

Proyect 2. COVID-19

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Abstract

Mathematical modeling has provided a wide range to test hypothesis about the factors/mechanisms underlying transmission disease dynamics. In this report, we describe different mathematical models using differential equations based on extensions of the classical compartmental model *SIR* to estimate transmission, recovery, latency and mortality rates due to the most recent coronavirus which cause Covid-19 disease.

1 Overview

Some observations from [WHO, 2020] regarding covid are

1. First case reported on 31 December 2019 to the WHO Country Office in China due to a pneumonia of unknown cause detected in Wuhan.
2. The outbreak was declared a Public Health Emergency of International Concern on 30 January 2020.

2 Introduction

This approach consists of two parts: first, the study of a database from China that include days where a maximum value of the incidence cases of COVID-19 was reached in that country, and the other one about the study of a database from the first month of the outbreak in Mexico, where a maximum value of incidence cases has not been reached.

3 COVID-19 in China

In the database from China (CoV2019.csv) we can see in row 27 the effect of the change in methodology for counting the number of infected that China implemented on February 17, 2020. In the following graphs we can see the differences among solutions using estimated parameters calculated with complete database and without row 27.

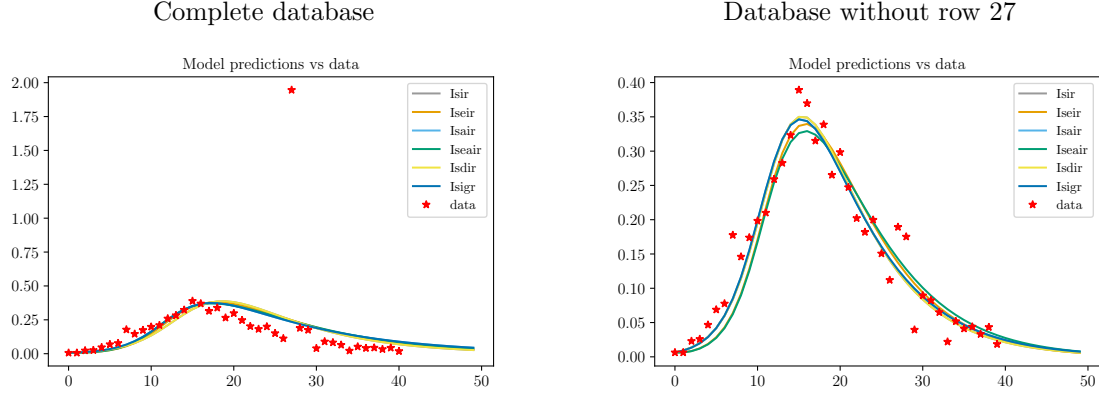


Figure 1: Predictions without mortality

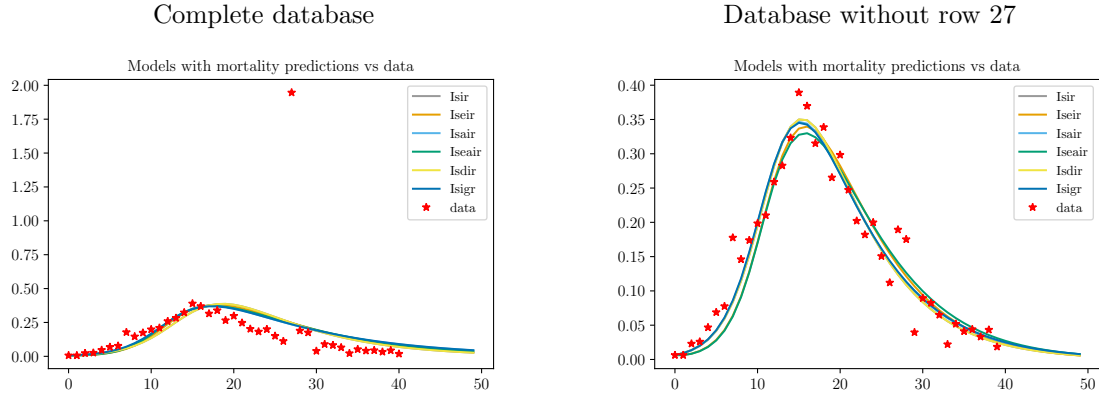


Figure 2: Predictions without mortality

Since this change in methodology does not show a significant change in the incidence of new cases from later days and also the approximations of the solutions are better using database without row 27, we decided not to consider this data for calculating estimates to compare.

3.1 Mathematical models

For the estimation of parameters we use compartmental models considering the proportion of deaths as a compartment of the model or as a parameter to be estimated. In addition we consider models that do not include mortality.

3.1.1 SIR

The first approach is to consider the SIR compartmental model (1) and two variants of it. One of them the SIRM model (2) with parameter μ as a proportion of population death. The other one, the SIMR model with the compartment for mortality (3).

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI \\
\frac{dI}{dt} &= \beta SI - \gamma I \\
\frac{dR}{dt} &= \gamma I
\end{aligned} \tag{1}$$

where the population is divided into three compartments: S susceptible, I infected and R recovered.

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI \\
\frac{dI}{dt} &= \beta SI - \gamma I - \mu I \\
\frac{dR}{dt} &= \gamma I
\end{aligned} \tag{2}$$

where the population also is divided into three compartments: S susceptible, I infected and R recovered.

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI \\
\frac{dI}{dt} &= \beta SI - \gamma I - \mu I \\
\frac{dM}{dt} &= \mu I \\
\frac{dR}{dt} &= \gamma I
\end{aligned} \tag{3}$$

where the population now is divided into four compartments: S susceptible, I infected, M deaths and R recovered.

The parameters used in previous models are as follows

$$\begin{aligned}
\beta &= \text{Contact rate} \times \text{Probability of transmission} \\
\gamma &= \text{Recovery rate} \\
\mu &= \text{Death proportion}
\end{aligned}$$

Using the library *PDEparams* for Python with normalized incidence data from China and establishing the initial conditions and bounds of parameters as in Table 1 we get the estimators showed in the same table.

