UNIVERSITÁ DEGLI STUDI DELL'AQUILA

DIPARTIMENTO DI INGEGNERIA E SCIENZE DELL'INFORMAZIONE E MATEMATICA

CORSO DI LAUREA IN INGEGNERIA MATEMATICA

Tesi di Laurea Magistrale

ANALYSIS OF THE INITIAL PHASE OF COVID-19 EPIDEMICS IN ITALY: A MODELING STUDY

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Anno Accademico 2021-2022

«[...] ma alla fine è solo una cosa passeggera,
quest'ombra, anche l'oscurità deve passare,
arriverà un nuovo giorno,
e quando il sole splenderà sarà ancora più luminoso [...]»
Il Signore degli Anelli: le due torri

Ringraziamenti

Voglio dedicare un pensiero a tutte le persone che ho incontrato e che mi sono state accanto durante questi anni di studio.

I would like to spend a few words for all those people who have been staying by my side throughout the years, and for those who I have the pleasure to meet on my academic path.

Grazie al Prof. Alessandro Borri per la sua pazienza e disponibilità. Questa tesi è frutto del suo prezioso aiuto. Lo ringrazio anche per avermi guidato e avermi dato il suo sincero punto di vista sulle mie opportunità future.

Thank you *to Prof. Alessandro Borri, for his patience and availability. This thesis was also possible due to his precious help. Thank you for leading me on this path and for giving me your most sincere perspective regarding my future opportunities.*

Grazie alla Dott.ssa Maíra Aguiar e al suo team (MTB group) per l'opportunità che mi è stata data di lavorare con loro al BCAM-Basque Center of Applied Mathematics. Sopratutto, grazie di avermi accolta a braccia aperte e di avermi fatto sentire a casa, anche a così tanti chilometri di distanza.

Thank you *to Dr. Maíra Aguiar and to her wonderful team, the MTB group; you gave me the opportunity to work and collaborate with you at the BCAM-Basque Center of Applied Mathematics. Moreover, thank you for welcoming and making me feel home, even though I was miles away from it.*

Grazie ai miei genitori, perchè sono quella che sono solo per merito loro. So di non essere la migliore delle figlie spesso. Vi chiedo, però, di ricordare sempre che vi voglio bene, che sono grata di essere vostra figlia e che questo traguardo è merito vostro quanto mio.

Thank you *to my beloved parents; I am what I am is because of them. I am aware I am not the best of the daughters. I ask you, indeed, to keep in mind that I deeply love you and that I am grateful to be your daughter. The achievement of this "milestone" is both yours and mine deserved.*

Grazie a i miei fratelli: David, Enrico e Michele perchè ho sempre guardato a loro come un modello da seguire. Senza saperlo mi avete spronato a dare il meglio di me e a non risparmiarmi mai in ogni aspetto della vita.

Thank you *to all my brothers; David, Enrico and Michele. I've always looked at you as "inspiration models". Without even knowing it, you have pushed me to always do and give my best and never spare me in each and every aspect of life.*

Un pensiero speciale ad Alessandro, per essere il mio migliore amico, la persona che mi conosce meglio al mondo e, nonostante questo, ogni giorno mi scegli e mi accetti per ciò che sono. Sei l'amore della mia vita. Tu sai starmi vicino e spronarmi anche quando le conseguenze possono farti stare male e mi metti al primo posto anche quando non lo merito. Per questo mi hai resa una persona migliore e più forte. Ed è questo che dovrebbe fare l'amore alle persone.

A special though *to Alessandro, for being my best friend. You are the person who knows me better than everyone in the entire world and, despite that, you keep choosing me everyday, accepting me for who I am.You know how to be my side, how to walk with me, you spur me even when the consequences could you feel bad. You always put me first, even when I do not deserve it; for this reason you surely make me a better and strong person. And that is, in my opinion, what love should do to people.*

Grazie a Martina, Sofia e Lorenzo, miei compagni di viaggio.
Martina e Sofia siete le sorelle che non ho mai avuto ma che ho sempre desiderato. Nonostante le nostre differenze, siete capaci di ascoltarmi e supportarmi senza mai giudicare e di accetare ogni mio difetto o mancanza. Sapete farmi ragionare e consigliarmi nel modo migliore, anche quando può farmi stare male. Con voi ho capito il vero senso della parola "AMICIZIA". Lorenzo, grazie per essere stato la prima persona a avvicinarmi appena messo piede in università e di essermi stato amico ancora prima che me ne rendessi conto. Sei una persona speciale, perchè fai sentire a casa e a proprio agio chiunque abbia la fortuna di conoscerti, con i tuoi modi esuberanti e un pò pazzi. Con voi tre ho condiviso i momenti migliori e più bui di questo percorso e spero che potremmo continuare a condividere le tappe più importanti delle nostre vite.

Thank you *to Martina, Sofia and Lorenzo, my traveling companions.*
Martina and Sofia, you are the sisters I never had but always wanted. In spite of our differences, you were able, and still are, to listen and support me without judging me, you accept each and every flaw I have. You know how to make me think and advise me in the best way, even when it may make me feel bad. With you I was able to understand the true meaning of the word "FRIENDSHIP".
Lorenzo, thank you for being the first person to approach me as soon as I set foot in the university and for being my friend even before I was able to realize it. You are a special person; you make everyone feel at home and ease with your exuberant and somewhat crazy ways of living.
I have shared the best and darkest moments of this journey with the three of you, and I hope we could continue to share the most important stages of our lives.

