Chapter 1
Lifting Lockdown Control Measure Assessment: From Finite to Infinite-dimensional Epidemic Models for COVID-19*

Redouane Qesmi and Aayah Hammoumi

Abstract The main focus of this chapter is on public health control strategies which are currently the main way to mitigate COVID-19 pandemic. We introduce and compare compartmental models of increasing complexity for COVID-19 transmission to describe dynamics of the disease spread. We begin by considering an SEAIR model including basic characteristics related to COVID-19. Next, we shall pay attention to age-structure modeling to emphasis the role of age-group individuals on the disease spread. A Model with constant delay is also formulated to show the impact of the latency period on the severity of COVID-19. Since there is evidence that for COVID-19 disease, important relationships exist between what is happening in the host and what is occurring at the population level, we shall link the basic model to in-host dynamics through the so-called threshold-type delay models. Finally, we will include demographic effects to the most complex models and we will conduct rigorous bifurcation analysis to quantify possible factors responsible for disease progression.

1.1 Introduction

The SARS-CoV-2, designated as Severe Acute Respiratory Syndrome CoronaVirus-2, is a causative agent of COVID-19 disease that first emerged in China on December 2019 [28]. Up to date, 213 countries and territories are affected by the disease, with

Redouane Qesmi
Superior School of Technology, Sidi Mohamed Ben Abdellah University, Fez 30000, Morocco, e-mail: redouane.qesmi@usmba.ac.ma

Aayah Hammoumi
Department of Biology, Cadi Ayyad University, Semlalia, Marrakech 40000, Morocco e-mail: a.hammoumi@uca.ma

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nearly 19 million confirmed cases and more than 700,000 deaths. Unfortunately, there are no current effective therapeutic agents or vaccines for treatment of COVID-19 and, consequently, public health control strategies that diminish contact between infectious and susceptible individuals are actually the main way to contain and mitigate the pandemic [36]. Examples of such a control include the personal protective measures (e.g. hand hygiene, cough or sneeze etiquette and face coverings), social distancing measures (e.g increasing physical distance from other people, avoiding social gathering and stay at home) and environmental surface cleaning [12]. However, despite health control interventions seem to be successful in reducing the spread of the pandemic, they are also responsible of global economic crisis. It is estimated that COVID-19 could cost the global economy more than $10 trillion [1, 21]. Millions of individuals throughout the world have been forced to reduce their working hours or have lost their jobs and around 900 million students are affected by national school closures [30, 33]. Furthermore, because of the isolation and the increase of social class inequalities, the lockdown is badly lived by the majority of children and adults who have developed mental health disorders and familial problems [1, 8, 21]. Although many information related to COVID-19, such as its potential to reoccur, remain unclear, lifting lockdown measure became an urgent need to avoid the worsening of the global crisis caused by COVID-19 [22]. Governments around the world encountered serious difficulties to adopt the best lockdown lifting strategy balancing between economy recovery and health protection of citizens.

Fortunately, since the beginning of the outbreak of COVID-19, mathematical modeling proved to be an effective tool to predict the course as well as the severity of the epidemic and to help decision makers to evaluate the effectiveness of health control measures (See [4, 13, 15, 20, 32] and references therein). Generally, at the beginning of an emergent epidemic, the novel pathogenic agent lacks detailed knowledge. Mathematicians begin by using simplest compartmental models to estimate the key epidemiological parameters (such as the basic reproduction number $R_0$, peak time, peak size, latency period, infectious period, etc) which are necessary to set up public health strategies and monitor the disease progression [3]. Most such models consider individuals in a closed population that are classified according to their disease status: susceptible (S), latent or Exposed (E), infectious (I) and recovered (R). These basic models have the great advantage of being easy to investigate but, on the other hand, often oversimplify the existing complexity of disease processes which underestimate or overestimate the magnitude of the disease spread. However, more complex models can be considered in case the scientists provide more epidemiological evidences leading to detailed knowledge of Sars-Cov-2 pathogenic mechanism and its mode of transmission. Even if they are more difficult to analyze and need more detailed data, these models could be more realistic since they take into account more realistic epidemiological properties such as the heterogeneity of disease transmission, age-subgroups, latent periods and so on. The purpose of this chapter is to consider and compare different deterministic compartmental models of increasing complexity that will be useful to clarify how Sars-CoV-2 spread within individuals while considering the relaxation of the compulsory lockdown to prevent dissemination of the COVID-19 disease.
The main contribution of this chapter is organized as follows. In Section 1.3, we will consider and investigate an extended basic SEAIR model which is widely used for COVID-19 disease. Indeed, this model takes into account the standard epidemiological states such as the exposed individuals to the Sars-CoV-2 virus which are infected but cannot transmit the virus to others. In Section 1.4, we consider an extension of the previous model with particular focus on an identified route of COVID-19 transmission from children to adults and vice versa. In other words, we present a discrete age-structured model, by separating the population into two different age-subgroups with different contact rates, to look at the heterogeneity of COVID-19 transmission within a population. Indeed, it is proved that children are less affected by Sars-Cov-2 than adults and play a minor role in disease transmission [2, 17]. Seniors and person with existing chronic medical conditions develop more severe form of disease and are more likely to die [34]. Furthermore, individuals with different ages may also have different behaviors and behavioral changes which are crucial in the assessment of control scenarios targeted at particular groups, such as reopening schools or relaunch of economic activities. The impact of the latent period on disease transmission is also evaluated in Section 1.5 by incorporating a time delay to the basic SAIR model instead of considering the latent stage as a model component. In Section 1.6, we examine a threshold-type delay model by incorporating a series of smaller Sars-CoV-2 viral loads, due to close contact with infectious individuals, into the within-host virus dynamics. This type of model can be used for example to study the impact of COVID-19 exposure to health care workers who are daily in close contacts with COVID-19 patients, visitors or co-workers in a population and are more likely to be infected [2]. In Section 1.7, we include vital dynamics to the constant and threshold-type delay models by assuming that the COVID-19 disease could persist for a long period. Indeed, with the evidence of sensibility of Sars-CoV-2 to climatic factors such as temperature and humidity, scientists think that the COVID-19 allows a seasonal cycle and could reduce with climate change. But, even with the arrival of the warm weather, the disease still evolved and could persist for several months or years. This demonstrates that the climate change is not the main parameter which influences the disease transmission but also, the people’s behavior, the low immunity of individuals to a novel coronavirus and the immunity period (the amount of time that people remain immune after infection) [9, 11]. We will then conduct rigorous qualitative analysis including bifurcation investigation of both models with demographic effect to quantify possible factors responsible for disease progression and highlight long term qualitative behavior of COVID-19 spread. Next, in order to help scientists to avoid major blunders and generate models that fit the data reasonably accurately, we compare in Section 1.8 the proposed models to identify which one best fits the reported data and provide a better prediction for COVID-19. Results of our models will help to tackle health concerns that are of great importance and will draw of the hospitals research and surveillance data to create, optimize, and parameterize disease models, focusing on COVID-19.
1.2 Data Collection

The data of reported symptomatic infectious cases is collected each day at 11 pm from the official Coronavirus Portal of Morocco [27]. Data information covers the cumulative number of reported cases from March 2nd to June 10th, 2020. The data from March 2nd to March 20th (first day of lockdown measure) are used to estimate the basic reproduction number and adjust the investigated models to become closer to reality, while data from March 21st to June 10th (last day of lockdown measure) are used to adjust the models and estimate the lockdown rate during this period of lockdown.

1.3 Basic COVID-19 Model

The population, with size $N$, considered in this basic model is stratified into seven disease status. Individuals are classified as susceptible ($S$), exposed noninfectious ($E$), asymptomatic infectious ($A$), unreported symptomatic infectious ($I_u$), reported symptomatic infectious or hospitalized ($H$), recovered ($R$) and dead ($D$). We formulate the model to describe the course of COVID-19 epidemic under the assumptions:

1. Reported symptomatic infectious individuals are hospitalized and can not contact susceptibles anymore.
2. As confirmed by Rothe et al. [24], asymptomatic individuals can infect susceptible individuals.
3. Confined asymptomatic and confined unreported individuals can still spread the virus to their families.
4. Exposed infected individuals can not immediately spread the virus to other individuals.
5. As proved by MacIntyre in [18], asymptomatic and symptomatic infectious individuals share the same infection probability.