In the following graph we see that all three models adjust to data with an error less than 0.0009

3.1 Mathematical models

	w/o Mortality compartment			With Mortality compartment	
Bounds	Init cond	Estimators w/o μ	Estimators with μ	Init cond	Estimators
$\beta \in (0.3, 2)$	$s = 0.9937$	$\beta = 0.5538$	$\beta = 0.5539$	$s = 0.9937$	$\beta = 0.5538$
$\gamma \in (0.07, 0.2)$	$i = 0.0063$	$\gamma = 0.1615$	$\gamma = 0.0929$	$i = 0.0063$	$\gamma = 0.1615$
$\mu \in (0.001, 0.3)$	$r = 0$		$\mu = 0.0686$	$m = 0.0$	$\mu = 0.0686$
				$r = 0$	

Table 1: SIR, SIRm, SIMR China.

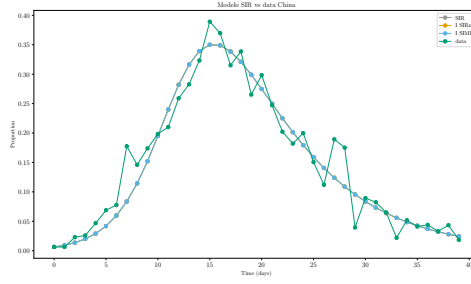


Figure 3: SIR China.

3.1.2 SEIR

The second approach is using the SEIR compartmental model (4) and two variants of it. The SEIRm model (5) with parameter μ as a proportion of population death. Whereas, the SEIMR model with the compartment for mortality (6).

$$\begin{aligned}
 \frac{dS}{dt} &= -\beta SI \\
 \frac{dE}{dt} &= \beta SI - \eta E \\
 \frac{dI}{dt} &= \eta E - \gamma I \\
 \frac{dR}{dt} &= \gamma I
 \end{aligned} \tag{4}$$

where the population is divided into four compartments: S susceptible, E exposed, I infected and R recovered.

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI \\
\frac{dE}{dt} &= \beta SI - \eta E \\
\frac{dI}{dt} &= \eta E - \gamma I - \mu I \\
\frac{dR}{dt} &= \gamma I
\end{aligned} \tag{5}$$

where the population again is divided into four compartments: S susceptible, E exposed, I infected and R recovered.

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI \\
\frac{dE}{dt} &= \beta SI - \eta E \\
\frac{dI}{dt} &= \eta E - \gamma I - \mu I \\
\frac{dM}{dt} &= \mu I \\
\frac{dR}{dt} &= \gamma I
\end{aligned} \tag{6}$$

where the population now is divided into five compartments: S susceptible, E exposed, I infected, M deaths and R recovered.

The parameters used in previous models are as follows

$$\begin{aligned}
\beta &= \text{Contact rate} \times \text{Probability of transmission} \\
\eta &= \text{Latency rate.} \\
\gamma &= \text{Recovery rate} \\
\mu &= \text{Death proportion}
\end{aligned}$$

Using the library *PDEparams* for Python with normalized incidence data from China and establishing the initial conditions and bounds of parameters as in Table 2 we get the estimators showed in the same table.

In the following graph we can see that all three models adjust to data with an errorless than 0.0009

3.1 Mathematical models

	w/o Mortality compartment			With Mortality compartment	
Bounds	Init cond	Estimators w/o μ	Estimators with μ	Init cond	Estimators
$\beta \in (0.3, 2)$	$s = 0.9937$	$\beta = 2.0$	$\beta = 2.0$	$s = 0.9937$	$\beta = 2.0$
$\eta \in (0.07, 0.2)$	$e = 0$	$\eta = 0.2$	$\eta = 0.2$	$e = 0$	$\eta = 0.2$
$\gamma \in (0.07, 0.2)$	$i = 0.0063$	$\gamma = 0.1696$	$\gamma = 0.085$	$i = 0.0063$	$\gamma = 0.1695$
$\mu \in (0.001, 0.3)$	$r = 0$		$\mu = 0.0846$	$m = 0.0$	$\mu = 0.0846$
				$r = 0$	

Table 2: SEIR, SEIRm, SEIMR China.

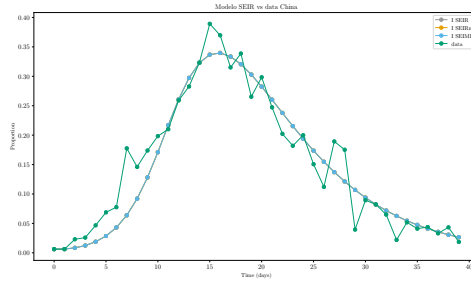


Figure 4: SEIR China.

3.1.3 SAIR

The next approach is using two models where the population is divided into four compartments (7) (8): S susceptible, A asymptomatic infected, I symptomatic infected and R recovered. And other one including deaths (9)

Here we consider that a proportion p of susceptible people have no symptoms of the disease and the remaining proportion $(1 - p)$ have severe symptoms like high fever or pneumonia. In addition, we set different contact rate for asymptomatic and symptomatic people, but both of them have the same recovery rate.

$$\begin{aligned}
 \frac{dS}{dt} &= -(\beta_a A + \beta_i I)S \\
 \frac{dA}{dt} &= p(\beta_a A + \beta_i I)S - \gamma A \\
 \frac{dI}{dt} &= (1 - p)(\beta_a A + \beta_i I)S - \gamma I \\
 \frac{dR}{dt} &= \gamma A + \gamma I
 \end{aligned} \tag{7}$$

$$\begin{aligned}
\frac{dS}{dt} &= -(\beta_a A + \beta_i I)S \\
\frac{dA}{dt} &= p(\beta_a A + \beta_i I)S - \gamma A \\
\frac{dI}{dt} &= (1-p)(\beta_a A + \beta_i I)S - \gamma I - \mu I \\
\frac{dR}{dt} &= \gamma A + \gamma I
\end{aligned} \tag{8}$$

$$\begin{aligned}
\frac{dS}{dt} &= -(\beta_a A + \beta_i I)S \\
\frac{dA}{dt} &= p(\beta_a A + \beta_i I)S - \gamma A \\
\frac{dI}{dt} &= (1-p)(\beta_a A + \beta_i I)S - \gamma I - \mu I \\
\frac{dM}{dt} &= \mu I \\
\frac{dR}{dt} &= \gamma A + \gamma I
\end{aligned} \tag{9}$$

The parameters used in previous models are as follows

β_a = Asymptomatic contact rate \times Probability of transmission

β_i = Symptomatic contact rate \times Probability of transmission

p = Proportion of asymptomatic patients

γ = Recovery rate

μ = Death proportion

Using the library *PDEparams* for Python with normalized incidence data from China and establishing the initial conditions and bounds of parameters as in Table 3 we get the estimators showed in the same table.