Grazie a Marta, mia insostituibile compagna di studio pazzo e disperatissimo. Senza di lei difficilmente avrei superato alcuni esami. Grazie per il tuo supporto, sia pratico che psicologico. Grazie per la tua dolcezza e la tua pazienza, anche quando ti tartassavo.

Thank you *to Marta, my irreplaceable companion of crazy and desperate study session. Without you, I wouldn't be able to pass certain exams. Thank*

you for your support, both practical and physiological. Thank you for your infinite kindness and patience. Even when I tortured you, you were always there.

Grazie ai miei amici di una vita, perchè i pomeriggi passati con voi ai muretti mi hanno spesso salvato da una crisi di nervi. Mi avete sopportato nei momenti no e mi avete distratto quando ne avevo bisogno, tirandomi sempre su di morale. Un ringraziamento particolare fra tutti va ad Andrea e alle sue conoscenze informatiche.

Moreover, I would like to spend few words for the long-lasting friends. ***Thank you*** *because spending all the afternoons at the "muretti" saved me from many breakdowns. You have put up with me in the bad times and distracted me when I needed it the most, always cheering me up. A special thanks. among all, go to Andrea and his computer skills.*

Infine, non posso che ringraziere me stessa per non aver mai mollato, nonostante tutto il mio bagaglio di insicurezze. In questi anni sono cresciuta e maturata, fino ad arrivare ad una buona consapevolezza di me stessa e posso dire di amare la persona che sono.
E come direbbe RuPaul "If you can't love yourself, how in the hell you gonna love somebody else?"

And last, but not least, I can only thank myself for never giving up, despite all my many insecurities. Over these years, I have grown and matured to a good self-awareness and I could say that I love the person I am.
And as RuPaul would say "If you can't love yourself, how in the hell you gonna love somebody else?"

Introduction

COVID-19 is a severe respiratory disease caused by the virus SARS-CoV-2, new coronavirus able to infect humans. COVID-19 was identified in December 2019 in China and spread rapidly around the globe.
COVID-19 cases in Italy were first identified in the North of the country, notified in the second half of February 2020. First cases were diagnosed in Lombardy on February 21, 2020, and by February 23, 2020, eleven municipalities were put into quarantine to prevent the spread of disease, i.e., nobody could enter and leave those territories. Quickly other cases occurred in the rest of the country, forcing the Authorities to establish quarantine status across the country.
Due to the high contagiousness of the infection, eventually enhanced by asymptomatic individuals, Italy became, in few weeks, the country with the greatest number of infected people in Europe. The large number of severe cases among infected people in Italy led to the hospitalization of thousands of patients, with a heavy burden on the National Health Service [22].
After the quarantine period, from March 2020 to May 2020, to control the spread of the infection, Italian Government established a ranking of the regions based on different colors, according to the risk degree. In addition to the social distancing and the obligation to wear mask, in the red zones the movements across regions were prohibited and the curfew was established.
The most affected regions were Lombardy and Emilia Romagna in the North of the Country, with more than half of the total cases.
It is reasonable to assume that the large spread of the novel Coronavirus in these regions was due to the development of the first outbreaks which caused a high number of people infected before the social distancing imposed by Government. But it is reasonable to think that the difference in the trend of the pandemic between North and South of Italy was due to the

different weather. Therefore, it is reasonable to assume that the COVID-19 trend is seasonal.

Until now, there are 156.493 deceased individuals for SARS-CoV-2 in Italy from the beginning of surveillance to 10 January 2022, reported by the integrated surveillance COVID-19 Coordinated by the Higher Health Institute (ISS). The reports from ISS shows that the average age of deceased individuals is 80 years old. Moreover, it seems that the mortality rate is increased when there are patients with pre-existing health conditions. Therefore, it could be significant analyzing the COVID-19 trend for different population classes, according to age and pre-existing health conditions [2] [16].

Predictive mathematical models for epidemics are fundamental to understand the course of the epidemic and to plan effective control strategies. One commonly used model is the SIR model for human-to-human transmission, which describes the flow of individuals through three mutually exclusive stages of infection: susceptible, infected and recovered. More complex models can accurately portray the dynamic spread of specific epidemics. For the COVID-19 pandemic, several models have been developed [9].
In this study, we start to describing the SIS model, in which the population is divided only into two classes (susceptible and infected) and the SIR model. Then, we proceed to describe a more complex model, the SHAR model in which the infected class is stratified into two classes: hospitalized and asymptomatic. The latter model is more accurate for the analysis of COVID-19 disease.
We model the countrywide spread of the COVID-19 epidemic in Italy, for which detailed epidemiological data are continuously updated and made public, thanks to *Protezione Civile* (Civil Protection) department and *Istituto Superiore di Sanità*, ISS (Italian National Institute of Health).
Notice that, mainly at the beginning of the pandemic and until the end of the lockdown, this data are only a proxy of the epidemiological conditions because:

1. the number of infected people on records depends on the sampling effort, namely the number of specimen collections (swabs) from individuals under investigation;

2. the effects of systematic errors or bias in the official data results mainly in under-reporting.