Taking account of the previous assumptions, the dynamics of COVID-19 can be described as follows: Individuals are confined at rate $\delta$. Unconfined (resp. confined) susceptibles $(1-p)S$ (resp. $(pS)$) contacted with either unreported symptomatic ($I_u$) or asymptomatic infectious individuals ($A$) are infected with infection probability, $\beta_N$ (resp. $\beta_c$), and move to the exposed infected class ($E$). Exposed individuals then become asymptomatic infectious at rate $k$. After an average period $1/\delta$ days the asymptomatic infectious individuals ($A$) become symptomatic and proceed either to the unreported symptomatic infectious ($I_u$), at rate $\delta_1$, or to the reported symptomatic infectious ($H$) at rate $\delta_2$ with $\delta = \delta_1 + \delta_2$. Once becoming symptomatic, individuals of class $I_u$ and $H$ remain symptomatic for $1/\mu$ days on average before they are recovered or dead at rate $d$. The parameter $\gamma$ corresponds to the lifting rate while parameter $\theta$ corresponds to the contact reduction, due to wearing masks, washing hands, and social distancing practices of unconfined individuals. The general basic
model equations including parameters control is given as follow

\[
\begin{align*}
\frac{dS}{dt} &= -((1 - \gamma) p\beta_c + (1 - \theta) (1 - (1 - \gamma) p) \beta_N) S(t) (A(t) + I_u(t)) / N, \\
\frac{dE}{dt} &= ((1 - \gamma) p\beta_c + (1 - \theta) (1 - (1 - \gamma) p) \beta_N) S(t) (A(t) + I_u(t)) / N - kE, \\
\frac{dA}{dt} &= kE - \delta A(t), \\
\frac{dI_u}{dt} &= \delta_1 A(t) - \mu I_u(t) - dI_u(t), \\
\frac{dH}{dt} &= \delta_2 A(t) - \mu H - dH, \\
\frac{dR}{dt} &= \mu (H + I_u), \\
\frac{dD}{dt} &= d(H + I_u).
\end{align*}
\]  

(1.1)

1.3.1 Reproduction Numbers

The basic reproduction number, \( R_0 \), is the average number of secondary infections produced when one infectious individual is introduced into a host susceptible population. This quantity determines whether a given disease may spread, or die out in a population. To compute this number, we assume that \( p = \theta = \gamma = 0 \) and we apply the next generation matrix method in [31]. We obtain

\[
R_0 = \frac{(a + k) (a + \delta) (a + \mu + d)}{k (\delta_1 + a + \mu + d) (1 + \frac{\delta_1}{\delta})}
\]

(1.2)

where \( a \) is an estimated constant given in Subsection 1.3.2. Here, \( R_0 \) can be explained as follows: Assume that one asymptomatic infectious individual is introduced into the susceptible population. This asymptomatic individual produces, on average, \( \beta_N S_0 \frac{1}{\delta} \) asymptomatic individuals during his average lifespan \( 1/\delta \). These asymptomatic individuals then become unreported symptomatic infectious individuals over their lifespan \( 1/\delta \) at a rate \( \delta_1 \) and then each infectious symptomatic produces, on average, \( \beta_N S_0 \frac{1}{\mu} \) asymptomatic individuals during his lifespan \( 1/\mu \).

Let us show the formula of \( R_0 \). The linearized system related to infectious individuals, around \( (S_0, 0, 0) \), of system (1.1) is given by
model given by \( SPSS \) software (Statistical Package for the Social Sciences) we found that exponential is given, for \( A(t) \) and we follow the procedure by [15]. The cumulative reported infectious population increases slowly and then accelerates rapidly with time. Hence, we will use exponential regression with an exponential function that best fits the data, from March 2nd to March 20 (before the start of lockdown).

For the estimation of \( R_c \) whether a control policy, such as lockdown, lifting, behavioral practices, etc, will be efficient to decrease the number of secondary infections to be less than one. Computation method of \( R_c \) is similar to the one of \( R_0 \) and leads to the following formula

\[
R_c = (1 - \gamma) \mu \beta_c + (1 - \theta) (1 - (1 - \gamma) \rho) \beta_N) \left( \frac{1}{\delta} + \frac{\delta_1}{\delta} \right).
\]

1.3.2 Parameter and Initial Data Estimation

To estimate the model parameters we will consider two different stages. The first stage is between the beginning of the COVID-19 epidemic and the first time of containment control (i.e \( p = 0 \) and \( \theta = 0 \)) for which we will estimate the initial data of the model, the parameters related to infection and the basic reproduction number. The second stage will be during the lockdown period (\( \gamma = 0 \) and \( \theta = 0 \)) for which we will estimate the lockdown rate.

Since the first and the only symptomatic infectious individual is reported on March 2nd, 2020, which corresponds to \( t = 0 \), then \( H(0) = 1 \), \( R(0) = 0 \) and \( D(0) = 0 \). For the estimation of \( \beta_N \), \( E(0) \), \( A(0) \) and \( I_u(0) \) we will use the data of cumulative reported cases collected from March 2nd to March 20 (before the start of lockdown) and we follow the procedure by [15]. The cumulative reported infectious population is given, for \( t \geq 0 \), by \( F(t) = \delta_2 \int_0^t A(s)ds + 1 \). It is obvious that cumulative reported infectious population increases slowly and then accelerates rapidly with time. Hence, we will use exponential regression with 95% of confidence level to find an exponential function that best fits the data, from March 2nd to June 10th. Using SPSS software (Statistical Package for the Social Sciences) we found that exponential model given by \( be^{at} \) with \( a = 0.263 \) with confidence interval \( CI (0.229 - 0.297) \) and
\( b = 0.507 \) with CI \((0.3444 - 0.7475)\) fits well the data with a correlation coefficient given by \( R = 0.97 \). It follows from \( F(t) = \delta_2 \int_0^t A(s) ds + 1 = be^{at} \) that

\[
A(t) = \frac{ba}{\delta_2} e^{at}.
\]  

(1.3)

Since the initial susceptible population is not dramatically affected in the early phase of the epidemic, we will assume that \( S(t) \approx S(0) \). Let \( S_0 := S(0), E(0) := E_0, A(0) := A_0 \) and \( I_u(0) := I_0 \). From the second and the third equations of system (1.1) we obtain after simplification

\[
\left( \frac{a + \delta}{k} + (a + \delta) \right) A(t) = \beta_N S(0) \left( A(t) + I_u(t) \right),
\]

(1.4)

\[
E(t) = E_0 e^{at} \quad \text{and} \quad I_u(t) = I_0 e^{at},
\]

(1.5)

where

\[
E_0 = \frac{a + \delta}{k} \frac{ba}{\delta_2} \quad \text{and} \quad I_0 = \frac{ba \left( \frac{a + \delta}{k} + (a + \delta) - \beta_N S(0) \right)}{\delta_2 \beta_N S_0}.
\]

(1.6)

Now, using formulas (1.5) and the third equation of system (1.1), we obtain after simplification

\[
aE_0 = \beta_N S_0 \left( A_0 + I_0 \right) - kE_0 \]

(1.7)

and

\[
\alpha I_0 = \delta_1 A_0 - (\mu + d)I_0.
\]

(1.8)

Solving equations (1.6), (1.7) and (1.8) for \( \beta_N \) and \( I_0 \) lead to

\[
\beta_N = \frac{(a + k) (a + \delta) (a + \mu + d)}{k (\delta_1 + a + \mu + d)} \quad \text{and} \quad I_0 = \frac{\delta_1}{a + \mu + d} A_0.
\]

(1.9)

To estimate the transmission rate, \( \beta_c \), and the lockdown rate, \( \rho \) during the lockdown period, we assume that \( \gamma = 0 \) and \( \theta = 0 \) and we use the nonlinear least squares solver “lsqcurvefit” in MATLAB R2019b software. The values of the estimated parameters are summarized in Table 1.1.

Define the sum of squared residuals (SSR) as

\[
SSR = \frac{1}{n} \sum_{i=1}^{n} \left( \delta_2 A(t) - \text{Newcase}(i) \right)^2
\]

where \( \text{Newcase}(i) \) is the number of new reported cases on the day \( i \) and \( n \) is the number of collected new cases. This number measures the discrepancy between the data and the estimation model of new reported cases per day and will serve us to compare the suggested models of this chapter. A small SSR indicates a better fit of the model to the data. A computation of this measure for model (1.1) leads to \( SSR_{\text{basic}} = 93.4 \).
Table 1.1 Parameter definitions and values of model (1.1).

| Symbol | Definition | Parameter value | Confidence interval | Reference |
|--------|------------|-----------------|---------------------|-----------|
| $S(0)$ | Initial susceptible population | 35865191 | | [5] |
| $E(0)$ | Initial exposed noninfectious population | 0.3175 | 0.8 – 1.37 | Estimated |
| $A(0)$ | Initial asymptomatic population | 11.9921 | 9.42 – 15.03 | Estimated |
| $I_a(0)$ | Initial unreported symptomatic population | 0.8414 | 0.592 – 1.3 | Estimated |
| $H(0)$ | Initial reported symptomatic population | 1 | | See text |
| $R(0)$ | Initial recovered population | 0 | | See text |
| $D(0)$ | Initial dead population | 0 | | See text |
| $\beta_N$ | Infection rate for unconfined population | 2.87 | 0.5 – 4.2 | Estimated |
| $\beta_c$ | Infection rate for confined population | 0.57 | 0.1 – 0.84 | Estimated |
| $1/\delta$ | Asymptomatic duration | 6 days | | [28] |
| $k$ | Exposed noninfectious rate | 3 | 2 – 4 | See text |
| $\delta_1$ | Asymptomatic unreported rate | 0.017 per day | | Assumed |
| $\delta_2$ | Symptomatic reported rate | 0.15 per day | | Assumed |
| $1/\mu$ | Symptomatic duration | 14 days | | [35] |
| $p$ | Proportion of lockdown | 0.7 | 0.5 – 0.76 | Estimated |
| $R_0$ | Basic reproduction number | 2.88 | 2.55 – 2.99 | Estimated |

1.4 Discrete Age Structure COVID-19 Model

Basic discrete age-structured compartmental models seem to be more appropriate for COVID-19 disease since it is claimed that adults have a greater risk of transmitting SARS-CoV-2 virus than children do toward susceptibles (See Section 1.1). This suggest that in order to give more appropriate description of COVID-19 transmission it is important to separate the population into two different age-subgroups.