	w/o Mortality compartment			With Mortality compartment	
Bounds	Init cond	Estimators w/o μ	Estimators with μ	Init cond	Estimators
$\beta_a \in (0.3, 2)$	$s = 0.9937$	$\beta_a = 0.3$	$\beta_a =$	$s = 0.9937$	$\beta_a = 0.3001$
$\beta_i \in (0.3, 2)$	$a = 0$	$\beta_i = 0.5762$	$\beta_i =$	$a = 0$	$\beta_i = 0.5761$
$p \in (0.1, 0.9)$	$i = 0.0063$	$p = 0.1$	$p = 0.1$	$i = 0.0063$	$p = 0.1$
$\gamma \in (0.07, 0.2)$	$r = 0$	$\gamma = 0.1453$	$\gamma = 0.1443$	$m = 0.0$	$\gamma = 0.1443$
$\mu \in (0.001, 0.3)$			$\mu = 0.001$	$r = 0$	$\mu = 0.001$

Table 3: SAIR, SAIRm, SAIMR China.

In the following graph we can see that all three models adjust to data with an error less than 0.0009

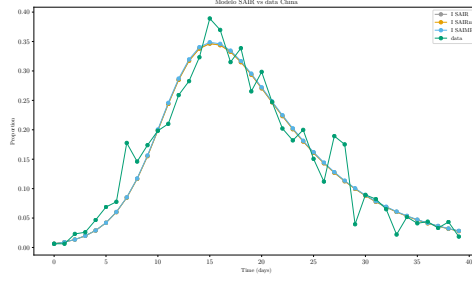


Figure 5: SAIR China.

3.1.4 SEAIR

For models (10) and (12) the population is divided into five compartments: S susceptible, E exposed, A asymptomatic infected, I symptomatic infected and R recovered. And for model (??) the compartment for deaths is added.

Unlike the SAIR model, any infected person go through a state of latency. However we consider again that a proportion p of susceptible people have no symptoms of the disease and also that symptomatic and asymptomatic people have different contact rate, but the same recovery rate.

$$\begin{aligned}
\frac{dS}{dt} &= -(\beta_a A + \beta_i I)S \\
\frac{dE}{dt} &= (\beta_a A + \beta_i I)S - \eta E \\
\frac{dA}{dt} &= p\eta E - \gamma A \\
\frac{dI}{dt} &= (1-p)\eta E - \gamma I \\
\frac{dR}{dt} &= \gamma A + \gamma I
\end{aligned} \tag{10}$$

$$\begin{aligned}
\frac{dS}{dt} &= -(\beta_a A + \beta_i I)S \\
\frac{dE}{dt} &= (\beta_a A + \beta_i I)S - \eta E \\
\frac{dA}{dt} &= p\eta E - \gamma A \\
\frac{dI}{dt} &= (1-p)\eta E - \gamma I - \mu I \\
\frac{dR}{dt} &= \gamma A + \gamma I
\end{aligned} \tag{11}$$

$$\begin{aligned}
\frac{dS}{dt} &= -(\beta_a A + \beta_i I)S \\
\frac{dE}{dt} &= (\beta_a A + \beta_i I)S - \eta E \\
\frac{dA}{dt} &= p\eta E - \gamma A \\
\frac{dI}{dt} &= (1-p)\eta E - \gamma I - \mu I \\
\frac{dM}{dt} &= \mu I \\
\frac{dR}{dt} &= \gamma A + \gamma I
\end{aligned} \tag{12}$$

The parameters used in previous models are as follows

- β_a = Asymptomatic contact rate \times Probability of transmission
- β_i = Symptomatic contact rate \times Probability of transmission
- p = Proportion of asymptomatic patients
- η = Latency rate
- γ = Recovery rate
- μ = Death proportion

Using the library *PDEparams* for Python with normalized incidence data from China and establishing the initial conditions and bounds of parameters as in Table 4 we get the estimators showed in the same table.

	w/o Mortality compartment			With Mortality compartment	
Bounds	Init cond	Estimators w/o μ	Estimators with μ	Init cond	Estimators
$\beta_a \in (0.3, 2)$	$s = 0.9937$	$\beta_a = 2.0$	$\beta_a =$	$s = 0.9937$	$\beta_a = 2.0$
$\beta_i \in (0.3, 2)$	$e = 0$	$\beta_i = 2.0$	$\beta_i =$	$e = 0$	$\beta_i = 2.0$
$\eta \in (0.07, 0.2)$	$a = 0$	$\eta = 0.2$	$\eta = 0.2$	$a = 0$	$\eta = 0.2$
$p \in (0.1, 0.9)$	$i = 0$	$p = 0.1$	$p = 0.1$	$i = 0.0063$	$p = 0.1$
$\gamma \in (0.07, 0.2)$	$r = 0$	$\gamma = 0.1515$	$\gamma = 0.0714$	$m = 0.0$	$\gamma = 0.1515$
$\mu \in (0.001, 0.3)$			$\mu = 0.0802$	$r = 0$	$\mu = 0.1452$

Table 4: SEAIR, SEAIRm, SEAIMR China.

In the following graph we can see that all three models adjust to data with an error less than 0.0009

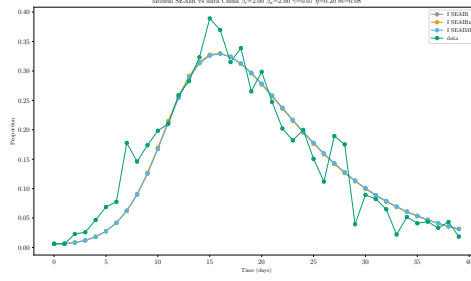


Figure 6: SEAIR China.

3.1.5 SIR with two types of susceptible (SDIR)

In this model we consider that there is a proportion of susceptible people who is more likely to get covid-19 because they suffer from other diseases like diabetes, high blood pressure, cancer or HIV. However both susceptible infected people pass into the same compartment of infected. As in previous models, (13) and (15) do not include a compartment for deaths but (??) do.