In fact, under-reporting may apply even to fatality counts, yet to a lesser extend with respect to reported infections. Hospitalizations are known, but may underestimate the situation because cases with mild symptoms are not hospitalized, for example due to saturation of the carrying capacity of the sanitary structures. Moreover, people with very mild symptoms or asymptomatic people was not always subjected to a COVID test [19].

This thesis describes the first years of COVID-19 pandemic in Italy. We started looking at the data given by the Italian Civil Protection and according to the trend we finally described the epidemiological curve through a SHAR model. In this model, the infection rate β changing according to different period that we identified during the first year of pandemic. To model β, we have taken into account the effect of control measures (Lockdown, social distancing, protection devices) and seasonality.
This study is structured as follow:

- In Chapter 1, we give a summary of the situation of Italy during the first year of pandemic.
- In Chapter 2, we describe the simple SIS model and its extension as SIR model. Then, we show the equilibrium states of these models and the biological meaning of these points in an epidemiological point of view. These two models are basic for the formulation of the SHAR model.
- In Chapter 3, we describe the SHAR model and how we used it for this study. Then, we present the results that we obtained.
- In Chapter 4, we described future projects and possible applications of our study. Firstly, we modify the SHAR model to continue the analysis for the whole emergency period. Then, we describe the stochastic formulation of the SHAR model and an optimization problem that can be used to determine a balance between economic cost and health cost. Finally, we describe the spatial formulation of the SHAR model.

Acknowledgments

This research was partially supported by the Basque Government through the "Mathematical Modeling Applied to Health" Project, BERC 2022-2025 program and by Spanish Ministry of Sciences, Innovation and Universities: BCAM Severo Ochoa accreditation SEV-2017-0718.

Acronyms

ISS: Istituto Superiore di Sanità;
DEE: Disease Endemic Equilibrium;
DFE: Disease Free Equilibrium;
WHO: World Health Organization;
ICU: Intensive Care Units;
ODE: Ordinary Differential Equation;
SDE: Stochastic Differential Equation.

Contents

Chapter 1

Overview of COVID-19 in Italy

In order to find the right model to describe a phenomenon it is necessary to understand well the phenomenon itself. For this reason we present here an outline of the first year of the pandemic in Italy.

1.1 Time line

On 31 December 2019, the Health Commission of Wuhan (Hubei, China) informed the WHO about a cluster of acute pneumonia cases with unknown origin in its province. On 9 January 2020, the Chinese Center for Disease Control and Prevention (CCDC) reported the identification of a novel coronavirus, later identified as the SARS-CoV-2, as the cause.
The virus was first confirmed to have spread in Italy on 31 January 2020, when two Chinese tourists in Rome tested positive. One week later an Italian man repatriated to Italy from the city of Wuhan was hospitalized and confirmed as the third case in Italy. Clusters of cases were later detected in Lombardy and Veneto on 21 February, with the first deaths on 22 February. By the beginning of March, the virus had spread to all regions of Italy.
On 22 February, the Italian government announced a new decree imposing the quarantine of more than 50,000 people from 11 municipalities in Northern Italy. The quarantine zones are called the Red Zones and the areas of Lombardy and Veneto outside them are called the Yellow Zones. The decree "absolutely avoided any movement into and out of the areas" [8]. It was possible to move into and out of the areas only for emergencies or "proven working needs" [3]. The decree also established the closure of all

gyms, swimming pools, spas and wellness centres. Shopping centres had to be closed on weekends, while other commercial activities could remain open if a distance of one metre between customers could be guaranteed. The decree imposed the closure of museums, cultural centres and ski resorts in the lockdown areas and the closure of cinemas, theatres, pubs, dance schools, game rooms, betting rooms and bingo halls, discos and similar places in the entire country. Civil and religious ceremonies, including funeral ceremonies, were suspended. All organised events were also suspended, as well as events in public or private places, including those of a cultural, recreational, sporting and religious nature, even if held in closed places. Penalties for violations range was established and the Italian military and law enforcement agencies were instructed to secure and implement the lockdown.
But this was not enough to stop the spread of the contagion.
In the evening of 9 March, the prime minister Giuseppe Conte announced in a press conference that all measures previously applied only in the so-called Red Zones were extended to the whole country.
This measure was described as the largest lockdown in the history of Europe, as well as the most aggressive response taken in any region beyond China, and paralysed the wealthiest parts of the country as Italy attempted to constrain the rapid spread of the disease.

The lockdown was hard causing psychological problems like stress and depression in the populations that were forced to face changes in everyday life and to stay forcedly at home in order to reduce contagion [21].
The worst episode in this period was the Army that was deployed in the city of Bergamo, the worst hit Italian city by COVID-19, as the local authorities could no longer process the number of dead residents. Army trucks transported bodies to crematoriums in several other cities, as cemeteries in the city were full.