The population considered in this section is stratified into two age categories and ten disease status. Individuals are classified as susceptible children ($T$), susceptible adult ($S$), exposed noninfectious ($E_T$), exposed noninfectious adult ($E_a$), asymptomatic infectious adult ($A$), asymptomatic infectious children ($B$), unreported symptomatic infectious ($I_a$), hospitalized symptomatic infectious ($H$), recovered individuals ($R$) and dead individuals ($D$). We assume that infected children do not show symptoms and can still transmit the disease. COVID-19 disease dynamics can be described as follows: Let $\beta^i$ be the transmission rate from infectious individuals to confined susceptible individuals and $\beta^N$ be the transmission rate from infectious individuals to unconfined susceptible individuals. Then, for $i \in \{\chi, N\}$, susceptibles adults ($S$) (resp. susceptible children ($T$)) are infected through contact with infectious adults ($A + I_a$) at a transmission rate $\beta_{aa}$ (resp. $\beta_{ca}$) or through contact with infectious children ($B$) at a transmission rate $\beta_{ac}$ (resp. $\beta_{cc}$) and move to
the exposed noninfectious adult class \((E_a)\) (resp. the exposed noninfectious children class \((E_T)\)). Adult exposed individuals (resp. children exposed individuals) then become asymptomatic infectious at rate \(k_s\) (resp. \(k_T\)). After an average period \(1/\delta\) days the asymptomatic infectious individuals \((A)\) become symptomatic and proceed either to the unreported symptomatic infectious \((I_u)\), at rate \(\delta_1\), or to the hospitalized individual \((H)\) at rate \(\delta_2\) with \(\delta = \delta_1 + \delta_2\). Once becoming symptomatic, individuals of class \(I_u\) and \(H\) either remain asymptomatic for \(1/\mu\) days on average before they are recovered or remain asymptomatic for \(1/d\) days on average before they are dead. Asymptomatic children can either be recovered without being hospitalized at rate \(\delta\) or detected and hospitalized at rate \(\sigma\). The control parameters are as defined in Section 1.3. The subscripts \(c\) and \(a\), respectively, characterize children and adults. The model will be given by the following equations

\[
\begin{align*}
\frac{dT}{dt} &= - (1 - \gamma_c) \rho_c (\beta_{ac}^N T(t) (A(t) + I_u(t)) + \beta_{cc}^N T(t) B(t)) \\
&\quad - (1 - \theta_c) (1 - (1 - \gamma_c) \rho_c) (\beta_{ac}^N T(t) (A(t) + I_u(t)) + \beta_{cc}^N T(t) B(t)) , \\
\frac{dE_T}{dt} &= (1 - \gamma_c) \rho_c (\beta_{ac}^N T(t) (A(t) + I_u(t)) + \beta_{cc}^N T(t) B(t)) \\
&\quad + (1 - \theta_c) (1 - (1 - \gamma_c) \rho_c) (\beta_{ac}^N T(t) (A(t) + I_u(t)) + \beta_{cc}^N T(t) B(t)) - k_T E_T , \\
\frac{dB}{dt} &= k_T E_T - (\sigma + \delta) B(t) , \\
\frac{dS}{dt} &= - (1 - \gamma_a) \rho_a (\beta_{aa}^N S(t) (A(t) + I_u(t)) + \beta_{ca}^N S(t) B(t)) \\
&\quad - (1 - \theta_a) (1 - (1 - \gamma_a) \rho_a) (\beta_{aa}^N S(t) (A(t) + I_u(t)) + \beta_{ca}^N S(t) B(t)) , \\
\frac{dE_a}{dt} &= (1 - \gamma_a) \rho_a (\beta_{aa}^N S(t) (A(t) + I_u(t)) + \beta_{ca}^N S(t) B(t)) \\
&\quad + (1 - \theta_a) (1 - (1 - \gamma_a) \rho_a) (\beta_{aa}^N S(t) (A(t) + I_u(t)) + \beta_{ca}^N S(t) B(t)) - k_s E_s , \\
\frac{dA}{dt} &= k_s E_s - \delta A(t) , \\
\frac{dI_u}{dt} &= \delta_1 A(t) - \mu I_u(t) - dI_u(t) , \\
\frac{dH}{dt} &= \delta_2 A(t) + \sigma B(t) - \mu H - dH , \\
\frac{dR}{dt} &= \delta B(t) + \mu (H + I_u) , \\
\frac{dD}{dt} &= d(H + I_u) .
\end{align*}
\]

(1.10)

### 1.4.1 Reproduction Numbers

Here, the basic and control reproduction numbers will be given by
\[ R_0 = \frac{\beta_{cc}^N T(0)/N}{\sigma + \delta} + \frac{\beta_{aa}^N S(0)/N}{\delta} + \frac{\delta_1 \beta_{aa}^N S(0)/N}{\delta (\mu + d)} \]  

(1.11)

and

\[ R_c = \frac{(1 - \gamma_c) p_c \beta_{cc}^N (1 - \theta_c) (1 - (1 - \gamma_c) p_c) \beta_{cc}^N T(0)/N}{\sigma + \delta} + \frac{(\delta_1 + \mu + d) ((1 - \gamma_a) p_a \beta_{aa}^N + (1 - \theta_a) (1 - (1 - \gamma_a) p_a) \beta_{aa}^N) S(0)/N}{\delta (\mu + d)} \]  

(1.12)

Let us show the formula of \( R_0 \). By setting \( \gamma = \theta = 0 \), the linearized system related to infectious individuals, around \( (T(0), 0, 0, S_0, 0, 0, 0) \) of system (1.3) is given by:

\[
\begin{align*}
\frac{dE_T}{dt} &= -k_T E_T + \beta_{cc}^N T(0)B(t)/N + \beta_{ac}^N T(0)A(t)/N + \beta_{aa}^N T(0)I_a(t)/N \\
\frac{dB}{dt} &= k_T E_T - (\sigma + \delta)B(t), \\
\frac{dE_S}{dt} &= \beta_{ca}^N S(0)B(t)/N - k_s E_S + \beta_{aa}^N S(0)A(t)/N + \beta_{aa}^N S(0)I_a(t)/N \\
\frac{dA}{dt} &= k_s E_S - \delta A(t), \\
\frac{dI_u}{dt} &= \delta_1 A(t) - (\mu + d) I_a(t). 
\end{align*}
\]

Moreover, the associated Jacobian matrix will be given by \( M = F - E \) where

\[
F = \begin{pmatrix}
0 & \beta_{cc}^N T(0)/N & 0 & \beta_{ac}^N T(0)/N & 0 & \beta_{ac}^N T(0)/N \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & \beta_{ca}^N S(0)/N & 0 & \beta_{aa}^N S(0)/N & 0 & \beta_{aa}^N S(0)/N \\
0 & 0 & 0 & 0 & k_s & 0 \\
0 & 0 & 0 & 0 & 0 & \delta_1 \\
0 & 0 & 0 & 0 & 0 & 0 \\
\end{pmatrix}
\]

and \( E = \begin{pmatrix}
k_T & 0 & 0 & 0 & 0 & 0 \\
0 & \sigma + \delta & 0 & 0 & 0 & 0 \\
0 & 0 & k_s & 0 & 0 & 0 \\
0 & 0 & 0 & \delta & 0 & 0 \\
0 & 0 & 0 & 0 & \mu + d & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
\end{pmatrix} \).

Therefore,

\[
FE^{-1} = \frac{1}{N} \begin{pmatrix}
\beta_{cc}^N T(0)/N & \alpha_c \beta_{cc} T(0)/N & (d + \mu + \delta_1) \beta_{ac}^N T(0)/N & (d + \mu + \delta_1) \beta_{ac}^N T(0)/N & \beta_{ac}^N T(0)/N \\
\delta + \sigma & \delta + \sigma & \delta (d + \mu) & \delta (d + \mu) & \delta (d + \mu) \\
0 & 0 & 0 & 0 & 0 \\
\beta_{ca}^N S(0)/N & \beta_{ca}^N S(0)/N & (d + \mu + \delta_1) \beta_{aa}^N S(0)/N & (d + \mu + \delta_1) \beta_{aa}^N S(0)/N & \beta_{aa}^N S(0)/N \\
\delta + \sigma & \delta + \sigma & \delta (d + \mu) & \delta (d + \mu) & \delta (d + \mu) \\
0 & 0 & 0 & 0 & 0 \\
\end{pmatrix}
\]

and \( R_0 \) is its spectral radius which is given by formula (1.11). Moreover, assuming that \( \gamma_c \theta_c, \theta_a \neq 0 \) and following the same process above, the control reproduction number will be given by formula (1.12).
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Table 1.2 Parameter definitions and values of model (1.10).  