Therefore we define five compartments: S healthy susceptible, SD sick susceptible, I infected, M deaths and R recovered.

$$\begin{aligned}
 \frac{dS}{dt} &= -\beta SI \\
 \frac{dSd}{dt} &= p\beta SdI \\
 \frac{dI}{dt} &= \beta SI + p\beta SdI - \gamma I \\
 \frac{dR}{dt} &= \gamma I
 \end{aligned} \tag{13}$$

$$\begin{aligned}
 \frac{dS}{dt} &= -\beta SI \\
 \frac{dSd}{dt} &= p\beta SdI \\
 \frac{dI}{dt} &= \beta SI + p\beta SdI - \gamma I - \mu I \\
 \frac{dR}{dt} &= \gamma I
 \end{aligned} \tag{14}$$

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI \\
\frac{dSd}{dt} &= p\beta SdI \\
\frac{dI}{dt} &= \beta SI + p\beta SdI - \gamma I - \mu I \\
\frac{dM}{dt} &= \mu I \\
\frac{dR}{dt} &= \gamma I
\end{aligned} \tag{15}$$

The parameters involved in the model are as follows

β = Contact rate \times Probability of transmission
 p = Factor of susceptibility for sick people ($p > 1$)
 γ = Recovery rate
 μ = Death proportion

Using the library *PDEparams* for Python with normalized incidence data from China and establishing the initial conditions and bounds of parameters as in Table 5 we get the estimators showed in the same table.

	w/o Mortality compartment			With Mortality compartment	
Bounds	Init cond	Estimators w/o μ	Estimators with μ	Init cond	Estimators
$\beta_i \in (0.3, 2)$	$s = 0.9937$	$\beta_i = 0.5538$	$\beta_i = 0.5536$	$s = 0.9937$	$\beta_i = 0.5538$
$p \in (0.1, 0.9)$	$sd = 0$	$p = 1.4904$	$p = 1.9358$	$sd = 0$	$p = 1.3566$
$\gamma \in (0.07, 0.2)$	$i = 0.0063$	$\gamma = 0.1615$	$\gamma = 0.1075$	$i = 0.0063$	$\gamma = 0.1596$
$\mu \in (0.001, 0.3)$	$r = 0$		$\mu = 0.0539$	$m = 0.0$	$\mu = 0.0019$
				$r = 0$	

Table 5: SDIR, SDIRm, SDIMR China.

In the following graph we can see that all three models adjust to data with an error less than 0.0009

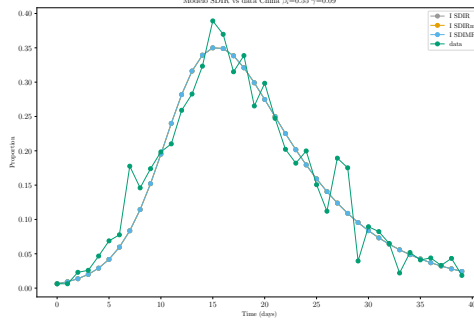


Figure 7: SDIR China.

3.1.6 SIR with two types of infected (SIGR)

Unlike the previous model, in this one we consider only one compartment of susceptible people, but two compartments of infected people. One of them for the proportion of people p with a weak immune system and the other one for the remaining infected people. Therefore we define four compartments: S susceptible, I infected with a good immune system, I_g infected with a weak immune system, R recovered.

As in previous models, (16) and (17) do not include a compartment for deaths but (18) do.

$$\begin{aligned}
 \frac{dS}{dt} &= -(\beta_i I + \beta_g I_g) S \\
 \frac{dI}{dt} &= (1-p)(\beta_i I + \beta_g I_g) S - \gamma I \\
 \frac{dI_g}{dt} &= p(\beta_i I + \beta_g I_g) S - \gamma I_g \\
 \frac{dR}{dt} &= \gamma(I + I_g)
 \end{aligned} \tag{16}$$

$$\begin{aligned}
 \frac{dS}{dt} &= -(\beta_i I + \beta_g I_g) S \\
 \frac{dI}{dt} &= (1-p)(\beta_i I + \beta_g I_g) S - \gamma I \\
 \frac{dI_g}{dt} &= p(\beta_i I + \beta_g I_g) S - \gamma I_g - \mu I_g \\
 \frac{dR}{dt} &= \gamma(I + I_g)
 \end{aligned} \tag{17}$$

$$\begin{aligned}
\frac{dS}{dt} &= -(\beta_i I + \beta_g Ig)S \\
\frac{dI}{dt} &= (1-p)(\beta_i I + \beta_g Ig)S - \gamma I \\
\frac{dIg}{dt} &= p(\beta_i I + \beta_g Ig)S - \gamma Ig - \mu Ig \\
\frac{dM}{dt} &= \mu Ig \\
\frac{dR}{dt} &= \gamma(I + Ig)
\end{aligned} \tag{18}$$

The parameters involved in the model are as follows

β_i = Contact rate of infected people with a good immune system \times Probability of transmission

β_g = Contact rate infected with a weak immune system \times Probability of transmission

p = proportion of people with a weak immune system

γ = Recovery rate

μ = Death proportion

Using the library *PDEparams* for Python with normalized incidence data from China and establishing the initial conditions and bounds of parameters as in Table 6 we get the estimators showed in the same table.

	w/o Mortality compartment			With Mortality compartment	
Bounds	Init cond	Estimators w/o μ	Estimators with μ	Init cond	Estimators
$\beta_i \in (0.3, 2)$	$s = 0.9937$	$\beta_i = 0.5763$	$\beta_i = 0.5854$	$s = 0.9937$	$\beta_i = 0.5766$
$\beta_g \in (0.3, 2)$	$i = 0.0063$	$\beta_g = 0.3005$	$\beta_g = 0.3$	$i = 0.0063$	$\beta_g = 0.3054$
$p \in (0.1, 0.9)$	$id = 0.0063$	$p = 0.1$	$p = 0.1$	$id = 0$	$p = 0.1$
$\gamma \in (0.07, 0.2)$	$r = 0$	$\gamma = 0.1453$	$\gamma = 0.1445$	$m = 0.0$	$\gamma = 0.1452$
$\mu \in (0.001, 0.3)$			$\mu = 0.3$	$r = 0$	$\mu = 0.0196$

Table 6: SIGR, SIGRm, SIGMR China.

