# 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 [4]. We identify a constant transmission rate ...

*Recently, a various mathematical models has been proposed and used for modeling and forecasting COVID-19 disease. But, all of this forecasting results have been interpreted and computed with fixed data (based on governmental data sources) until a specified day and time and there are not taking account of the recent changed data and the evolution of the pandemie situation. The first aims of this platform is develop an interactive application wich is able to simulate and forecasting the spread of Covid-19, based on the classical models likes SIR, SEIR and their variants at each time with the actual update of real data that come from different API. The Simulator-Covid page allow to simulate the presented mathematical models for a various values of the model parameter?s. To find the parameters adopted for each countries ( in particular in morocco and its regions ) and we fit the models for each country with respect to the actual real data given by the API . The second aims is to present some recents models (developed by our team) describes the spreading of coronavirus under the effect of a various government measures related to stoping coronavirus spreading, likes lockdowns or confinement. We also evaluate the government measures a each country and investigate the clustering of country with respect to the evolution of the pandemic.*

*Key words:* ..., ...

## 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

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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.

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

## 2. Mathematical model

### *2.1. The SIR model*

⟨sir⟩

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 $t$

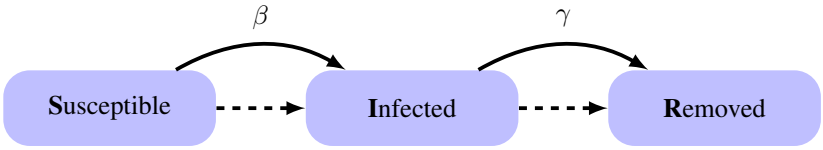


Figure 1: Compartemental diagram for SIR model

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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 [4]:

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

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 $\beta$ is the infection rate (to be estimated) and $\gamma$ 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 $S(0) = N$, $I(0) = 0$ 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?

Based on available data, this exponential growth is observed in the first days of starting COVID-19 outbreak data from various countries.

### *2.2. The SIRD model*

Now, let us consider the SIR model (2.1) with additional class $D(t)$ of deaths individuals due to the epidemic and $\sigma$ the mortality rate of the infected. We will note by $\mathbf{R}(t)$ the recovered class and model can be expressed by

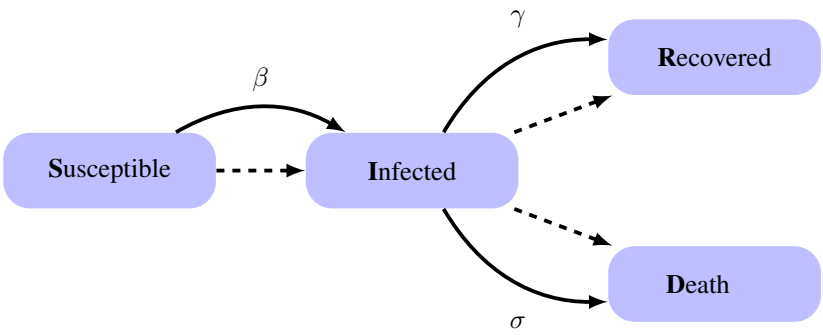


Figure 2: Compartemental diagram for SIRD model

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The dynamics of $D(t)$ depends on $I(t)$ and the SIRD System can be written as

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

Adding all equations in the model, we observe that the total population $N = S + I + R + D$ is a constant. Indeed, we see that

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

Now, thanks to [3], the basic reproduction number of (2.4) can be computed by

$$\mathcal{R}_0 = \frac{\beta S(0)}{(\gamma + \sigma)N}.$$

Similarly as in subsection (2.1 ), we have $I(t) \sim I(0)\ \exp((\beta - \gamma - \sigma)t)$ for $S(0) \sim N$. In this case, we see that the number of infected will grow for $\beta > \gamma + \sigma$ i.e. $\mathcal{R}_0 > 1$ and when $\beta - \gamma - \sigma < 0$ i.e. $\mathcal{R}_0 < 1$ it will decay which plays the key role behind disease propagation. For more analysis about this see, for instance[5, 3, 2].