| Symbol | Definition | Parameter value | Confidence interval | Reference |
|--------|------------|-----------------|---------------------|-----------|
| $\beta_{aa}^N, \beta_{ac}^N$ | Infection rate from infectious adults to unconfined population | 0.41 | 0.1 – 0.63 | Estimated |
| $\beta_{ca}^N, \beta_{cc}^N$ | Infection rate from infectious children to unconfined population | 0.2 | 0.05 – 0.31 | Estimated |
| $\beta_{aa}^X, \beta_{ac}^X$ | Infection rate from infectious adults to confined population | 0.1 | 0.007 – 0.15 | Estimated |
| $\beta_{ca}^X, \beta_{cc}^X$ | Infection rate from infectious children to confined population | 0.014 | 0.002 – 0.16 | Estimated |
| $p$ | Proportion of lockdown | 0.65 | 0.57 – 0.86 | Estimated |
| $k$ | Exposed noninfectious individuals | 3 | 2 – 4 | See text |
| $R_0$ | Basic reproduction number | 2.06 | 0.5 – 3.19 | Estimated |

1.4.2 Parameter and Initial Data Estimation

Note that the first infected child was reported 22 days since the beginning of the epidemic. Furthermore, the maximum asymptomatic duration including the exposure period is about 14 days. Consequently, there were neither exposed nor asymptomatic infected children under 15 years old at $t = 0$. Thus, the initial data values related to infected adult individuals are the same as those in system 1.3. Furthermore, $E_0 = B_0 = 0$, $T_0 = 9683602$ and $S_0 = 26181589$. As mentioned in Section 1.1, we assume that $\beta_{ac}^i = \beta_{aa}^i, \beta_{ca}^i = \beta_{cc}^i$ where $i \in \{X, N\}$. Using the same fitting solver as in Section 1.3.2 we obtain the parameter values shown in Table 1.2. The SSR related to this model is estimated to be $SSR_{age} = 98.76$.

1.5 COVID-19 Model with Constant Delay

In order to enable the study of the effect of the period time, in which infected individuals are asymptomatic and noninfectious, on the COVID-19 dynamics, we will incorporate the time delay (latency period) in the basic model instead of considering the noninfectious latent state as a model component. Let $\eta$ denotes the death rate of noninfectious exposed individuals. Once infected through contact with infectious individuals at rate $\beta$, the susceptible individuals that survive with probability $e^{-\eta \tau}$ become infectious (able to transmit the infection) when the time since exposure exceeds an exposure period time $\tau$. The dynamics of the model are described by the following system of differential equation with delay.
The control and basic reproduction numbers for system (1.13) are, successively given by:

\[
\begin{align*}
\frac{dS}{dt} &= -\alpha e^{-\eta t} S(t) (A(t) + I_u(t)) / N, \\
\frac{dA}{dt} &= \alpha e^{-\eta t} S(t - \tau) (A(t - \tau) + I_u(t - \tau)) - \delta A(t), \\
\frac{dH_u}{dt} &= \delta_1 A(t) - \mu I_u(t) - dI_u(t), \\
\frac{dH}{dt} &= \delta_2 A(t) - \mu H - dH, \\
\frac{dR}{dt} &= \mu (H + I_u), \\
\frac{dD}{dt} &= d(H + I_u)
\end{align*}
\]  

(1.13)

where \( \alpha = (1 - \gamma) p \beta_c + (1 - \theta) (1 - (1 - \gamma) p) \beta_N \) and all the model parameters, except \( \eta \) and \( \tau \), are described similarly to those in Section 1.3.

### 1.5.1 Reproduction Numbers

The control and basic reproduction numbers for system (1.13) are, successively given by:

\[
R_c = \frac{\alpha S_0 e^{-\eta t}}{N} \left( \frac{1}{\delta} + \frac{\delta_1}{\delta (\mu + d)} \right) \quad \text{and} \quad R_0 = \frac{\beta_N S_0 e^{-\eta t}}{N} \left( \frac{1}{\delta} + \frac{\delta_1}{\delta (\mu + d)} \right).
\]

To compute the Basic reproduction number, we apply the survival function approach described by Heffernan, Smith, and Wahl [6]. Let \( R_{01} \) (respectively, \( R_{02} \)) be the average number of secondary infections produced when one asymptomatic infected (respectively, symptomatic unreported infected) individual is introduced into the host virgin population. Following the work in [6], we have \( R_{01} = \int_0^\infty F(s) ds \) where \( F(s) \) is the probability that a newly asymptomatic infected individual has been produced by an existing asymptomatic infectious individual and lives for at least time \( s \). The probability function \( F(s) \) can be expressed as \( F(s) = \int_0^s P_1(t) P_2(s, t) dt \), where \( P_1(t) \) is the probability that an asymptomatic infected individual of age \( t \) infects a susceptible individual and is given by \( \frac{\beta_N S_0}{N} \) and \( P_2 (s,t) \) is the probability that exposed infected individual lives to age \( s - t \) and is given by \( e^{-\eta t} e^{-\delta(s-t)} \) before becoming infectious. Consequently \( R_{01} = \frac{\beta_N S_0 e^{-\eta t}}{N} \int_0^\infty \int_0^s e^{-\delta(s-t)} dt ds \) which can be reduced to \( R_{01} = \frac{\beta_N S_0 e^{-\eta t}}{N} \). Since asymptomatic individuals can become unreported symptomatic infectious individuals over their lifespan \( 1/\delta \) at a rate \( \delta_1 \) and each infectious symptomatic individual produces, on average, \( \beta_N S_0 \frac{1}{\mu + d} \) asymptomatic individuals during his lifespan \( 1/(\mu + d) \) then, similarly, we can express \( R_{02} \) as \( R_{02} = \frac{\beta_N S_0 e^{-\eta t} \delta_1}{\delta(\mu + d)} \). Thus, the basic reproduction number \( R_0 \) will be given by
\[ R_0 = \frac{ \beta N S_0 e^{-\eta \tau}}{N} \left( \frac{1}{\delta} + \frac{\delta_1}{\delta (\mu + d)} \right). \]

Similarly, we can obtain the control reproduction number for system (1.13).

### 1.5.2 Parameter and Initial Data Estimation

Since the parameters \( \delta, \delta_1, \delta_2, \mu \) and \( d \) are not affected by the age then their values are the same as those in Subsection 1.3.2. Note that since there were no death of exposed individuals then it is meaningful to assume that \( \eta = 0 \). To estimate the initial data we will use the same process as in Subsection 1.3.2 so that \( A(t) \) will be given by (1.3) for \( t \) close to 0. Thus, using the second and the third equations of system (1.13) we obtain, for \( t \) close to 0,

\[ aA(t) = \beta N S(0) \left( A(t - \tau) + I_0(t - \tau) \right) / N - \delta A(t), \quad (1.14) \]

and

\[ I_0(t + \theta) = I_0(\theta) e^{a\theta}, \quad (1.15) \]

where

\[ I_0(\theta) = \frac{\delta_1}{a + \mu + d} \frac{b a}{\delta_2} e^{a\theta}. \quad (1.16) \]

Now, using equations (1.14) and (1.15) and the third equation of system (1.13), we obtain after simplification

\[ aA_0 = \beta N S_0 \left( A_0 + \frac{\delta_1}{a + \mu + d} A_0 \right) e^{-a\tau} / N - \delta A_0 \quad (1.17) \]

and

\[ aI_0 = \delta_1 A_0 - \mu I_0 - dI_0. \quad (1.18) \]

Solving equations (1.16), (1.17) and (1.18) for \( \beta_N \) and \( A_0 \) lead to

\[ \beta_N = \frac{(a + \delta) (a + \mu + d)}{a + \mu + d + \delta_1} e^{a\tau} \quad \text{and} \quad I_0 = \frac{\delta_1}{a + \mu + d} A_0. \quad (1.19) \]

Furthermore, the initial data \( A_0(\theta) \) and \( I_0(\theta) \) are given for \( \theta \in [-\tau, 0] \) by \( A_0(\theta) = \frac{ba}{\delta_2} e^{a\theta} \) and \( I_0(\theta) = \frac{\delta_1}{a + \mu + d} A_0(\theta) \). We will assume, as in Section 1.3, that the latency duration varies between 6 and 12 hours. Consequently, \( \beta_N \) is estimated to be between 0.4492 and 0.48 with an average of 0.4596. In this case, the basic reproduction number varies between 2.96 and 3.174 with 3.03 in average. Finally, by repeating the same above process between the first and last day of lockdown we can estimate the parameters \( \beta_c \) and \( p \) (See Table 1.3). Here, the sum of squared
### Table 1.3 Parameter definitions and values of model (1.13)

| Symbol | Definition                                      | Parameter value | Confidence Interval (95%) | Reference |
|--------|------------------------------------------------|-----------------|---------------------------|-----------|
| $\beta_N$ | Infection rate for unconfined population | 0.4596          | 0.4492 – 0.48           | Estimated |
| $\beta_c$ | Infection rate for confined population       | 0.091           | 0.089 – 0.096           | Estimated |
| $\tau$   | latency period                                | 0.33            | 0.25 – 0.5             | See text |
| $R_0$   | Basic reproduction number                     | 3.03            | 2.96 – 3.174           | Estimated |
| $p$     | Proportion of lockdown                        | 0.75            | 0.53 – 0.82            | Estimated |

residuals is estimated to be $SSR_{dde} = 92.63$. When considering 6 hours and 12 hours as latency periods then their $SSR$ are given respectively by $SSR_{\tau=0.25} = 93.23$ and $SSR_{\tau=0.5} = 95.55$.