In the following graph we can see that all three models adjust to data with an error less than 0.0009

3.2 Comparing models

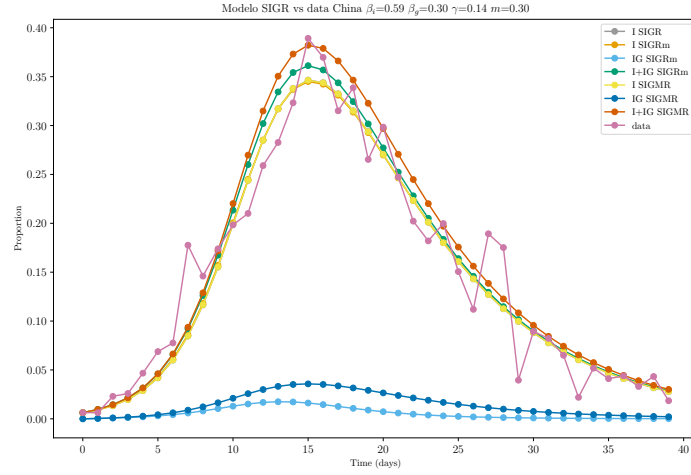


Figure 8: SIGR China.

3.2 Comparing models

Plotting all graphs together we get the following graphs

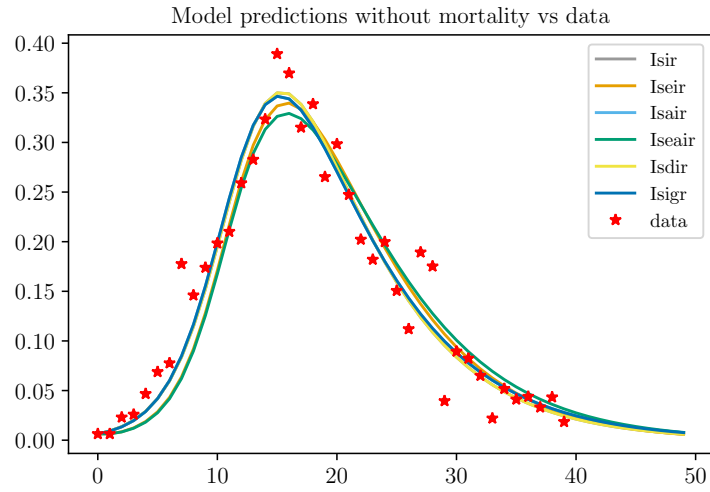


Figure 9: Models without mortality

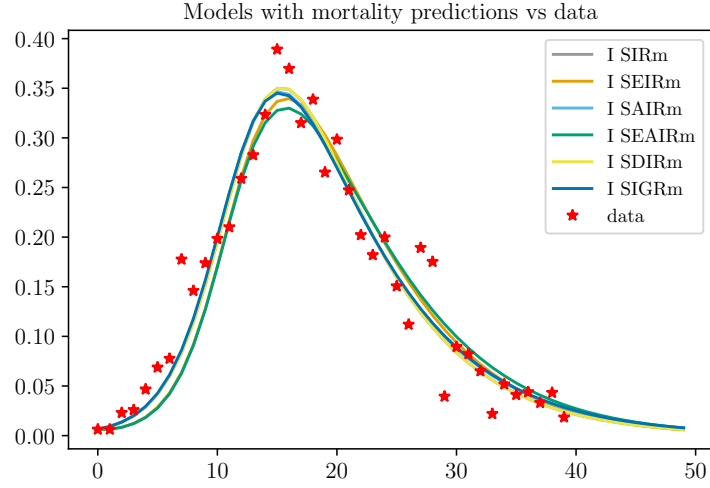


Figure 10: Models with mortality parameter

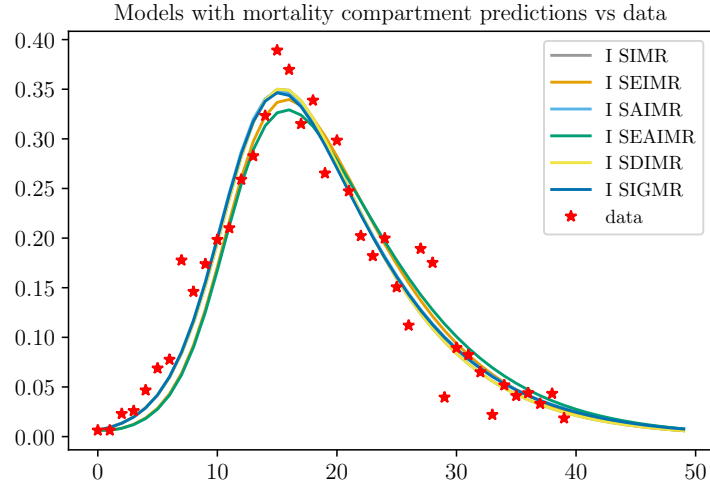


Figure 11: Models with mortality compartment

Calculating the AIC value for each model with mortality either with mortality parameter or compartment regard we get the followings AIC value of each model considering mortality:

Im	Iseirm	Isairm	Iseairm	Isdirm	Isigrm
-127.80834908	-120.46250425	-122.617106	-113.87726642	-125.33205175	-122.75223531

Figure 12: Models without deaths compartment

Im2	Iseimr	Isaimr	Iseaimr	Isdimr	Isigmr
-127.80834546	-120.46250354	-122.5762573	-113.4258779	-125.33215443	-122.62821313

Figure 13: Models with deaths compartment

With respect to these values, we concluded that the best models to approximate the data are SIRM (2), SIMR (3) and SDIRM (15). Therefor we use the values of the parameters estimated with these models to adjust the Mexico database in the next section.

4 COVID-19 in Mexico

Currently the outbreak of COVID-19 epidemic in Mexico has begun. Taking the database available in the webpage <https://www.ecdc.europa.eu/en/publications-data> we can apply the mathematical models of the previous section for Mexico and compare the resulting parameters with the corresponding ones for China, as well as visualize possible scenarios of the epidemic.

However for this approach we use the library *PDEparams* to estimate all parameters in either models that include mortality as a parameter or not.

The database consist in the daily incidence of COVID-19 since the first day infection was detected in Mexico until April 1st.

Initial conditions, bound of parameters, estimators and error for each model are shown in the following tables.

