carried out by scientists and researchers around the world. However, modeling and forecasting the spread of COVID-19 remains an urgent challenge to draw up data based on data in other countries over the long term. In our project, we present a basic models of epidemic transmission that can be linked to data provided by international scientific reports and to data from different cities in Morocco.

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2. Mathematical model

2.1. The SIR model

The SIR model is one of the most epidemiological compartmental models for the investigation of the spread of disease caused by virus. This model was introduced by Kermack and McKendrick in 1927 to describes the evolution of the relative proportions of three disjoint classes which change with time t

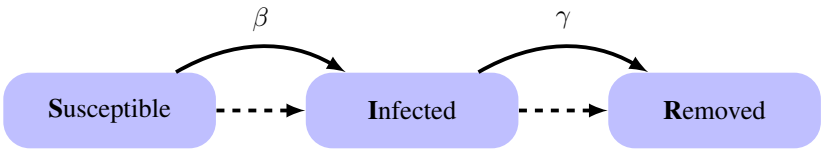

Figure 1: Compartemental diagram for SIR model

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In the SIR model, the population is subdivided into the following three epidemiologically distinct types of individuals and this classes are be represented by

1. The susceptible class $\mathbf{S}(t)$ the individuals have not yet infected by the disease of interest .
2. The infected class $\mathbf{I}(t)$ the individuals who are currently infected and capable to transmitting the disease to others.
3. The removed class $\mathbf{R}(t)$ the individuals formally infected who are deceased, or have recovered and are either permanently immune.

Mathematically, the model can formulated as a system of three equations [3]:

$$\begin{cases} \dfrac{dS(t)}{dt} = -\dfrac{\beta}{N} S(t)\, I(t) \\ \dfrac{dI(t)}{dt} = \dfrac{\beta}{N} S(t)\, I(t) - \gamma I(t) \\ \dfrac{dR(t)}{dt} = \gamma I(t). \end{cases} \tag{2.1}$$

Sir-system

The term $\frac{\beta}{N} S(t)\, I(t)$ represents the disease transmission rate by contact between susceptible and infected individuals. The parameter β is the infection rate (to be estimated) and γ is the recovery rate which can be computed with respect to the period of viral shedding ($\gamma \sim \frac{1}{10} days^{-1}$ in the case of Covid-19). Adding all equations in the model, we observe that the total population $N = S + I + R$ is a constant. Indeed, we see that

$$\frac{dS(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} = 0 \qquad \text{and} \quad S(t) + I(t) + R(t) = N \text{ for each time } t.$$

The system (2.1) are completed by the initial conditions. Starting the model when the first infected individual appears in the population, which correspond to $S(0) = N$, $I(0) = N - 1$ and $R(0) = 0$. The case where the number of infected and recovered is neglected with respect to the total population the number of susceptible S in can be approximated by a constant, $S(t) \sim S(0) = N$. The first equation (2.1) can be written as

$$\frac{dI(t)}{dt} \sim \beta\, I(t) - \gamma I(t). \tag{2.2}$$

?Sir-simplified?

We obtain an ordinary differential equation with constant coefficients and the solution can be expressed as

$$I(t) \sim I(0)\ \exp((\beta - \gamma)t) \tag{2.3}$$

Sir-sol

Now, let us consider the class $D(t)$ of deaths individuals due to the epidemic and σ the mortality rate of the infected. We will note by $\mathbf{R}(t)$ the recovered class. The dynamics of $D(t)$ depends on $I(t)$ and the SIRD System becomes

$$\begin{cases} \dfrac{dS(t)}{dt} = -\dfrac{\beta}{N} S(t)\, I(t) \\ \dfrac{dI(t)}{dt} = \dfrac{\beta}{N} S(t)\, I(t) - (\gamma + \sigma) I(t) \\ \dfrac{dR(t)}{dt} = \gamma I(t) \\ \dfrac{dD(t)}{dt} = \sigma I(t). \end{cases} \tag{2.4}$$

SirD-system

Thanks to [2], the basic reproduction number of (2.4)can be computed by

$$\mathcal{R}_0 = \frac{\beta}{\gamma + \sigma}.$$

From (2.3), we see that the number of infected will grow for $\beta > \gamma$ i.e. $\mathcal{R}_0 > 1$ and when $\beta - \gamma < 0$ i.e. $\mathcal{R}_0 < 1$ it will decay which plays the key role behind disease propagation.