### *2.3. The proposed non linear 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 SIRD model with social distancing 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 such that $p(0) = 1$ and $p(t) \to p^\star$ as $t \to \infty$. The function $p(t)$ describe the social distancing and the sensitivity to disease. For $p(t) = 1$, we recover the SIRD model (2.4). 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 $p(t) = p^\star$ for $t \geq t_c$, where $t_c$ is the time of beginning confinement. A typical example is

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

?p?

#### *2.3.1. The reproduction number and phase plane*

Observe that the non trivial equilibrium values of the system (2.5) is given by $(S^\star, 0, R^\star, D^\star)$ where

$$S^\star = N\big(\frac{\gamma + \sigma}{\beta}\big)^{\frac{1}{p^\star}} \quad \text{and} \ \ R^\star + D^\star = N(1 - \big(\frac{\gamma + \sigma}{\beta}\big)^{\frac{1}{p^\star}}).$$

Recall that, the total population $S(t) + I(t) + R(t) + D(t) = N$ of each $t$, we focus only on the equation in $S$ and $I$. Following [1, 2], the right side of the system (2.5) can be decomposed as $\mathcal{F} + \mathcal{V}^+ + \mathcal{V}^-$ where

$$\mathcal{F}(S, I) = (0, \beta\big[\frac{S}{N}\big]^p I), \quad \mathcal{V}^+(S, I) = (0, 0) \quad \text{and} \quad \mathcal{V}^-(S, I) = (-\beta\big[\frac{S}{N}\big]^p I, -(\gamma + \sigma) I).$$

then, we have $F = \beta\big[\frac{S^*}{N}\big]^{p^*}$ and $V = -(\gamma+\sigma)$, we deduce that

$$\mathcal{R}_0 = \rho(-FV^{-1}) = \frac{\beta}{\gamma+\sigma}\big[\frac{S}{N}\big]^{p^*}.$$

where $\rho$ is a spectral radius. Moreover, the number of people in a population who can be infected by an individual at time $t$ can be represented by the effective reproduction number:

$$R_t^p = \frac{\beta}{\gamma+\sigma}\big[\frac{S(t)}{N}\big]^{p(t)}.$$

We observe that the social distancing affect $R_t$, since $S(t) \leq N$ and when $p \to \infty$ we observe that $R_t^p \to 0$.

Now, we investigate the phase plane, dividing the first equation by the second in (2.5), the phase portrait for the epidemic, can be formulated as

$$\frac{dI}{dS} = \frac{\gamma+\sigma}{\beta}\big[\frac{S}{N}\big]^{-p(t)} - 1. \tag{2.7}$$ ?IS?

Integrating this equation with respect to $S$, for any $t > t_c$ we have

$$\begin{aligned} I(t) &= I(t_0) + \frac{N}{\mathcal{R}_0}\int_{t_0}^{t_c}\frac{1}{S}dS + \frac{1}{\mathcal{R}_0}\lim_{\varepsilon\to 0}\int_{t_c+\varepsilon}^{t}\big[\frac{S}{N}\big]^{-p(t)}dS - \int_{t_0}^{t}dS \\ &= I(t_0) + \frac{N}{\mathcal{R}_0}\ln\big(\frac{S(t_c)}{S(t_0)}\big) + \frac{N}{\mathcal{R}_0(1-p(t))}\big[\frac{S(t)}{N}\big]^{1-p(t)} \\ &- \lim_{\varepsilon\to 0}\frac{N}{\mathcal{R}_0(1-p(t_c+\varepsilon))}\big[\frac{S(t_c+\varepsilon)}{N}\big]^{1-p(t_c+\varepsilon)} + S(t_0) - S(t) \\ &= I(t_0) + \frac{N}{\mathcal{R}_0}\ln\big(\frac{N}{S(t_0)}\big) - \frac{N}{\mathcal{R}_0(1-p(t))}\big[\frac{S(t)}{N}\big]^{1-p(t)} + S(t_0) - S(t) \end{aligned} \tag{2.8}$$ {?}