Initial conditions	Bounds of the parameters	Estimators w/o μ	Estimators with μ
$S = 1 - \frac{2}{10^9}$	$\beta \in (0.3, 2)$	$\beta = 0.357618$	$\beta = 0.482471$
$I = \frac{2}{10^9}$	$\gamma \in (1/14, 1/5)$	$\gamma = 0.169533$	$\beta = 0.102204$
$R = 0$	$\mu \in (0.001, 0.3)$	NA	$\mu = 0.192145$
Error w/o μ:	$6.157570744838375e - 16$	Error with μ:	$6.157552695786656e - 16$

Table 7: Estimators for Mexico using models (1) and (2).

Model's Solutions using estimated parameters for infected compartment adjust data in the following way.

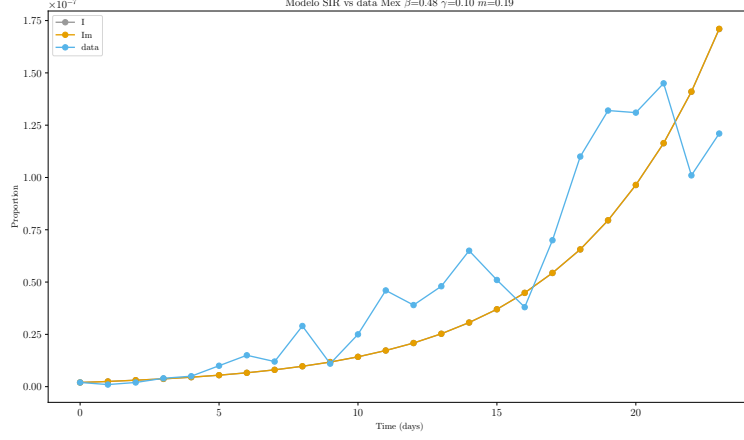


Figure 14: SIR and SIRm for Mexico.

Initial conditions	Bounds of the parameters	Estimators w/o μ	Estimators with μ
$S = 1 - \frac{2}{10^9}$	$\beta \in (0.3, 2)$	$\beta = 0.568903$	$\beta = 0.564751$
$E = 0$	$\eta \in (1/14, 1/5)$	$\eta = 0.192063$	$\eta = 0.199257$
$I = \frac{2}{10^9}$	$\gamma \in (1/14, 1/5)$	$\gamma = 0.071653$	$\gamma = 0.072731$
$R = 0$	$\mu \in (0.001, 0.3)$	NA	$\mu = 0.002483$
Error w/o μ:	$7.233848374790644e - 16$	Error with μ:	$7.225348313332751e - 16$

Table 8: Estimators for Mexico using models (4) and (5).

Model's Solutions using estimated parameters for infected compartment adjust data in the following way.

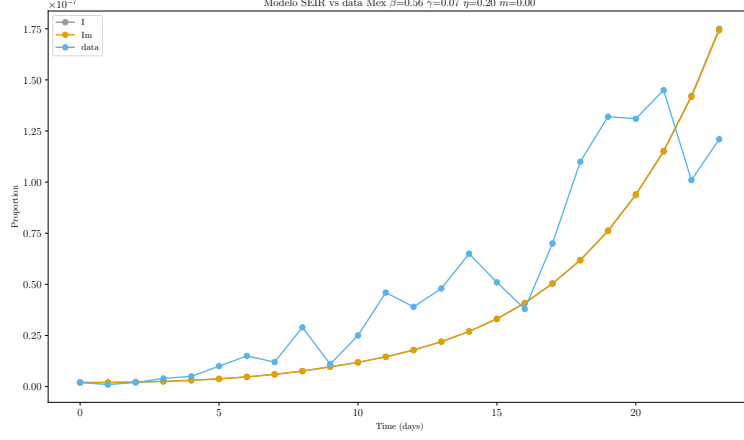


Figure 15: SEIR and SEIRm for Mexico.

Initial conditions	Bounds of the parameters	Estimators w/o μ	Estimators with μ
$S = 1 - \frac{2}{10^9}$	$\beta_a \in (0.3, 2)$	$\beta_a = 0.308686$	$\beta_a = 0.313312$
$A = 0$	$\beta_i \in (0.3, 2)$	$\beta_i = 0.391231$	$\beta_i = 0.408574$
$I = \frac{2}{10^9}$	$p \in (0.1, 0.9)$	$p = 0.10095$	$p = 0.100788$
$R = 0$	$\gamma \in (1/14, 1/5)$	$\gamma = 0.19093$	$\gamma = 0.194483$
	$\mu \in (0.001, 0.3)$	NA	$\mu = 0.013729$
Error w/o μ:	$6.401122922791813e - 16$	Error with μ:	$6.411750375344447e - 16$

Table 9: Estimators for Mexico using models (7) and (8).

Model's Solutions using estimated parameters for infected compartment adjust data in the following way.

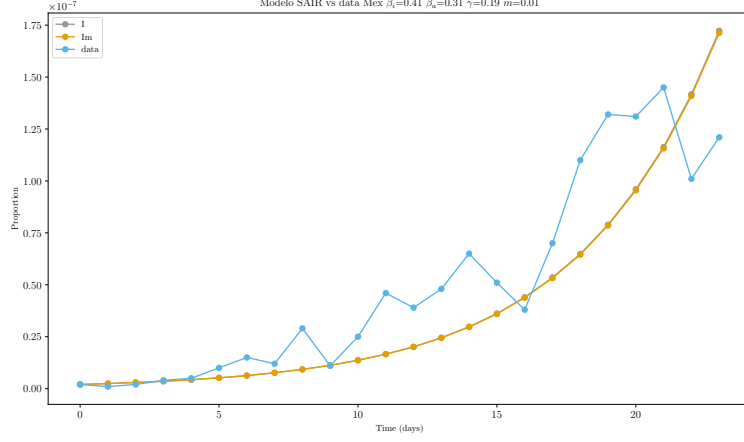


Figure 16: SAIR and SAIRm for Mexico

Initial conditions	Bounds of the parameters	Estimators w/o μ	Estimators with μ
$S = 1 - \frac{2}{10^9}$	$\beta_a \in (0.3, 2)$	$\beta_a = 0.314711$	0.328644
$E = 0$	$\beta_i \in (0.3, 2)$	$\beta_i = 0.743561$	0.735649
$A = 0$	$\eta \in (1/14, 1/5)$	$\eta = 0.197463$	0.199694
$I = \frac{2}{10^9}$	$p \in (0.1, 0.9)$	$p = 0.100174$	0.105928
$R = 0$	$\gamma \in (1/14, 1/5)$	$\gamma = 0.138006$	0.13049
	$\mu \in (0.001, 0.3)$	NA	$\mu = 0.005156$
Error w/o μ:	$7.379813707940692e - 16$	Error with μ:	$7.381321589506402e - 16$

Table 10: Estimators for Mexico using models (10) and (12)

Model's Solutions using estimated parameters for infected compartment adjust data in the following way.