On 16 May, Conte announced the government plan for the easing of restrictions. Starting from 18 May most businesses could reopen, and free movement was granted to all citizens within their region; movement across regions was still banned for non-essential motives. From that moment on, the contagions curve continues to decrease, thanks to the increase of the temperature too. But starting from July 2020, many countries in Europe,

including Italy, witnessed a new rise in detected COVID-19 cases. This was probably due to the free movement and tourism that was relaunched.
In October a new lockdown phase started, less severe than the previous. For this reason, the Italian government decided to establish again the classification of the region in colors depending on the degree of risk, avoiding a new total lockdown [4].

1.2 Why was the pandemic so severe in Italy?

As we had understood, Italy has been hit very hard by the coronavirus pandemic, with 17,147,477 documented cases (until 18 of May, 2022). The number of cases and deaths cannot be explained simply because of the epidemic starting in Italy earlier compared with other countries besides China. Some factors pertain to demographics and background disease in the population.
Italy has the most elderly population in Europe and the second most elderly population in the world after Japan. COVID-19 has a strong age dependence for the severity of the infection and the risk of death. The median age of people infected with SARS-CoV-2 who are dying in Italy has been 80 years, and the average age of patients requiring critical care support has been 67 years. Moreover, COVID-19 morbidity and mortality is strongly dependent on the presence of concomitant serious diseases, and Italy has a high proportion of patients with history of smoking and high rates of chronic obstructive pulmonary disease and ischemic heart disease.

A second factor is that Italian life is famous for its socialization and frequent congregations and clustering. It is possible also that in early stages, there was not much adoption of standard hygienic measures, and instructions to stay at home proved difficult to accept, with many complaints registered with the police.

A third set of factors pertains to the standard capacity of the health care system and decisions made during hospital management of the presenting cases. Italy has a state-run health care system, but it has only a modest number of ICU beds and very few subintensive care beds. Overall, 5090 ICU beds (8.4 per 100,000 individuals) are available in Italy, and 2601 beds in

coronary care units (4.3 per 100,000 individuals).
Given the little experience in dealing with the new virus, it is unavoidable that some strategic mistakes were made about which patients should be hospitalized. Apparently, many patients with relatively modest symptoms were admitted (because of the so-called "defensive medicine"). Hospital overcrowding may also explain the high infection rate of medical personnel. Nine percent of infections in Italy occurred among health care personnel.

Moreover, in Italy local authorities have decision-making powers on their territory; thus, preparedness and containment may have been hampered. There was a delay from the first case detection to the first containment decree from the government that closed the relevant villages 3 days later [25].

Chapter 2

Basic epidemiological models

In this chapter we intoduced some basic epidemiological models from which we get the model we used for this study. These models are the SIS model and the SIR model and for these two models we described the equilibrium states.

2.1 SIS Model

This model takes its name from the two classes of individuals that are taken into consideration, the class of the susceptible individuals $S(t)$ and the class of the infected individuals $I(t)$. Indeed, the SIS model is used for disease for which individuals do not acquire immunity after the end of the infection, but they become susceptible again. Therefore, the flow of individuals is described with two stages: susceptible and infected. The SIS model can describe disease like cold and seasonal influence, tuberculosis or gonorrhea. It assumes that the total population N is constant and at each time t results $N = S(t) + I(t)$. To visualize the model, we look at the state-flow diagram, where boxes represent states and arrows indicate the transitions of the individuals through a sequence of disease related stages, as in
Figure 2.1.1.

We call β *infection rate* and, since it assumed that the disease spread is proportional to the number of meeting between the susceptible and infected people, it depends on the total number of susceptible and infected.
Moreover, we call γ *recovery rate*, that is the rate with which the infected return in the susceptible class. The dynamics of the system is the following:

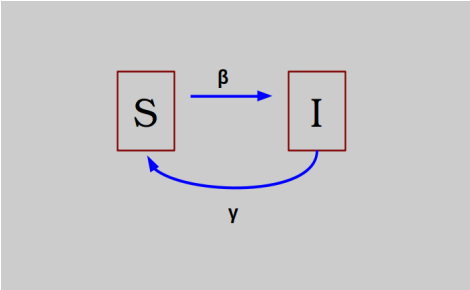

Figure 2.1.1: State-flow diagram for the SIS model

- in the unit of time, a constant portion β of the meeting between susceptible and infected is effective for the spread of the disease;
- in the unit of time, a constant portion γ of the infected heals and returns in the susceptible class.

Therefore, the model can be described by the following ODE system:

$$\begin{cases} \frac{dS(t)}{dt} &= -\frac{\beta}{N}S(t)I(t) + \gamma I(t) \\ \frac{dI(t)}{dt} &= \frac{\beta}{N}S(t)I(t) - \gamma I(t) \end{cases} \tag{2.1.1}$$

Since we have a constant population N, we can reduce the system to a single ODE considering:

$$\begin{cases} S(t) &= N - I(t) \\ \frac{dI(t)}{dt} &= \frac{\beta}{N}(N - I(t))I(t) - \gamma I(t) \end{cases} \tag{2.1.2}$$

One can easily find the steady state of the system (2.1.1) imposing:

$$\frac{dI(t)}{dt} = 0 \quad \Rightarrow \quad I_1^*\Big(\frac{\beta}{N}(N - I_2^*) - \gamma\Big) = 0$$

Therefore, there exists two steady states for the system. The first steady state is

$$(S_1^*, I_1^*) = (N, 0)$$

where S_1^* is finded replacing $I_1^* = 0$ in the first equation of the system (2.1.2). This steady state is called *Disease Free Equilibrium (DFE)* and it corresponds to the case in which the disease does not spread.