2.2. General SIRD model

In this work, we assume the human behavior to propagation of diseases and which individuals reduce their contacts with respect to the increasing of affected individuals, and we propose a modified SIR model which can expressed as

$$\begin{cases} \dfrac{dS(t)}{dt} = -\beta \big[\dfrac{S(t)}{N}\big]^{p(t)}\, I(t) \\ \dfrac{dI(t)}{dt} = \beta \big[\dfrac{S(t)}{N}\big]^{p(t)} I(t) \; - (\gamma + \sigma) I(t) \\ \dfrac{dR(t)}{dt} = \gamma I(t) \\ \dfrac{dD(t)}{dt} = \sigma I(t). \end{cases} \tag{2.5}$$

Sir-gen-system

where $p(t) \geq 1$ is a continuous function describe the social distancing and the sensitivity to disease. For $p(t) = 1$, we recover the SIR model (2.1). In general, after the start of the evolution of the epidemic, there is a large reduction in the population $S(t)$ by a social distancing measures. For that, we assume that $p(t) = 1$ for $t \leq t_c$ and $p(t) = \overline{p}$ for $t \geq t_c$, where t_c is the time of beginning confinement. A typical example is

$$p_\varepsilon(t) = \begin{cases} 1 & \text{if} \quad t \leq t_c \\ \dfrac{\overline{p} - 1}{\varepsilon}(t - t_c) + 1 & \text{if} \quad t_c \leq t \leq t_c + \varepsilon \\ \overline{p} & \text{if} \quad t \geq t_c + \varepsilon \end{cases} \tag{2.6}$$

?p?

2.3. Numerical simulations

Thanks to the implicit Euler method, discretizing the time variable as $t = k\tau$ where k is a number and τ is the time step. The discrete iterative scheme of the proposed model can be written as

$$\begin{cases} S_{k+1} = S_k - \tau\beta\big[\frac{S_{k+1}}{N}\big]^{p_{k+1}} I_{k+1} \\ I_{k+1} = I_k + \tau\beta\big[\frac{S_{k+1}}{N}\big]^{p_{k+1}} - \tau(\gamma+\sigma)I_{k+1} \\ R_{k+1} = R_k + \tau\gamma I_{k+1} \\ D_{k+1} = D_k + \tau\sigma I_{k+1} \end{cases} \tag{2.7}$$

Sir-system_d

where S_{k+1}, I_{k+1}, R_{k+1} and R_{k+1} are number of the susceptible, the infected and the recovered and death in the specific day $k+1$ respectively, p_{k+1} the value if p at day $k+1$. First, assume that $p_k = 1$ for any $k \geq 0$, the discrete () iterative scheme becomes

⟨Sir-system_d⟩

$$\begin{cases} S_{k+1} = S_k - \tau\dfrac{\beta}{N} S_{k+1} I_{k+1} \\ I_{k+1} = I_k + \tau\dfrac{\beta}{N} S_{k+1} I_{k+1} - \tau(\gamma+\sigma)I_{k+1} \\ R_{k+1} = R_k + \tau\gamma I_{k+1} \\ D_{k+1} = D_k + \tau\sigma I_{k+1} \end{cases} \tag{2.8}$$

?Sir-system-di2?