### 1.6 COVID-19 Model with Threshold-Type Delay

Threshold delay equations (TDEs) ensue in a natural way in compartmental models for which the time in residence in a particular compartment is determined by the stipulation that a fixed threshold load of an entity is racked up during the time spent in that compartment. A susceptible individual that is first exposed to a pathogen at time $t - \sigma$ will become infectious at time $t$ provided the individual receives a sufficient load of the virus during the time from $t - \sigma$ to $t$. We will assume that an individual is exposed to an infectious quantum, $c$, which is the unit of SARS-CoV-2 viral load needed to produce an infection. Therefore, we will assume that the infectious SARS-CoV-2 viral load will grow, overcoming the non-specific immune response. When the pathogen load has increased to a threshold $Q$, or equivalently, when the age since exposure is greater than the latency period $\tau$, we then consider the individual to be infectious. We assume, as mentioned in [7], that the repeated exposures to smaller viral loads increase the pathogen load in-host. Furthermore, since transmission occurs from infected individuals, the pathogen load due to an exposure will depend on the infected population.

Let $r$ be the internal growth rate of the SARS-CoV-2 virus, $b$ is the number of effective contacts between an exposed and infectious individuals, $k$ is an adjustable parameter which measures how soon saturation occurs. Following the modeling approach in [23], the threshold condition is governed by the following formula

$$\Psi(t) := ce^{r(A(t+I_{u,t})} + \int_{-\tau(A(t+I_{u,t})}^{0} e^{-\nu v} G(A(t+v) + I_{u}(t+v))dv - Q = 0$$

(1.20)
where \( A_t + I_{u,t} \) are the history functions of the infectious individuals defined for \( \xi \in [−\tau^\infty := −\max_{\phi \in C} \tau(\phi), 0] \) by

\[
A_t(\xi) + I_{u,t}(\xi) = A(t + \xi) + I_u(t + \xi)
\]

and \( \tau : C \mapsto \mathbb{R}^+ \) is a decreasing and continuously differential map on the space of continuous functions, \( C := C([−\tau^\infty, 0], \mathbb{R}^+) \), satisfying \( \tau(0) = \frac{1}{\gamma} \ln \left( \frac{\gamma}{\epsilon} \right) \). Furthermore, \( F \) is the additive SARS-CoV-2 viral load in the exposed individual due to multiple exposures to infectious individuals which is given, for \( x \geq 0 \), by the following Holling functional response-type 2

\[
G(x) = \frac{b \epsilon x}{k x + 1}.
\]

The COVID-19 model will then be given by the following threshold-type delay system

\[
\begin{aligned}
\frac{dS}{dt} &= -\alpha S(t) \left( A(t) + I_u(t) \right) / N, \\
\frac{dA}{dt} &= \alpha e^{-\eta \tau(t)} S(t - \tau(A_t + I_{u,t})) \left( A(t - \tau(A_t + I_{u,t})) + I_u(t - \tau(A_t + I_{u,t})) \right) - \delta A(t), \\
\frac{dI_t}{dt} &= \delta_1 A(t) - \mu I_t(t) - dI_t(t), \\
\frac{dH}{dt} &= \delta_2 A(t) - \mu H - dH, \\
\frac{dR}{dt} &= \delta B(t) + \mu (H + I_u), \\
\frac{dD}{dt} &= d(H + I_u), \\
\Psi(t) &= 0
\end{aligned}
\]

where \( \tau, A \) and \( I_u \) satisfy the threshold condition (1.20).

Applying the survival function approach described by Heffernan, Smith, and Wahl [5] as done in Subsection 1.5.1 the control and basic reproduction numbers are given by

\[
R_c = \frac{\alpha S_0 e^{-\eta \tau(0)} (\mu + d + \delta_1)}{\delta N (\mu + d)} \text{ and } R_0 = \frac{\beta N S_0 e^{-\eta \tau(0)} (\mu + d + \delta_1)}{\delta N (\mu + d)}.
\]

In order to estimate the model parameters and simulate its dynamics we use MATLAB ddesd solver [25] for state-dependent delay differential equations to compute the solutions of (1.21) numerically. However, we should note that simulating the behavior of solutions of system (1.21) for the general state-dependent delay \( \tau \) is a challenging task. To overcome this difficulty we will estimate the parameters and perform our simulations using constant initial data. Let \( \tilde{C} = \)
Table 1.4 Parameter definitions and values of model (1.21).

| Symbol | Definition | Parameter value | Confidence Interval (95%) | Reference |
|--------|------------|-----------------|---------------------------|-----------|
| $\beta_N$ | Infection rate for unconfined population | 0.4596 | 0.4492 – 0.48 | Estimated |
| $\beta_c$ | Infection rate for confined population | 0.091 | 0.089 – 0.096 | Estimated |
| $r$ | Internal growth rate | 1.02 | | Adjusted |
| $b$ | Effective contact number | 20 | | Adjusted |
| $k$ | Adjustable parameter | $10^{-5}$ | | Adjusted |
| $c$ | Viral load per contact | 49,79 | 18.31 – 135.33 | Estimated |
| $\tau(0)$ | Maximal latency duration | 0.33 days | 0.25 – 0.25 | See text |
| $R_0$ | Basic reproduction number | 3.03 | 2.96 – 3.174 | Estimated |
| $p$ | Proportion of lockdown | 0.73 | 0.51 – 0.78 | Estimated |

$\{\phi \in C : \phi(s) = \phi(0) \text{ for all } s \in [-\tau^\infty, 0]\}$ be the space of constant initial data. Thus, for $\phi \in C$, the equation $\Psi(\tau(\phi), \phi) = 0$ given by (1.20) is equivalent to

$$ce^{r\tau(\phi)} + \int_{-\tau(\phi)}^0 e^{-rv}G(\phi(0))dv - Q = 0.$$ 

Solving this equation for $\tau(\phi)$, we obtain

$$\tau(\phi) = \frac{1}{r} \ln \left( \frac{rQ + G(\phi(0))}{cr + G(\phi(0))} \right). \quad (1.22)$$

It is experimentally shown that the minimal viral load needed for the infection to occur in hamsters is 1000 particles (See [10] more details). Thus, we assume that $Q = 1000$. Furthermore, since the maximal latency duration $\tau(0)$ varies between 6 and 12 hours then, from formula (1.22) the viral load, $c$, per each contact will vary between $Qe^{-r/2}$ and $Qe^{-r/4}$ with an average of $Qe^{-r/3}$. However, another difficulty we encounter for this model is that the parameters $b$, $r$ and $k$ related to COVID-19 disease are still unknown and we are compelled to fairly adjust them to fit the reported cases. (See Table 1.4). In this case we will be able to follow the same process as the one in Subsection 1.5.2 to obtain the remaining model parameters (See Table 1.4). Furthermore we obtain $SSR_{sde} = 94.3$.

1.7 Models with Demographic Effects

In the previous section we have omitted births and deaths in our description of models because it was believed that the time scale of of COVID-19 epidemic is much shorter than the demographic time scale. Indeed, we have used a time scale on which the number of births and deaths in unit time is negligible. However, as mentioned in Section 1.3 there is a possibility that the COVID-19 may not go away
after a short time and could stay for years. Thus, we need to think on a longer time scale and include a birth rate parameter, $\nu_S$ and a death rate parameter $d_S$. In what follows, we will reconsider models (1.13) and (1.21) including demographic effects and we shall give a rigorous mathematical analysis to the both models. The reason for which we select these models is that model (1.13) is shown to be the best one to fit well the data while model (1.21), as we will see in Subsection 1.7.2, generates more complicated behavior then the three other models.

### 1.7.1 COVID-19 Model with Constant Delay

Let us analyze the following constant delay COVID-19 model

\[
\begin{align*}
\frac{dS}{dt} &= \pi_S - \alpha e^{-\gamma t} S(t) (A(t) + I_u(t)) / N - d_S S(t), \\
\frac{dA}{dt} &= \alpha e^{-\gamma t} S(t - \tau) (A(t - \tau) + I_u(t - \tau)) - \delta A(t) - d_S A(t), \\
\frac{dI_u}{dt} &= \delta_1 (A(t) - \mu I_u(t) - d_I u(t) - d_S I_u(t)), \\
\frac{dH}{dt} &= \delta_2 A(t) - \mu H(t) - d H(t) - d_S H(t), \\
\frac{dR}{dt} &= \mu (H(t) + I_u(t)) - d_S R(t), \\
\frac{dD}{dt} &= d (H(t) + I_u(t))
\end{align*}
\]

(1.23)

where

\[\alpha = (1 - \gamma) p \beta_c + (1 - \theta) (1 - (1 - \gamma) \beta_d) .\]

Since the three last components $H, R$ and $D$ do not appear in the three first equations of model (1.23) then we will focus our local stability study on the three first equations.