The second steady state can be found imposing

$$\begin{cases} \left(\frac{\beta}{N}(N - I_2^*) - \gamma\right) = 0 \\ S_2^* = N - I_2^* \end{cases}$$

Solving the system with respect to I_2^* and S_2^*, one can find that the second steady state is

$$(S_2^*, I_2^*) = \left(\frac{\gamma}{\beta}N, \left(1 - \frac{\gamma}{\beta}\right)N\right)$$

This second steady state is called *Disease Endemic Equilibrium (DEE)* and it correspond to the case in which the disease spreads.

2.1.1 Stability Analysis

Now, one can study the stability of the steady states of the SIS model. Consider a small perturbation around the equilibrium point

$$\Delta I = I(t) - I^*$$

One can prove that

$$\frac{d\Delta I(t)}{dt} = f(I^*) + \left[\frac{\beta}{N}(N - 2I^*) - \gamma\right]\Delta I - \frac{\beta}{N}\Delta I^2 \tag{2.1.3}$$

where

$$f(I^*) = \frac{\beta}{N}S^*(t)I^*(t) - \gamma I^*(t), \quad with \quad S^* = N - I^* \tag{2.1.4}$$

Neglecting the terms of order higher than one and noticing that $f(I^*) = 0$, we have the linearized differential equation

$$\frac{d\Delta I(t)}{dt} = \frac{df}{dt}_{|I=I^*} \cdot (\Delta I)$$

that is

$$\frac{d\Delta I}{dt} = \left[\frac{\beta}{N}(N - 2I^*) - \gamma\right]\Delta I \tag{2.1.5}$$

Consider the DFE point: calling $\Delta I = x$, we have the ordinary differential equation:

$$\frac{dx}{dt} = (\beta - \gamma)x \tag{2.1.6}$$

that has solution

$$x(t) = x(t_0) \cdot e^{(\beta-\gamma)(t-t_0)} \tag{2.1.7}$$

Therefore,

- for $\beta < \gamma$ the solution tends to zero as t tends to infinity $\Rightarrow$ we have a stable equilibrium point;
- for $\beta > \gamma$ the solution tends to infinity as t tends to infinity $\Rightarrow$ we have an unstable equilibrium point.

Moreover, $\beta = \gamma$ is the condition for which the stability of the system changes and it is called *bifurcation value*.
Now, consider the DEE point: calling again $\Delta I = x$, we have the following ordinary differential equation:

$$\frac{dx}{dt} = -(\beta - \gamma)x \tag{2.1.8}$$

that has solution

$$x(t) = x(t_0) \cdot e^{-(\beta-\gamma)(t-t_0)}$$

Therefore, contrary to the previous case,

- for $\beta < \gamma$ the equilibrium is unstable;
- for $\beta > \gamma$ the equilibrium is stable.

The Figure (2.1.2) graphically represents the results of the stability analysis. Indeed, for $\beta < \gamma$ the stationary solution $I_1 = 0$ is stable and it is represented with a solid line, meanwhile the stationary solution $I_2 = (1-\frac{\gamma}{\beta})N$ is unstable. Conversely, for $\beta > \gamma$ the solution I_1 becomes unstable and it is represented by a dashed line, meanwhile the solution I_2 is stable. Again, $\beta = \gamma$ is the bifurcation value for the stability of the point.
Notice that this is a local stability analysis and this solution approximately holds in a neighborhood of the equilibrium points. The solution of the non-linear system does not tends to infinity but it is limited by N.

In order to verify these different behaviours, it is possible to calculate the exact time dependent solution of $I(t)$ from the equation (2.1.2) through the method of separation of variables. Proceeding with the calculation, one can find that:

$$I(t) = \frac{N(1-\frac{\gamma}{\beta})}{1-(1-\frac{N}{I(t_0)}(1-\frac{\gamma}{\beta}))e^{-(t-t_0)(\beta-\gamma)}} \tag{2.1.9}$$

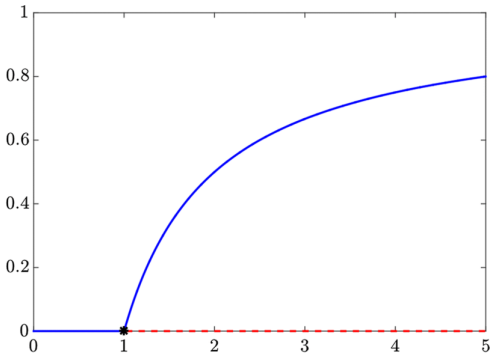

Figure 2.1.2: Bifurcation diagram SIS model when $\gamma = 1$

Notice that, for t tends to infinity, this solution is bounded by the population size N, as we said.

The analytic approach of the epidemic threshold is found when $I_1^* = I_2^*$, that is when $\beta = \beta_c = \gamma$, where β_c is called *critical value of* β. For the critical value, looking at the equation (2.1.2), we have the following ordinary differential equation for $I(t)$:

$$\frac{dI(t)}{dt} = -\frac{\beta}{N} I^2(t)$$

that has solution, using again the method of separation of variables:

$$I(t) = \frac{1}{\frac{1}{I(t_0)} + \frac{\beta}{N}(t - t_0)}$$

Therefore, we found that the analytic threshold for which the dynamic of the infected class change is given by $I(t) \approx t^{-1}$, as we can see from Figure 2.1.3.