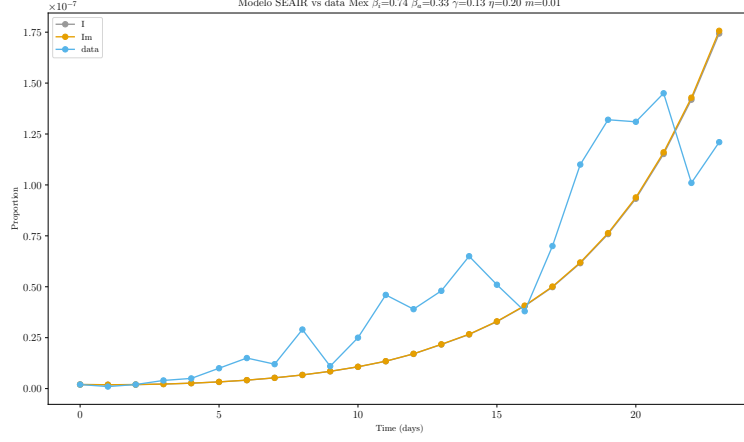


Figure 17: SEAIR and SEAIRm for Mexico.

Initial conditions	Bounds of the parameters	Estimators w/o μ	Estimators with μ
$S = 1 - \frac{2}{10^9}$	$\beta \in (0.3, 2)$	$\beta = 0.361629$	0.486852
$Sd = 0$	$p \in (1, 2)$	$p = 1.666214$	1.759334
$I = \frac{2}{10^9}$	$\gamma \in (1/14, 1/5)$	$\gamma = 0.173491$	0.166815
$R = 0$	$\mu \in (0.001, 0.3)$	NA	$\mu = 0.131919$
Error w/o μ:	6.157563964021295e - 16	Error with μ:	6.157551753201298e - 16

Table 11: Estimators for Mexico using models (13) and (15)

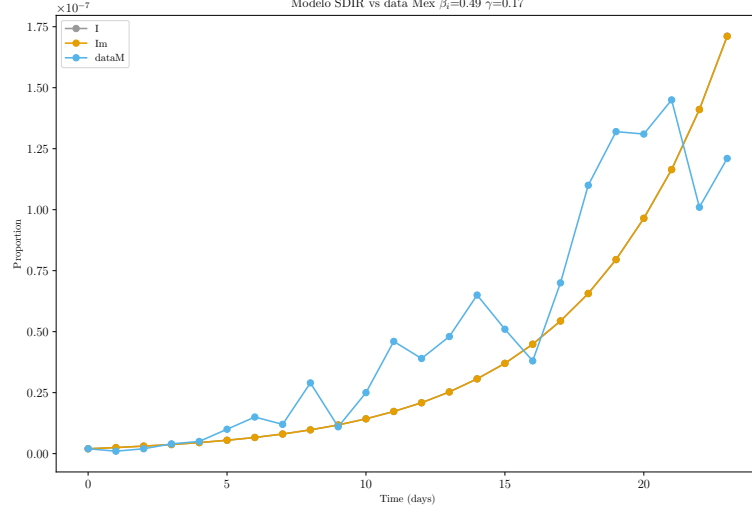


Figure 18: SDIR and SDIRm for Mexico.

Initial conditions	Bounds of the parameters	Estimators w/o μ	Estimators with μ
$S = 1 - \frac{2}{10^2}$	$\beta_i \in (0.3, 2)$	$\beta_i = 0.397098$	$\beta_i = 0.316651$
$Sd = 0$	$\beta_g \in (0.3, 2)$	$\beta_g = 0.314594$	$\beta_i = 0.330305$
$I = \frac{2}{10^9}$	$p \in (0.1, 0.9)$	$p = 0.100354$	$p = 0.100375$
$R = 0$	$\gamma \in (1/14, 1/5)$	$\gamma = 0.196915$	$gamma = 0.113718$
	$\mu = (0.001, 0.3)$	NA	$\mu = 0.246623$
Error w/o μ:	$6.432568006042808e - 16$	Error with μ:	$6.103887138175697e - 16$

Table 12: Estimators for Mexico using models (16) and (17)

4.1 Comparing models

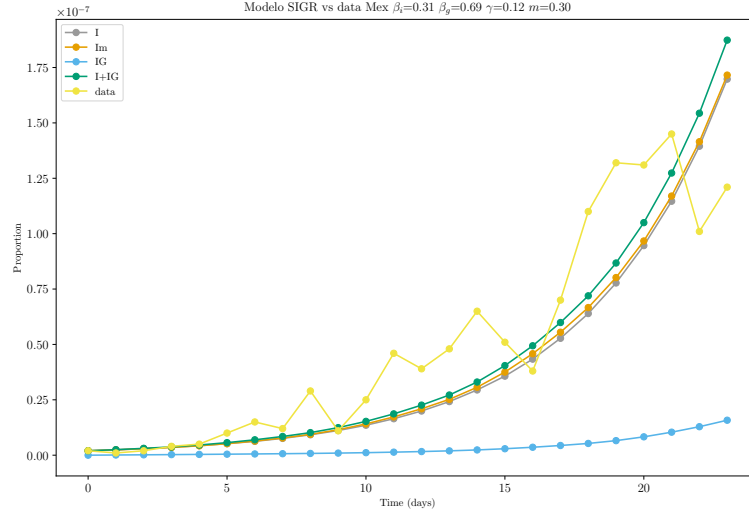


Figure 19: SGR and SIGRm for Mexico.

4.1 Comparing models

Assuming all parameters showed above we can plot the solutions until day 200 and see the follow behaviour.