#### 1.7.1.1 Equilibria

Computing the equilibria of system (1.23) we see that a positive steady state $\left(\hat{S}, \hat{A}, \hat{I}_u\right)$ must satisfy

\[
\begin{align*}
\pi_S - \alpha e^{-\gamma \tau} \hat{S} (\hat{A} + \hat{I}_u) / N - d_S \hat{S} &= 0, \\
\alpha e^{-\gamma \tau} \hat{S} (\hat{A} + \hat{I}_u) / N - (\delta + d_S) \hat{A} &= 0, \\
\delta_1 \hat{A} - (\mu + d + d_S) \hat{I}_u &= 0.
\end{align*}
\]

A straightforward calculation of the above system leads to the following result.
Proof. The characteristic equation associated with the DFE is given by
\[ \Delta = (\lambda + d_S) (\lambda + \delta + d_S - \alpha e^{-\eta \tau} S \lambda + \mu + d + d_S) e^{-\lambda \tau} / N, \]
and locally asymptotically stable when \( R_c < 1 \) and a unique endemic equilibrium of (1.23) appears when \( R_c > 1 \).

Moreover, the endemic equilibrium, \( E^* = (K, S^*, I^*) \), satisfies
\[ S^* = \frac{\delta}{\alpha e^{-\eta \tau} (1 + \frac{\delta_1}{\mu + d + d_S})} / N, \quad \tilde{A} = \delta (\pi_S - d_S S^*) / N \text{ and } \tilde{I}_u = \frac{\delta_1}{\mu + d + d_S} \tilde{A}, \]
(1.24)

### 1.7.1.2 Control Thresholds

Following the work done in Subsection 1.5.1, we can easily obtain the basic reproduction number related to model (1.23) as follows
\[ R_0 = \frac{\pi_S \beta N e^{-\eta \tau}}{d_S N} \left( \frac{1}{\delta + d_S} + \frac{\delta_1}{(\delta + d_S) (\mu + d + d_S)} \right). \]
The control reproduction number is given by
\[ R_c = \frac{\pi_S \alpha e^{-\eta \tau}}{d_S N} \left( \frac{1}{\delta + d_S} + \frac{\delta_1}{(\delta + d_S) (\mu + d + d_S)} \right). \]

### 1.7.1.3 Bifurcation Analysis

In the following, we shall prove that system (1.23) produces a forward transcritical bifurcation. The linearization of system (1.23) around any steady state \( E = (S^*, A^*, I^*_u) \) characteristic equation
\[ \Delta (\lambda) = (\lambda + \delta + d_S) (\lambda + \alpha e^{-\eta \tau} (A^* + I^*_u) / N + d_S) (\lambda + \mu + d + d_S) \]
\[ -\alpha e^{-\eta \tau} S^* (\lambda + \mu + d + \delta_1 + d_S) (\lambda + d_S) e^{-\lambda \tau} / N. \]
The local behavior of the DFE of system (1.23) is given by the following theorem.

**Theorem 1.** The boundary steady state \( E \) of system (1.23) is unstable when \( R_c > 1 \) and locally asymptotically stable when \( R_c < 1 \).

**Proof.** The characteristic equation associated with the DFE is given by
\[ \Delta (\lambda) = (\lambda + d_S) (\lambda + \delta + d_S) (\lambda + \mu + d + d_S) - \alpha e^{-\eta \tau} S^* (\lambda + \mu + d + \delta_1 + d_S) e^{-\lambda \tau} / N. \]
Then the associated eigenvalues are given by \( \lambda = -d_S \) and the roots of
\[ \tilde{\Delta} (\lambda) = (\lambda + \delta + d_S) (\lambda + \mu + d + d_S) - \alpha e^{-\eta \tau} S^* (\lambda + \mu + d + \delta_1 + d_S) e^{-\lambda \tau} / N. \]
(1.26)
Let $\lambda$ be any eigenvalue associated to equation (1.26) with nonnegative real part (i.e. $\Re e (\lambda) \geq 0$) and assume that $R_c < 1$. Then $e^{-\Re e (\lambda) \tau} \leq 1$ and

$$\frac{|\lambda + \delta + dS| |\lambda + \mu + d + dS|}{|\lambda + \mu + d + \delta_1 + dS|} \leq ae^{-\eta \tau S}/N.$$

On the other hand, it follows from $R_c < 1$ that

$$ae^{-\eta \tau S}/N < \frac{(\delta + dS) (\mu + d + dS)}{\mu + d + \delta_1 + dS}.$$

This is a contradiction since the map $\lambda \mapsto \frac{|\lambda + \delta + dS| |\lambda + \mu + d + dS|}{|\lambda + \mu + d + \delta_1 + dS|}$ is increasing. Consequently, the DFE is locally asymptotically stable. On the other hand if $R_c > 1$ then

$$\delta (0) = \delta (\mu + d + dS) (1 - R_c) < 0.$$

Then $\delta$ has one positive root and the DFE is unstable.

The forward transcritical bifurcation of the endemic equilibrium as $R_c$ moves through 1 is stated as follows.

**Theorem 2.** When $R_c < 1$, the endemic equilibrium of system (1.23) is locally asymptotically stable while the DFE is unstable, and for $R_c > 1$ the DFE is unique and locally asymptotically stable. That is, forward transcritical bifurcation occurs at $R_c = 1$.

**Proof.** The characteristic equation associated with the endemic equilibrium is given by

$$\Delta (\lambda) = \frac{(\lambda + \delta + dS) \left( \lambda + \alpha e^{-\eta \tau} (\tilde{A} + \tilde{I}_u) /N + dS \right) (\lambda + \mu + d + dS)}{(\lambda + \mu + d + \delta_1 + dS) (\lambda + dS)} - ae^{-\eta \tau S}/N e^{-\lambda \tau}.$$

Let $\lambda$ be any eigenvalue associated to equation (1.26) with nonnegative real part. Then

$$\frac{|\lambda + \delta + dS| |\lambda + \mu + d + dS|}{|\lambda + \mu + d + \delta_1 + dS|} \leq \frac{|\lambda + \delta + dS| |\lambda + \alpha e^{-\eta \tau} (\tilde{A} + \tilde{I}_u) /N + dS| |\lambda + \mu + d + dS|}{|\lambda + \mu + d + \delta_1 + dS| |\lambda + dS|} = ae^{-\eta \tau S}/N e^{-\lambda \tau} |/N$$

$$\leq \frac{(\mu + d + dS) \delta}{\mu + d + \delta_1 + dS}.$$

However, $\lambda \mapsto \frac{|\lambda + \delta + dS| |\lambda + \mu + d + dS|}{|\lambda + \mu + d + \delta_1 + dS|}$ is increasing which is a contradiction.

It follows that all characteristic roots of $\Delta$ are negative. Thus, the local asymptotic stability of the positive steady state immediately follows. Furthermore, from Theorem 1 we deduce the local behavior of the DFE. This completes the proof.
\subsection*{1.7.2 COVID-19 Model with Threshold-Type Delay}

In this section we will perform qualitative analysis of the following threshold-type delay COVID-19 model. We shall prove that system (1.23) produces two potential cases of bifurcation depending on the chosen parameter values.

\begin{equation}
\begin{align*}
\frac{dS}{dt} &= \pi_S - \alpha S(t) \left( A(t) + I_u(t) \right) / N - d_S S, \\
\frac{dA}{dt} &= \alpha e^{-\eta \tau (A(t)+I_u(t))} S(t - \sigma(t)) \left( A(t - \sigma(t)) + I_u(t - \sigma(t)) \right) \\
&\quad - (\delta + d_S) A(t), \\
\frac{dI_u}{dt} &= \delta_1 A(t) - \mu I_u(t) - (d + d_S) I_u(t), \\
\frac{dH}{dt} &= \delta_2 A(t) - \mu H - (d + d_S) H, \\
\frac{dR}{dt} &= \delta B(t) + \mu (H + I_u), \\
\frac{dD}{dt} &= d (H + I_u)
\end{align*}
\end{equation}

(1.27)

where \( \sigma(t) = \tau \left( A(t) + I_u(t) \right) \).

\subsection*{1.7.2.1 Equilibria}

As mentioned in Subsection 1.7.1 we will focus our study only on the three first equations. Computing the equilibria of the system (1.27) we see that an endemic equilibrium \( (\hat{S}, \hat{A}, \hat{I}_u) \) must satisfy

\[
\begin{align*}
\pi_S - \alpha \hat{S} \left( \hat{A} + \hat{I}_u \right) / N - d_S \hat{S} &= 0, \\
\alpha e^{-\eta \tau (\hat{A}+\hat{I}_u)} \hat{S} \left( \hat{A} + \hat{I}_u \right) / N - (\delta + d_S) \hat{A} &= 0, \\
\delta_1 \hat{A} - (\mu + d + d_S) \hat{I}_u &= 0.
\end{align*}
\]

Let, for \( y > 0, \nu(y) = \tau \left( \frac{\mu + d + \delta_1 + d_S}{\mu + d + d_S} \right) y \),

\[ W(y) = \eta \nu'(y) \left( \alpha \frac{\mu + d + \delta_1 + d_S}{\mu + d + d_S} y / N + d_S \right) + \alpha \frac{\mu + d + \delta_1 + d_S}{\mu + d + d_S} / N \]

and

\[ \chi(y) = \frac{\pi_S \alpha e^{-\eta \nu'(y) \left( \mu + d + \delta_1 + d_S \right)}}{\alpha \left( \frac{\mu + d + \delta_1 + d_S}{\mu + d + d_S} \right) y / N + d_S} \].
A straightforward calculation of the above system leads to the following result.