2.2 SIR Model

The SIR epidemic model is a variant of the SIS model in which it is present one more population class: the recovered individuals $R(t)$. This is because the SIR model can be applied to infectious disease where waning immunity can happen and the recovered can become susceptible again after a proper amount of time. One can notice that, when the waning immunity is very fast,

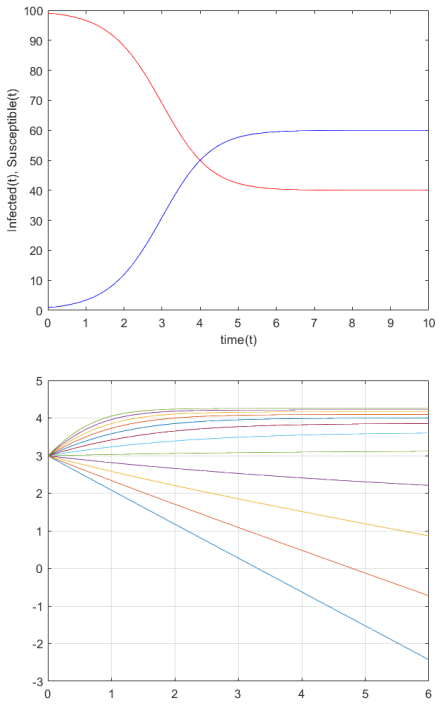

Figure 2.1.3: 1) Dynamics of SIS for $N = 100$, $\beta = 2.5$, $\gamma = 1$; 2) Trajectories of $I(t)$ for $\beta \in [0, 3.5]$

the SIR model can be approximated essentially by a SIS model. Therefore, the SIS model is a limit case of SIS. As before, we considering the state-flow diagram of the model, as we can see from Figure 2.2.1.

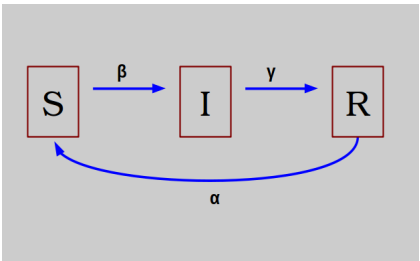

Figure 2.2.1: State-flow diagram for the SIR model

As before, β is the *infection rate*, γ is the *recovery rate*, whereas α is called *waning immunity rate* and it denotes the rate at which the immunity falls, so that the recovered become susceptible again.
The basic assumption of the model are:

- the total number of individuals in the population has constant size over time $N = I(t) + S(t) + R(t) \quad \forall t \in \mathbb{R}^+$;
- the population is homogeneously mixed among the infected and susceptible, that is every infected individual can equally transmit the disease to every susceptible individual.
- susceptible individuals get infected and infectious at rate β;
- infected individuals recovers at rate γ and develop immunity;
- recovered individuals became susceptible again at rate α.

The dynamics of the system is the following:

$$\begin{cases} \frac{dS(t)}{dt} &= -\frac{\beta}{N} I(t)S(t) + \alpha(N - S(t) - I(t)) \\ \frac{dI(t)}{dt} &= \frac{\beta}{N} I(t)S(t) - \gamma I(t) \\ R(t) &= N - S(t) - I(t) \end{cases} \tag{2.2.1}$$

In this model:

- $\frac{\beta}{N} I(t)S(t)$ is the number of infections caused by contact between infected and susceptible individuals in the population;
- $\gamma I(t)$ is the number of recovered individuals;
- $\alpha R(t)$ is the number of recovered individuals who re-enter into the susceptible state after waning immunity from infection.

One can compute the variation of the number of susceptible, infected and recovered individuals through the computation of *Euler scheme*:

$$\begin{cases} S(t + \Delta t) &= S(t) + \Delta t(- \frac{\beta}{N} S(t)I(t) + \alpha(N - S(t) - I(t))) \\ I(t + \Delta t) &= I(t) + \Delta t(\frac{\beta}{N} S(t)I(t) - \gamma I(t)) \\ R(t + \Delta t) &= N - S(t + \Delta t) - I(t + \Delta t) \end{cases}$$

This is useful in the computation of the numerical solution.

The model has two possible steady states: the *Disease Free Equilibrium*, where there are no infected individuals in the population, and the *Disease Endemic Equilibrium*, when the number of susceptible and infected individuals in this population get equilibrated at finite values. The basic SIR model has only fixed points as possible stationary solutions, that can be calculated by setting the rates of change $\frac{dS(t)}{dt}$ and $\frac{dI(t)}{dt}$ to zero.
For the DFE state the solution is given by

$$\begin{cases} S_1^* &= N \\ I_1^* &= 0 \\ R_1^* &= 0 \end{cases}$$

Meanwhile, for the DEE state the solution is given by

$$\begin{cases} S_2^* &= N\frac{\gamma}{\beta} \\ I_2^* &= N(1-\frac{\gamma}{\beta})\frac{\alpha}{(\gamma+\alpha)} \\ R_2^* &= N - S_2^* - I_2^* \end{cases}$$

Notice that the DEE of the SIR is similar to the DEE of the SIS with a "correction" term, that is $\frac{\alpha}{\gamma+\alpha}$. Therefore, it depends directly on the waning immunity.