Since

$$\frac{d^2I}{dS^2} = \frac{-p(t)}{N\mathcal{R}_0}\big[\frac{S}{N}\big]^{-p(t)-1} \leq 0,$$

we assume that the maximum $I_{max}$ reach after $t_c$ then $I_{max}$ occurs when $\frac{dI}{dt} = 0$ or in the other words $S^\star = N\mathcal{R}_0^{\frac{1}{p^\star}}$ then we can compute the maximum number of infective

$$I_{max} = I(t_0) + \frac{N}{\mathcal{R}_0}\ln\big(\frac{N}{S(t_0)}\big) + \frac{N}{(1-p^*)}\big[\mathcal{R}_0\big]^{\frac{1}{p^*}-2} + S(t_0) - N\mathcal{R}_0^{\frac{1}{p^\star}}$$

Starting the model when the first infected individual appears in the population, which correspond to $S(t_0) = N$ and $I(0) = 0$, then

$$I_{max} = \frac{N}{(1-p^*)}\big[\mathcal{R}_0\big]^{\frac{1}{p^*}-2} + N(1-\mathcal{R}_0^{\frac{1}{p^\star}}).$$

### *2.4. Numerical simulations*

Generally, explicit treatment of (2.1) usually means stricter conditions on time step and the parameters to achieve stability of time discretization schemes. To overcome this, we will use the implicit Euler method,

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

$$\begin{cases} S_{k+1} = S_k - \tau\beta\big[\frac{S_{k+1}}{N}\big]^{p_{k+1}} I_{k+1} \\ I_{k+1} = I_k + \tau\beta\big[\frac{S_{k+1}}{N}\big]^{p_{k+1}} I_{k+1} - \tau(\gamma+\sigma)I_{k+1} \\ R_{k+1} = R_k + \tau\gamma I_{k+1} \\ D_{k+1} = D_k + \tau\sigma I_{k+1} \end{cases} \tag{2.9}$$ 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⟩

$$\begin{cases} S_{k+1} = S_k - \tau\dfrac{\beta}{N} S_{k+1} I_{k+1} \\ I_{k+1} = I_k + \tau\dfrac{\beta}{N} S_{k+1} I_{k+1} - \tau(\gamma+\sigma)I_{k+1} \\ R_{k+1} = R_k + \tau\gamma I_{k+1} \\ D_{k+1} = D_k + \tau\sigma I_{k+1} \end{cases} \tag{2.10}$$ ?Sir-system-di2?

Adding the first and the second equations, we obtain

$$(1+\tau(\gamma+\sigma))I_{k+1} = I_k + S_k - S_{k+1}. \tag{2.11}$$ Eq1

From the first equation, we have

$$S_{k+1} = \frac{S_k}{1+\tau\frac{\beta}{N}I_{k+1}}. \tag{2.12}$$ Eq2

Replacing (2.12) in (2.11) and the fact that $S_k + I_k + R_k + D_k = N$, we can easily obtain that

$$I_{k+1} = \frac{\sqrt{\big(\tau(\gamma+\sigma)+1-\tau\frac{\beta}{N}(S_k+I_k)\big)^2 + 4\tau\frac{\beta}{N}(\tau(\gamma+\sigma)+1)I_k} - (\tau(\gamma+\sigma)+1-\tau\frac{\beta}{N}(S_k+I_k))}{2\tau\frac{\beta}{N}(1+\tau(\gamma+\sigma))} := \eta_k. \tag{2.13}$$ Eq3

Consequently, we have

$$S_{k+1} = \frac{S_k}{1+\tau\frac{\beta}{N}\eta_k}, \quad R_{k+1} = R_k + \tau\gamma\eta_k \quad \text{and} \quad D_{k+1} = D_k + \tau\sigma I_{k+1}, \tag{2.14}$$ ?Eq4?

which can be computed directly . Now taking $\Theta_{k+1} := \big[\frac{S_{k+1}}{N}\big]^{p_{k+1}-1}$ in (2.4) the system becomes

$$\begin{cases} S_{k+1} = S_k - \tau\dfrac{\beta}{N}\Theta_{k+1} S_{k+1} I_{k+1} \\ I_{k+1} = I_k + \tau\dfrac{\beta}{N}\Theta_{k+1} S_{k+1} I_{k+1} - \tau(\gamma+\sigma)I_{k+1} \\ R_{k+1} = R_k + \tau\gamma I_{k+1} \\ D_{k+1} = D_k + \tau\sigma I_{k+1}. \end{cases} \tag{2.15}$$ Sir-system-appro