Adding the first and the second equations, we obtain

$$(1+\tau(\gamma+\sigma))I_{k+1} = I_k + S_k - S_{k+1}. \tag{2.9}$$

Eq1

From the first equation, we have

$$S_{k+1} = \frac{S_k}{1+\tau\frac{\beta}{N}I_{k+1}}. \tag{2.10}$$

Eq2

Replacing (2.10) in (2.9) and the fact that $S_k + I_k + R_k + D_k = N$, we can easily obtain that

$$I_{k+1} = \frac{\sqrt{\big(\tau(\gamma+\sigma)+1-\tau\frac{\beta}{N}(S_k+I_k)\big)^2 + 4\tau\frac{\beta}{N}(\tau(\gamma+\sigma)+1)I_k} - (\tau(\gamma+\sigma)+1-\tau\frac{\beta}{N}(S_k+I_k))}{2\tau\frac{\beta}{N}(1+\tau(\gamma+\sigma))} := \eta_k. \tag{2.11}$$

Eq3

Consequently, we have

$$S_{k+1} = \frac{S_k}{1+\tau\frac{\beta}{N}\eta_k}, \quad R_{k+1} = R_k + \tau\gamma\eta_k \quad \text{and} \quad D_{k+1} = D_k + \tau\sigma I_{k+1}, \tag{2.12}$$

?Eq4?

which can be computed directly . Now taking $\Theta_{k+1} := \left[\frac{S_{k+1}}{N}\right]^{p_{k+1}-1}$ in (2.3) the system becomes

$$\begin{cases} S_{k+1} = S_k - \tau\dfrac{\beta}{N}\,\Theta_{k+1}\,S_{k+1}\,I_{k+1} \\ I_{k+1} = I_k + \tau\dfrac{\beta}{N}\,\Theta_{k+1}\,S_{k+1}\,I_{k+1} - \tau(\gamma+\sigma)I_{k+1} \\ R_{k+1} = R_k + \tau\gamma I_{k+1} \\ D_{k+1} = D_k + \tau\sigma I_{k+1}. \end{cases} \tag{2.13}$$ Sir-system-appro

The solution of (2.13) can be obtained using the following fixed point method:

$$\begin{cases} S_{k+1}^{n+1} = S_k - \tau\dfrac{\beta}{N}\,\Theta_{k+1}^{n}\,S_{k+1}^{n+1}\,I_{k+1}^{n+1} \\ I_{k+1}^{n+1} = I_k + \tau\dfrac{\beta}{N}\,\Theta_{k+1}^{n}\,S_{k+1}^{n+1}\,I_{k+1}^{n+1} - \tau(\gamma+\sigma)I_{k+1}^{n+1} \\ R_{k+1}^{n+1} = R_k + \tau\gamma I_{k+1}^{n+1} \\ D_{k+1}^{n+1} = D_k + \tau\sigma I_{k+1}^{n+1}. \end{cases} \tag{2.14}$$?Sir-system-fixed?

for $n \in \mathbb{N}$, with $\Theta_{k+1}^{n} := \left[\frac{S_{k+1}^{n}}{N}\right]^{p_{k+1}-1}$. We shall see further that all results obtained for the scheme (2.9)- (2.11) are also true, with convenient adaptations, for the fully implicit scheme. Now, we present the algorithm used to solve our proposed model.

Require : $S(0) = N-1$, $I(0) = 1$, $R(0) = 0$, $D(0) = 0$, $p(0) = 1$, $Er = 1$, $\epsilon = 10^{-6}$ $n = 0$
Calculate $\Theta_{k+1}^{0} := \left[\frac{S_k}{N}\right]^{p_k-1}$
$\tilde{I} = I_k$
while $\big(Err < \epsilon\big)$ **do**

$$I_{k+1}^{n+1} = \frac{\sqrt{\left(\tau(\gamma+\sigma)+1-\tau\frac{\beta}{N}(S_k+I_k)\Theta_{k+1}^{n}\right)^2 + 4\tau\frac{\beta}{N}(\tau(\gamma+\sigma)+1)\Theta_{k+1}^{n}I_k} - (\tau(\gamma+\sigma)+1-\tau\frac{\beta}{N}(S_k+I_k)\Theta_{k+1}^{n})}{2\tau\frac{\beta}{N}(1+\tau(\gamma+\sigma))};$$