2.2.1 Stability Analysis

In order to analyze the stability of the equilibrium states, since we work now on a two dimensional system, we look at the Jacobian matrix and its eigenvalues.
According to linearization via Taylor's expansion around the fixed point (S^*, I^*), as we did for the SIS model, we have that the linearized system is given by

$$\frac{d}{dt}\begin{bmatrix} S(t)-S^* \\ I(t)-I^* \end{bmatrix} = \begin{bmatrix} \frac{\partial f}{\partial S} & \frac{\partial f}{\partial I} \\ \frac{\partial g}{\partial S} & \frac{\partial g}{\partial I} \end{bmatrix}\Big|_{(S,I)=(S^*,I^*)} \cdot \begin{bmatrix} S(t)-S^* \\ I(t)-I^* \end{bmatrix} \tag{2.2.2}$$

The Jacobian matrix is given by

$$A := \begin{bmatrix} \frac{\partial f}{\partial S} & \frac{\partial f}{\partial I} \\ \frac{\partial g}{\partial S} & \frac{\partial g}{\partial I} \end{bmatrix}\Big|_{(S,I)=(S^*,I^*)} = \begin{bmatrix} -\frac{\beta}{N}I^* - \alpha & -\frac{\beta}{N}S^* - \alpha \\ \frac{\beta}{N}I^* & \frac{\beta}{N}S^* - \gamma \end{bmatrix} \tag{2.2.3}$$

One can calculated the eigenvalues of the matrix A solving $A\vec{u} = \lambda\vec{u}$ and setting

$$det|A - \lambda\mathbb{I}| = 0 \tag{2.2.4}$$

For the DFE state $(S_1^*, I_1^*, R_1^*) = (N, 0, 0)$, the characteristic equation, given by the equation (2.2.4), is

$$\lambda^2 + \lambda\alpha\Big(\frac{\beta - \gamma}{\gamma + \alpha} + 1\Big) - \alpha(\beta - \gamma) = 0$$

Therefore, the corresponding eigenvalues are

$$\begin{cases} \lambda_1 &= -\alpha \\ \lambda_2 &= \beta - \gamma \end{cases}$$

In general, the fixed point is stable when the eigenvalues have negative real part and unstable when at least one eigenvalue is positive. Therefore, the stability of the system changes when one of the eigenvalues becomes zero: this is a *transcritical bifurcation*.
Therefore, we have that

- for $\beta < \gamma$ the DFE is stable;
- for $\beta > \gamma$ the DFE is unstable.

In Figure 2.2.2 one can see that for $\beta < \gamma$ the solution tends to the DFE in a short time, whereas for $\beta > \gamma$ the solution shows an oscillatory behaviour.
If the eigenvalues provide information about the stability of the linearized system, the corrisponding eigenvectors generate the stability, instability and central subspaces of the linearized system. Gives $\lambda_j = a_j + ib_j$ eigenvalues and $w_j = u_j + iv_j$ the corresponding eigenvectors, than
$E_s =< u_j, v_j : a_j < 0 >$ is called stable subspace, $E_u =< u_j, v_j : a_j > 0 >$ is called unstable subspace and $E_c =< u_j, v_j : a_j = 0 >$ is called central subspace of the linearized system.
To calculate the corresponding eigenvectors we use the equation

$$(A - \lambda_i\mathbb{I})\vec{u_i} = 0 \quad i = 1, 2$$

where $\vec{u_i}$ is the eigenvector that we want to find.

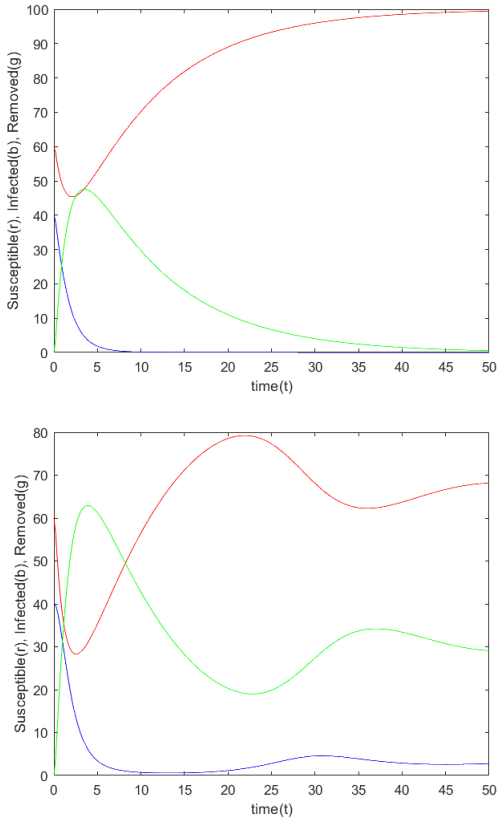

Figure 2.2.2: Numerical solution of the SIR model by Euler scheme with $\gamma = 1$, $\beta = 0.8$ and $\beta = 1.5$