**Proposition 2.** The model (1.27) has a disease free equilibrium (DFE) given by,

\[
E = \left( \frac{\pi_S}{d_S}, 0, 0 \right)
\]

in which there is no disease. Furthermore,

(i) if \( R_c \leq 1 \) and \( W(\hat{A}) > 0 \) then there is no endemic equilibrium,

(ii) if \( R_c > 1 \) and \( W(\hat{A}) > 0 \) then there exists only one endemic equilibrium,

(iii) if \( R_c < 1 \) and there exist \( \hat{A}^* > 0 \) such that \( \chi(\hat{A}^*) > \delta N (\mu + d) \) then there exist at least two endemic equilibria,

(vi) if \( R_c \leq 1 \) and, for all \( y > 0 \), \( \chi(y) < \delta N (\mu + d) \) then there is no endemic equilibria.

Moreover, the endemic equilibrium, \( E^* = \left( \hat{S}, \hat{A}, \hat{I}_u \right) \), satisfies

\[
\hat{S} = \frac{\pi_S}{\alpha \left( \frac{\mu + d + \delta_1 + d_S}{\mu + d + d_S} \right) \hat{A}/N + d_S}, \quad \hat{I}_u = \frac{\delta_1}{\mu + d + d_S} \hat{A} \quad \text{and} \quad \chi(\hat{A}) = \delta N (\mu + d + d_S).
\]

_**Proof.**_ After few calculation we obtain

\[
\chi(0) = \frac{\pi_S a e^{-\eta y(0)} (\mu + d + \delta_1 + d_S)}{d_S} = R_c \delta N (\mu + d + d_S),
\]

\[
\lim_{y \to \infty} \chi(y) = 0 \quad \text{and} \quad \chi'(\hat{A}) = -\frac{\pi_S a (\mu + d + \delta_1 + d_S) e^{-\eta y(\hat{A})}}{\left( \alpha \left( \frac{\mu + d + \delta_1 + d_S}{\mu + d + d_S} \right) \hat{A}/N + d_S \right)^2} W(\hat{A}).
\]

This proves all the assertions of the proposition.

### 1.7.2.2 Control Thresholds

Similarly to the proof in Subsection [1.5.1](#) the basic and control reproduction numbers for system (1.27) are successively given by

\[
R_0 = \frac{\pi_S \beta N e^{-\eta y(0)} (\mu + d + \delta_1 + d_S)}{\delta N (\mu + d + d_S) d_S} \quad \text{and} \quad R_c = \frac{\pi_S a e^{-\eta y(0)} (\frac{1}{\delta + d_S} + \frac{\delta_1}{(\delta + d_S) (\mu + d + d_S)})}{Nd_S}.
\]
1.7.2.3 Bifurcations

Here we focus on local asymptotic stability and bifurcation analysis of equilibria of system (1.27).

**Theorem 3.** The DFE $\tilde{E} = (\tilde{S}, 0, 0)$ of (1.27) is unstable when $R_c > 1$, and locally asymptotically stable when $R_c < 1$.

**Proof.** The characteristic equation associated with the DFE is given by

$$\Delta (\lambda) = (\lambda + \delta + d_S)(\lambda + \mu + d + d_S) - \alpha e^{-\eta r(0)}\overline{r}\lambda e^{-\lambda r(0)}(\lambda + \mu + d + \delta_1 + d_S) / N$$

$$= \lambda^2 + (\mu + d + \delta + d_S - a\overline{S}/N)\lambda + \alpha e^{-\eta r(0)}\overline{r}/N(\lambda + \mu + d + \delta_1 + d_S)e^{-\lambda r(0)} + (\delta + d_S)(\mu + d + d_S).$$

When $r = 0$ then $\Delta (\lambda) = \lambda^2 + (\mu + d + \delta + d_S - a\overline{S}/N)\lambda + \delta (\mu + d + d_S) (1 - R_c)$. Furthermore, we have

$$\mu + d + \delta + d_S - \overline{S}\alpha/N = \frac{(\delta + d_S)(\mu + d + d_S)(\mu + d + \delta + d_S)(\mu + d + \delta_1 + d_S)}{\mu + d + \delta_1 + d_S}(\delta + d_S)(\mu + d + d_S) > \frac{(\delta + d_S)(\mu + d + d_S)}{\mu + d + \delta_1 + d_S}(1 - R_c).$$

Thus, the DFE is stable when $r = 0$ and $R_c < 1$. Assume that $r > 0$ and let $\omega > 0$. Separating real and imaginary parts, equality $\Delta(i\omega) = 0$ is equivalent to

$$\omega^4 + \left((\mu + d + d_S)^2 + (\delta + d_S)^2 - \left(\alpha e^{-\eta r(0)}\overline{S}/N\right)^2\right)\omega^2 + (\delta + d_S)^2(\mu + d + d_S)^2$$

$$- \left(\alpha e^{-\eta r(0)}\overline{S}/N(\mu + d + \delta_1 + d_S)\right)^2 = 0.$$ 

A simple calculation of the discriminant $\tilde{\delta}$ leads to

$$\tilde{\delta} = \left((\mu + d + d_S)^2 - (\delta + d_S)^2 - \left(\alpha e^{-\eta r(0)}\overline{S}/N\right)^2\right)^2 + 4(\delta + d_S)^2\left(\alpha e^{-\eta r(0)}\overline{S}/N\right)^2$$

$$+ 4\left(\alpha e^{-\eta r(0)}\overline{S}/N(\mu + d + \delta_1 + d_S)\right)^2$$

which is positive. It follows that $i\omega$ is not a root of $\Delta$ and, consequently, the DFE is LAS for all $r > 0$ such that $R_c < 1$. On the other hand, if $R_c > 1$ then

$$\Delta(0) = \delta (\mu + d + d_S) \left(1 - \frac{\alpha e^{-\eta r(0)}\overline{S}}{d_S \delta (\mu + d + d_S)}\right)$$

$$= (\delta + d_S)(\mu + d + d_S)(1 - R_c)$$

which is negative. It follows that $\Delta$ has a positive root and the DFE is unstable.
Theorem 4. When $R_c = 1$ and $W(\hat{A}) > 0$, the endemic equilibrium undergoes a forward transcritical bifurcation, that is for $R_c > 1$, $R_c$ close to 1, the endemic equilibrium is locally asymptotically stable whereas the DFE is unstable, and for $R_c < 1$ the DFE is locally asymptotically stable and is the only steady state of (1.27).

Proof. The characteristic equation is given by

$$\Delta(\lambda) = (\lambda + \delta + d_S)(\lambda + \mu + d + d_S) - \alpha \tilde{S}e^{-\eta v(\hat{A})}e^{-\lambda v(\hat{A})}(\lambda + \mu + d + \delta_1 + d_S)/N + Q(\lambda)$$

where

$$Q(\lambda) = \alpha e^{-\eta v(\hat{A})} \left(\tilde{A} + \tilde{I}_a\right) \tilde{S}(\lambda + \mu + d + \delta_1 + d_S) \left(e^{-\lambda v(\hat{A})} \frac{\alpha/N}{\lambda + \alpha(\tilde{A} + \tilde{I}_a)/N + d_S} + \eta v'(\hat{A})\right)/N.$$  

Then

$$\Delta(0) = \delta(\mu + d + d_s) - \alpha e^{-\eta v(\hat{A})} \tilde{S}(\mu + d + \delta_1 + d_S)/N + \alpha e^{-\eta v(\hat{A})} \left(\tilde{A} + \tilde{I}_a\right) \tilde{S}(\mu + d + d_S) \left(\frac{\alpha(\mu + d + \delta_1 + d_S)/N}{\alpha(\tilde{A} + \tilde{I}_a)/N + d_S} + \eta v'(\hat{A})\right)/N.$$  

On the other hand, from the equilibrium equation (1.28), we have

$$\alpha e^{-\eta v(\hat{A})} \tilde{S}(\mu + d + \delta_1 + d_S)/N - (\delta + d_S)(\mu + d + d_S) = 0.$$  

Then

$$\Delta(0) = \alpha e^{-\eta v(\hat{A})} \left(\tilde{A} + \tilde{I}_a\right) \tilde{S}(\mu + d + d_S) \left(\frac{\alpha(\mu + d + \delta_1 + d_S)/N}{\alpha(\tilde{A} + \tilde{I}_a)/N + d_S} + \eta v'(\hat{A})\right)/N.$$  

It follows from condition (ii) in Proposition 2 that $\Delta(0) > 0$. This proves that $\lambda = 0$ is not a root of $\Delta(\lambda) = 0$.

Now, let $\lambda$ be a root of $\Delta(.)$ with nonnegative real part and $Z = |\lambda + \mu + d + \delta_1 + d_S|\alpha e^{-\eta v(\hat{A})}\tilde{S}/N$. Thus, $|e^{-\lambda v(\hat{A})}| \leq 1$ and

$$|Q(\lambda)| \leq Z \left|\frac{\alpha(\tilde{A} + \tilde{I}_a)/N}{\lambda + \alpha(\tilde{A} + \tilde{I}_a)/N + d_S}\right| < Z.$$
are locally asymptotically stable whereas a second endemic equilibrium exists and is unstable.