$Err = ||\tilde{I} - I_{k+1}^{n+1}||$
$\tilde{I} = I_{k+1}^{n+1}$
$S_{k+1}^{n+1} = \dfrac{S_k}{1+\tau\frac{\beta}{N}\Theta_{k+1}^{n}I_{k+1}^{n+1}};$
$R_{k+1}^{n+1} = R_k + \tau\gamma I_{k+1}^{n+1};$
$D_{k+1}^{n+1} = D_k + \tau\sigma I_{k+1}^{n+1};$
$n = n+1;$
$\Theta_{k+1}^{n} := \left[\frac{S_{k+1}^{n}}{N}\right]^{p_{k+1}-1;}$
end

Algorithm 1: Iterative Algorithm

2.3.1. Phase Plane

Dividing the first equation in (2.5) by the second, the phase portrait for the epidemic, can be formulated as

$$\frac{dI}{dS} = \frac{\gamma + \sigma}{\beta}\big[\frac{S}{N}\big]^{-p(t)}\, I(t) - 1 \tag{2.15}$$ {?}

Then

$$I = \int \frac{\gamma + \sigma}{\beta}\big[\frac{S}{N}\big]^{-p(t)}\, I(t) - 1 \tag{2.16}$$ {?}

2.4. Fitting the model

In this subsection, we present the technic to fitting the SIR model to Covid-19 data and defend its use in this context.
In terms of the SIR model, the total number of infected specimens, regardless of strain, represent the Infectious (I) category of the model. However, the total number of specimens tested does not accurately represent the Susceptible (S) category of the model. This is a result of data collection from different regions of the nation using different testing practices, resulting in varying amounts of specimens tested as well as seemingly varying rates of infection.9 This is also a result of under-reporting that occurs with the influenza virus.2 Therefore the population size needs to be estimated. The method to estimate population size used in this paper will be addressed further in Chapter III

2.5. Parameter estimation

The model parameters $\vartheta := (\beta, \gamma, N)$ can be estimated via least-square fitting of the model solution to the observed data [5]. This is can be expressed by finding for the set of parameters $\vartheta^\star := (\beta^\star, \gamma^\star, N^\star)$ that minimizes the sum of squared differences between the real data $(\zeta_1, \zeta_2, ..., \zeta_k)$ and the corresponding model solution named by $(\zeta_\vartheta(t_1),\ \zeta_\vartheta(t_2), ..., \zeta_\vartheta(t_k))$. That is, the objective function is written as

$$\mathcal{L}(\vartheta) = \min_{\vartheta} \sum_{i}^{k} |\zeta_\vartheta(t) - \zeta(t_i)|^2 \qquad \text{subject to } \zeta_\vartheta(t) := (S_\vartheta(t), I_\vartheta(t), R_\vartheta(t)) \text{ solution of } (2.1)$$

When no vaccine is available, the isolation of diagnosed infectives and social distancing are the only control measures available.

1. Namely, the susceptible individuals S, capable of contracting the disease and becoming infectious; the asymptomatic E and symptomatic I infectious, capable of transmitting the disease to susceptible; and the recovered R, permanently immune (after healing or dying). Such a simple model represents well a generic behavior of epidemics (plainly as a series of transitions between these populations), and a related advantage consists in a small number of parameters to be identified (three transition rates in Fig. 1: s, g and b). This is an important outcome in the case of a virus attack with a limited amount of data available. That is the case of the current worldwide situation1 under the presence of the SARS-CoV-2 virus.

In our study, we use a compartmental epidemic model given in Figure **??** (Ajoute la figure) to study the transmissibility of Covid-19.

We propose a conceptual model describing compartments of different species in different communities.

The following mathematical model describes the dynamic of infection of Covid-19:

$$\begin{cases} \dfrac{d\,S(t)}{d\,t} = -\beta(t)S^p(t)\,I(t) \\ \dfrac{d\,E(t)}{d\,t} = -rE(t) + \beta(t)S^p(t)\,I(t) \\ \dfrac{d\,I(t)}{d\,t} = -(\delta+\gamma)I(t) + rE(t) \\ \dfrac{d\,R(t)}{d\,t} = -\gamma R(t) + \delta\,I(t), \end{cases} \tag{2.17}$$

?Covid-system?

with social distancing Epidemic model formulation

3. Discussion

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