The solution of (2.15) can be obtained using the following fixed point method:

$$\begin{cases} S_{k+1}^{n+1} = S_k - \tau \dfrac{\beta}{N}\, \Theta_{k+1}^{n}\, S_{k+1}^{n+1}\, I_{k+1}^{n+1} \\ I_{k+1}^{n+1} = I_k + \tau \dfrac{\beta}{N}\, \Theta_{k+1}^{n}\, S_{k+1}^{n+1}\, I_{k+1}^{n+1} - \tau(\gamma+\sigma) I_{k+1}^{n+1} \\ R_{k+1}^{n+1} = R_k + \tau\gamma I_{k+1}^{n+1} \\ D_{k+1}^{n+1} = D_k + \tau\sigma I_{k+1}^{n+1}. \end{cases} \tag{2.16}$$

?Sir-system-fixed?

for $n \in \mathbb{N}$, with $\Theta_{k+1}^{n} := \big[\frac{S_{k+1}^{n}}{N}\big]^{p_{k+1}-1}$. We shall see further that all results obtained for the scheme (2.11)- (2.13) 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 $\Theta_{k+1}^{0} := \big[\frac{S_k}{N}\big]^{p_k - 1}$
$\tilde{I} = I_k$
**while** $\big(Err < \epsilon\big)$ **do**

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

$Err = ||\tilde{I} - I_{k+1}^{n+1}||$
$\tilde{I} = I_{k+1}^{n+1}$

$$S_{k+1}^{n+1} = \frac{S_k}{1+\tau\frac{\beta}{N}\Theta_{k+1}^{n} I_{k+1}^{n+1}};$$

$R_{k+1}^{n+1} = R_k + \tau\gamma I_{k+1}^{n+1};$
$D_{k+1}^{n+1} = D_k + \tau\sigma I_{k+1}^{n+1};$
$n = n+1;$
$\Theta_{k+1}^{n} := \big[\frac{S_{k+1}^{n}}{N}\big]^{p_{k+1}-1;}$
**end**

**Algorithm 1:** Fixed point iterative Algorithm

### *2.5. 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 —- 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.*

**?**⟨Fig0⟩**?**

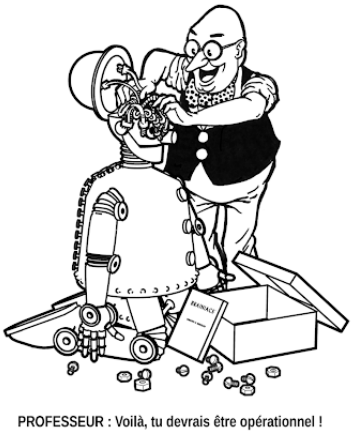


Figure 3: Active/ Deaths cases at first 15 days (Italy France Spain Chile Brazil Mexico Morocco Algeria Oman) .

### *2.6. Parameter estimation*

The model parameters $\vartheta := (\beta, \gamma, p)$ can be estimated via least-square fitting of the model solution to the observed data [7]. This is can be expressed by finding for the set of parameters $\vartheta^\star := (\beta^\star, \gamma^\star, p^\star)$ 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

$$\min_{\vartheta} \sum_{j=1}^{k} ||\zeta_\vartheta(t_j) - \zeta_j||^2 := z^1 \sum_{j=1}^{k} w^1_{t_j} (S_\vartheta(t_j) - S_j)^2 + z^2 \sum_{j=1}^{k} w^2_{t_j} (I_\vartheta(t_j) - I_j)^2 + z^3 \sum_{j=1}^{k} w^3_{t_j} (R_\vartheta(t_j) - R_j)^2$$

where $\zeta_\vartheta(t) := (S_\vartheta(t), I_\vartheta(t), R_\vartheta(t))$ is a solution of the system (2.1), $t_i$ is the time of observed data and $i$ is the number of data points. The corresponding weight is given by

$$w^m_{t_{k-j}} = \delta^m (1 - \delta^m)^{j-1} \qquad \text{for } j = 1, ..., k-1 \text{ and } m \in \{1, 2, 3\}$$

where $0 < \delta^m < 1$ for $m \in \{1, 2, 3\}$ When each data point should not be given equal weight in the estimation of model parameters, weighted least squares can be useful to assign relative weights to each data point in our dataset. For instance, weights could reflect variable quality (e.g., precision of the measurements) of the time series so that less weight is given to those data points associated with inferior quality or precision. We define the nonnegative weights given to each data point as wti so that the objective function for weighted least squares fitting is given by