Theorem 5. Assume that case (iiii) in Proposition 2 holds true. When \( R_c = 1 \), the system (1.27) undergoes a backward bifurcation. That is, for \( R_c > 1 \), \( R_c \) close to 1, the endemic equilibrium is the unique equilibrium which is locally asymptotically stable; and for \( R_c < 1 \), \( R_c \) close to 1, the DFE together with an endemic equilibrium are locally asymptotically stable whereas a second endemic equilibrium exists and is unstable.

Proof. When case (iii) hold, then there exists at least two positive steady states, \( E_m = (S^m, A^m, I^m_u) \) and \( E_M = (S^M, A^M, I^M_u) \). The selected equilibria \( E_m \) and \( E_M \) we will use are the first two solutions \( A^m \) and \( A^M \) of equation \( \chi(y) = \delta N (\mu + d) \) such that \( \chi'(A^m) < 0 \) and \( \chi'(A^M) > 0 \). Thus, the proof of the LAS of equilibrium \( E^M \) is similar to the one of Theorem 4.

The characteristic equation associated to \( E_m \) satisfies

\[
\Delta(0) = \alpha e^{-\eta\nu(A_m(\zeta))} (A_m(\zeta) + I_m(\zeta)) S_m(\zeta) (\mu + d + dS) \chi'(A^m)/N.
\]

Consequently \( \Delta(0) < 0 \) and, since \( \lim_{1 \to \infty} \Delta(\lambda) = +\infty \), then there exists \( \lambda^* > 0 \) such that \( \Delta(\lambda^*) = 0 \). This concludes the proof of the theorem.

The existence of a backward bifurcation is an interesting artifact since this means that repeated exposures of susceptibles to the SARS-CoV-2 virus can cause bistability dynamics and, subsequently, infection persistence even when the control reproduction number \( R_c \) is less than unity. An interesting query that emanates from the backward bifurcation is “What is the maximum effective contact number, \( b \), or viral load per each contact, \( c \), below which the COVID-19 disappear one we reduce \( R_c \) below one?” Note that, as mentioned and proved in (23), in the case of single exposure model (1.27) is a system of constant-delay differential equations which is equivalent to system (1.23). Moreover, no backward bifurcation occurs. Generally, there is a threshold \( \lambda^* \) below which the backward bifurcation disappear (The proof is similar to the one in (23)). This result could have a significant biological interpretation since, as stated in (19), minimization of exposure to SARS-COV-2 is key to reducing the chance of infection and developing disease.
1.8 Discussion

Since the beginning of COVID-19 pandemic, numerous mathematical models with increasing complexity are developed worldwide to understand the course of COVID-19 disease. The modeling results have shown a wide range of variations, especially in the basic reproduction numbers. This leads to ask some questions such as: Why these variations exist between models? Which model is the most realistic for the COVID-19 disease? WHO had reported that the basic reproduction number is estimated to be between 1.4 and 2.5 [26], while other interesting contributions reported that the COVID-19 is more transmissible than what WHO mentioned. In [16], the authors estimated, through a comparison study of 12 different results, that the median value of $R_0$ for COVID-19 is expected to be around $2−3$. However, only 6 among these studies have used mathematical models leading to a higher variation of $R_0$ (1.5−6.49), with an average of 4.2. Another systematic review in [14] screened 75 mathematical and statistical models published between December 1st 2019 and February 21st 2020 and concluded that the median of $R_0$ for COVID-19 was 3.77.

![Fig. 1.1 Time series plot for model (1.1), starting from March 21, 2020, of the numbers of reported individuals change using different lifting rates at different times as follows: 30% of the total population is lifted on June 10 (dot line) and a fraction $\gamma$ of the remaining confined individuals ($\gamma = 0.3$, $\gamma = 0.4$, and $\gamma = 0.5$, solid line, dashed line and dot-dashed line respectively) is lifted on September 1st.](image)

In this chapter, we developed, fitted and compared four mathematical models with increasing complexity, that incorporate lifting lockdown strategy, to check out which one among them provides the best prediction for COVID-19 disease. We considered a progressive relaxation of the compulsory lockdown performed in two stages and supported by a reduction of 60% of the contact rate. In the first stage 30% of the total confined population lifted the lockdown on June 10th while, in the second stage another 30% lifted the lockdown on September 1st. Our investigation of the proposed models showed a small variation of $R_0$ ranging from 2.06 to 3.03, and according to the SSR measure (see Section 1.3), the best fit of reported data is achieved for the model with constant delay (1.13) with $SSR = 92.63$. Consequently, our results show that model (1.13) is the most reliable to estimate the value of $R_0$ ($R_0 = 3.03$), which is higher than those estimated by models (1.1), (1.10) and (1.21).
Fig. 1.2 Time series plot for model (1.10), starting from March 21, 2020, of the numbers of reported individuals change using different lifting rates at different times as follows: 30% of children and 30% of adults are lifted on June 10 (dot line) and a fraction $\gamma$ of the remaining confined individuals $((\gamma_0 = 0.115, \gamma_c = 0.8)$, $(\gamma_0 = 0.25, \gamma_c = 0.8)$, and $(\gamma_0 = 0.39, \gamma_c = 0.8)$, solid line, dashed line, dot-dashed line respectively) is lifted on September 1st.

Although it is believed that the discrete structured-age model (1.10) is more realistic, our investigations show that this model is the least accurate of any of the models used to estimate the basic reproduction number $R_0$ since its $SSR$ is the highest one with $SSR = 98.76$. This lead us to think to extend the proposed models by gathering both age and constant delay factors at once. On the other hand, using our proposed models, the examination of the lockdown lifting scenario shows a prominent difference between disease predictions. Furthermore, no eradication of COVID19 disease is observed before the end of the year when relaxing the compulsory lockdown on September 1st. The discrete structure-age model (1.10), which have estimate the lowest $R_0$ value, predict a less severe disease persistence when comparing with the other models. Lifting 30% of the total confined population on June 10th will lead to a slight second wave of infection followed by a rapid decrease till the eradication of the disease before the end of the year.

Fig. 1.3 Time series plot for model (1.13), starting from March 21, 2020, of the numbers of reported individuals change using different lifting rates at different times as follows: 30% of the total population is lifted on June 10 (dot line) and a fraction $\gamma$ of the remaining confined individuals ($\gamma = 0.3$, $\gamma = 0.4$, and $\gamma = 0.5$, solid line, dashed line, dot-dashed line respectively) is lifted on September 1st.
However, if this strategy is accompanied with a second lockdown lifting of at least 30% of the total confined population (11.5% of adults and 80% of children under 15 years old) on September 1st then the extinction of the virus cannot happen (Fig. 1.2) and a third wave could arise. However, it is obvious that the reopening of primary and junior high schools does not lead to an important wave of infection, when comparing with models (1.1), (1.13) and (1.21). Figures (1.4), (1.3) and (1.4) show, however, that no second wave will reoccur but a longer lasting persistence of the infection occurs when 30% of the population lifted on June 10th.

Fig. 1.4 Time series plot for model (1.21), starting from March 21, 2020, of the numbers of reported individuals change using different lifting rates at different times as follows: 30% of the total population is lifted on June 10 (dot line) and a fraction \( \gamma \) of the remaining confined individuals (\( \gamma = 0.3 \), \( \gamma = 0.4 \), and \( \gamma = 0.5 \), solid line, dashed line, dot-dashed line respectively) is lifted on September 1st.

However, when comparing with the both basic model (1.1) and constant delay model (1.13) threshold-type delay model (1.21) show a higher size of reported cases as well as an important second wave when a second stage of lifting lockdown strategy occurs on September 1st. Furthermore, it seems that the latency period influence the model fitting to data. Figure (1.5) and the SSR measure (SSR\( \tau = 0.33 \) = 92.63), related to the delay model (1.13), shows that the constant delay model with latency period of 8 hours is the best fit to data and, thus, this period gives a better prediction than 6 or 12 hours of latency.

Fig. 1.5 Time series plot for model (1.13), starting from March 21, 2020, of the numbers of reported individuals change using different latent periods (\( \tau = 0.25 \), \( \tau = 0.33 \), and \( \tau = 0.5 \), dashed line, solid line, dot-dashed line respectively) with 30% of the total population is lifted on June 10.
In summary, there are no mathematical models able to correctly capture all complexity of COVID-19 disease in general. Each model, either simple or complex, has its own advantages and disadvantages. Besides the availability of data, the choice of model depends on the goal sought by scientists to answer a question of interest. Furthermore, the use of complex models does not necessarily provide the most precise answers than the simplest. Indeed, since many biological and epidemiological issues related to SARS-CoV-2 remain to be clarified, parameters considered in the proposed model can be underestimated or overestimated and, consequently, can lead to wrong results. An unsuccessful evaluation of the disease behavior could cost serious damage because it lead to an incorrect estimate of the control health measures that are necessary to contain the disease transmission. However, although a lot of issues must be considered to provide the built model a maximum of realism, mathematical modeling remains a crucial tool to understand and control the behavior of COVID-19 disease.

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