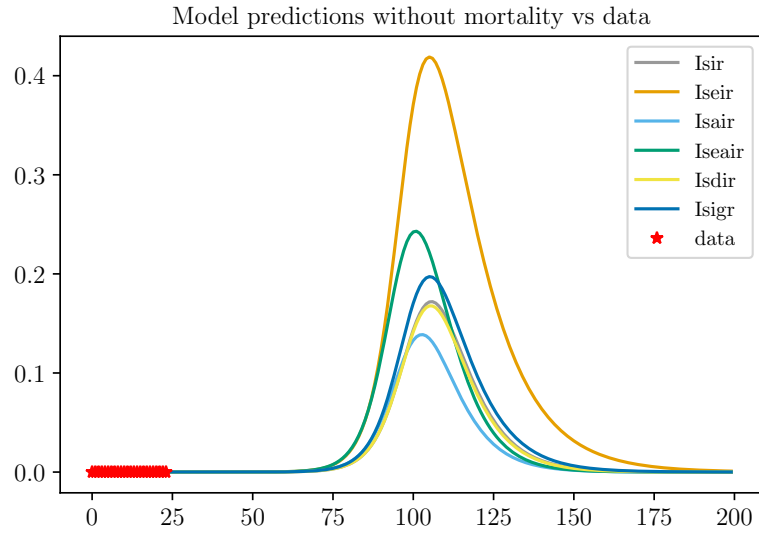


Figure 20: Solutions behaviour of models without mortality.

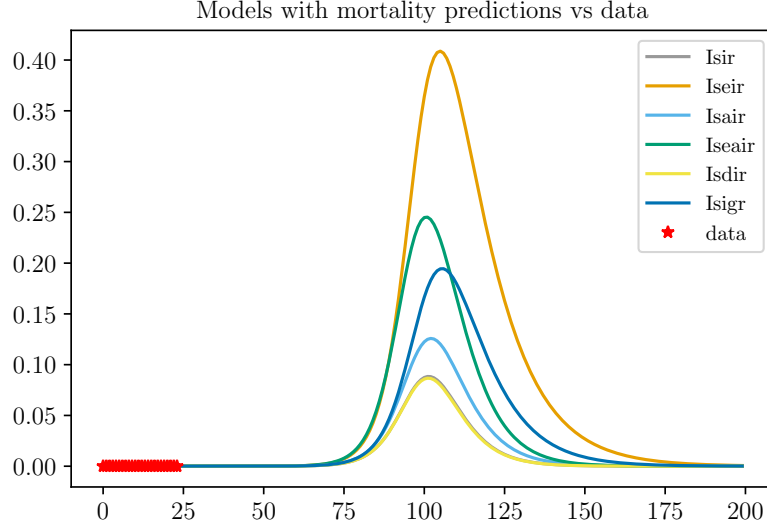


Figure 21: Solutions behaviour of model without mortality parameter

It is necessary to emphasize that because of in Mexico the stage of the epidemic has not yet reached a peak, then the estimates for mortality and recovery rates tend to vary considerably among models and therefore the behavior of the solutions looks variable.

4.2 Conclusions

For the models with mortality compartments we obtained the following:

- For the SIR models the estimation rates are $\beta \sim 0.55$, $1/\gamma \sim 6.25$ d and $\mu \sim 0.086$
- For the SEIR models the estimation rates are $\beta \sim 0.2$, $1/\eta \sim 5$, $1/\gamma \sim 6.25$ d and $\mu \sim 0.084$
- For the SAIR models the estimation rates are $\beta_a \sim 0.3$, $\beta_i \sim 0.57$, asymptomatic proportion $p = 0.1$, $1/\gamma \sim 7.14$ d and $\mu \sim 0.001$
- For the SEAIR models the estimation rates are $\beta_a \sim 2$, $\beta_i \sim 2$, asymptomatic proportion $p = 0.1$, $1/\eta = 5$ d, $1/\gamma \sim 6.6$ d and $\mu \sim 0.14$
- For the SDIR models the estimation rates are $\beta_i \sim 0.5$, $1/\gamma \sim 6.2, 6.6$ d and $\mu \sim 0.0019$

In summary, the transmission parameter varies from about 0.5 to 2 depending on the models structure, whereas the infectious periods range is about 5 to 7 days, whereas latency period is about 5 days and mortality rates varies from 0.001 to 0.14. The interpretation of these estimations requires further discussion.

4.3 Discussion

Since data bases from China were reported as number of cases, we calculate incidence from these data to estimate the indicated parameters. We explore different compartmental structures to estimate different parameters which allow us to explore further scenarios using estimated parameters from the best models and incorporate different assumptions regarding other parameters such as proportion of asymptomatic individuals, susceptible types of people due to chronic diseases and severity of infections.

An important remark is that although the accuracy for data from both China and Mexico, predictions for Mexico number of cases strongly depends on model assumptions since these data contains information for the exponential growth. This model comparison allows us to show examples in which there are good accuracy but predictions rely on more assumptions to be explored.

Possible extensions for the modelling approaches:

1. Tests hypothesis such as assuming 80-85 % of infections are asymptomatic, or 15% will require hospitalization to explore possible outcomes using asymptomatic modeling (SAIR,SEAIR) , susceptible types (SDIR) and types of infection symptoms (SIGR) models.
2. Pose models including quarantine

Quarantine model: quarantine susceptibles and severe infectives

$$\begin{aligned}
 \frac{dS}{dt} &= -(\beta_1 I + \beta_2 G)S - qS \\
 \frac{dI}{dt} &= (1-p)(\beta_1 I + \beta_2 G)S - \gamma I - qI \\
 \frac{dG}{dt} &= p(\beta_1 I + \beta_2 G)S - \gamma G - mG \\
 \frac{dQ}{dt} &= qS + qI \\
 \frac{dM}{dt} &= mG \\
 \frac{dR}{dt} &= \gamma I
 \end{aligned} \tag{19}$$

Material and Methods

- Mexico Data from [ECDC, 2020]
- Parameter estimation is performed using the Differential Evolution (PDE) algorithm .
- Solver for ordinary differential equations is performed using odeint from python.
- Description of the methodology for comparing the models using The Akaike information criterion (AIC) is described in [Esteban A. Hernandez-Vargas,]

Author contributions

- Model structured discussed by NLGM and RCM
- Simulations for models with incidence data from China and Mexico performed by NLGM

REFERENCES

- Simulations for models with incidence and incorporating mortality data from China and Mexico performed by RCM
- Report written mostly by RCM
- Discussion by all authors

References

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[WHO, 2020] WHO (2020). WHO covid.