## 3. Numerical results

we illustrate various numerical tests based on some real data. First, we fix the parameters $\beta$ and $\gamma$ and we illustare the effect of $p$ after confinement

| | France | Italy | Morocco | Allemagne | Espagne |
|---|---|---|---|---|---|
| Pandemic quantity | | | | | |
| $\beta\ (indiv^{-1}day^{-1})$ | 4.00168509 | 16.9943614 | 3.41860628 | | |
| $\gamma\ (day^{-1})$ | 0.67707324 | 0.64610399 | 0.50386318 | | |
| $p$ | 0.97463955 | 0.76667556 | 0.50000186 | | |

In this simulation, we estimate ...

?⟨Fig1⟩?

Figure 4: Simulation Covid-19 spreading .

## 4. Next model

### *4.1. SIER Model*

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:

$$\begin{cases} \frac{d\,S(t)}{d\,t} = -\beta(t)\big[\frac{S(t)}{N}\big]^{p(t)}\ I(t) \\ \frac{d\,E(t)}{d\,t} = -rE(t) + \beta(t)\big[\frac{S(t)}{N}\big]^{p(t)}\ I(t) \\ \frac{d\,I(t)}{d\,t} = -(\delta+\gamma)I(t) + rE(t) \\ \frac{d\,R(t)}{d\,t} = -\gamma R(t) + \delta\ I(t), \end{cases} \tag{4.1}$$

Covid-SEIR-system

Herein, $S$, $E$, $I$, $R$ are the susceptible, exposed, clinically ill and infectious and recovered respectively. Regarding the class $S$, $\beta$ is the transmission rate and for $i = 1, 2$ $\varepsilon_i$ is a reduction factor in the transmissibility of infectious..

In this, work we will decompose $I(t) = I_A(t) + \delta I_C(t)$ and the model (4.2), can be expressed as

$$\begin{cases} \frac{d\,S(t)}{d\,t} = -\beta(t)\big[\frac{S(t)}{N}\big]^{p(t)}\,(I_A(t) + \delta I_C(t)) \\ \frac{d\,E(t)}{d\,t} = -rE(t) + \beta(t)\big[\frac{S(t)}{N}\big]^{p(t)}\,(I_A(t) + \delta I_C(t)) \\ \frac{d\,I_A(t)}{d\,t} = -\gamma_A I_A(t) + r(1-\rho)E(t) \\ \frac{d\,I_C(t)}{d\,t} = -(\eta + \gamma_I + \sigma_I)I_C(t) + r\rho E(t) \\ \frac{d\,R(t)}{d\,t} = -\gamma_I R(t) + \eta\, I_C(t), \end{cases} \tag{4.2}$$

Covid-SEIR-system

The function $\mathcal{A}$ describe the of social distancing models. In the In the first model, individuals reduce their interaction with others proportionally with the cumulative percentage of affected (infectious and recovered) individuals,

*4.2. Generalized Richards model (Yassir peut soccuper de mettre en place ce modele. Ici $I_c$ c'est le cumulatif des infectees , donnera des resultats meilleures que beni mellal )*

$$\frac{d\,I_c(t)}{d\,t} = -rI_c^{p(t)}\big(1 - \big(\frac{I_c}{K}\big)^{\gamma}\big) \tag{4.3}$$

?Covid-GR-system?

1-where $0 \leq p(t) \leq 1$ where r represents the intrinsic growth rate in the absence of any limitation to disease spread, K is the size of the epidemic,
-Richards, 1959
- Dinh et al., 2016; Hsieh - Cheng, 2006; Ma et al., 2014; Turner et al., 1976; Wang, Wu, -Yang, 2012)
-Viboud et al., 2016
-Chowell et al., 2016b; Pell et al., 2016.

## 5. Discussion

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