For λ_1, the corresponding eigenvector is given by

$$\vec{u_1} = \frac{1}{\sqrt{1 + (\frac{\gamma-\beta-\alpha}{\beta+\alpha})^2}} \begin{bmatrix} 1 \\ (\frac{\gamma-\beta-\alpha}{\beta+\alpha}) \end{bmatrix}$$

Meanwhile, for λ_2 the corresponding eigenvector is given by

$$\vec{u_2} = \begin{bmatrix} 1 \\ 0 \end{bmatrix}$$

Looking at Figure 2.2.3, one can see that for $\beta < \gamma$ the infected solution tends to the same eigenvector direction. If β starts to increase we can see that the solution takes longer to reach the equilibrium. When β exceeds γ the solution of the infected change its direction and goes aways from the

eigenvectors direction and the equilibrium.

For the DEE state the eigenvalues are given by

$$\begin{cases} \lambda_1 = a + \sqrt{b} \\ \lambda_2 = a - \sqrt{b} \end{cases}$$

where $a := -\frac{\alpha}{2}(1 + \frac{\beta-\gamma}{\alpha+\gamma})$ and $b := [\frac{\alpha}{2}(1 + \frac{\beta-\gamma}{\alpha+\gamma})]^2 - (\beta - \gamma)\alpha$. Again, the equilibrium point is stable if the real part of the eigenvalues is negative. In this case we have $a < 0$ if

$$1 + \frac{\beta - \gamma}{\alpha + \gamma} > 0$$

that is is always true.
Therefore, the DEE state is stable. Moreovere,

- if $b > 0$ the eigenvalues are real numbers, giving the contraction or expansion of the trajectories near to the considered fixed point;
- if $b < 0$ the eigenvalues became complex, where the real part gives the contraction or expansion of the trajectories near to the equilibrium whereas the immaginary part causes oscillations of the trajectories spiraling into the fixed point.

$$\begin{cases} \lambda_1 = a + i\sqrt{|b|} \\ \lambda_2 = a - i\sqrt{|b|} \end{cases}$$

The correspondent eigenvectors of the DEE state can be calculated as before. For the first eigenvalue λ_1 the correspondent eigenvector $\vec{u_1}$ is given by

$$\vec{u_1} = \frac{1}{\sqrt{1 + (\frac{a-\sqrt{b}}{\gamma+\alpha})^2}} \cdot \begin{bmatrix} 1 \\ \frac{1}{\sqrt{1+(\frac{a-\sqrt{b}}{\gamma+\alpha})^2}} \end{bmatrix}$$

Meanwhile, for the eigenvalue λ_2 the correspondent eigenvector $\vec{u_2}$ is given by

$$\vec{u_2} = \frac{1}{\sqrt{1 + (\frac{a+\sqrt{b}}{\gamma+\alpha})}} \cdot \begin{bmatrix} 1 \\ \frac{a+\sqrt{b}}{\gamma+\alpha} \end{bmatrix}$$

Looking at Figure 2.2.4, we can see that until $b > 0$ the infected solution tends to the equilibrium point, that is the eigenvectors direction, that approximately following a straight line. When $\beta < 0$ the solution spiral to-

wards the equilibrium.
The epidemic dynamics as a function of the parameter β shows the spread of the epidemic when $\beta > \gamma$ and its extinction when $\beta < \gamma$. Moreover, for $\alpha > 0$ we assume that the disease gives a waning immunity and we observe oscillations resembling new epidemic waves.

2.2.2 Basic Reproduction Number

It is defined *Basic Reproduction number* the number of secondary cases $I_s(t \to \infty)$ generated from a primary case with $I_p(t_0) = 1$ in a completely susceptible population $\frac{S}{N} \approx 1$.

$$R_0 := \frac{I_s(t \to \infty)}{I_p(t_0)} \tag{2.2.5}$$

During the COVID-19 pandemic, the *Basic Reproduction Number* is monitored by to determine measures to be taken to control the spread of the pandemic.
Considering the equation for $\frac{dI}{dt}$ in the system (2.2.1) when $S \approx N$, we call

$$\begin{cases} \frac{dI_p}{dt} = -\gamma I_p \\ \frac{dI_s}{dt} = \beta I_p \end{cases} \tag{2.2.6}$$

By solving the ordinary differential equations we have that

$$\begin{cases} I_p(t) = I_p(t_0)e^{-\gamma(t-t_0)} \\ I_s(t) = \frac{\beta}{\gamma} I_p(t_0)(1 - e^{-\gamma(t-t_0)}) \end{cases} \tag{2.2.7}$$

Considering the limit as $t \to \infty$ we have that

$$R_0 = \frac{\beta}{\gamma} \frac{I_p(t_0)}{I_p(t_0)} = \frac{\beta}{\gamma} \tag{2.2.8}$$

One can notice that

- if $R_0 < 1$, the infection will die out in the long run;
- if $R_0 > 1$, the infection will be able to spread in a population.

In general, when the initial susceptible size S_0 does not coincide with the total population size ($S_0 \neq N$), one can consider

the *Momentary reproduction ratio* $r(t)$, defined as

$$r(t) = \frac{\beta}{\gamma}\frac{S_0}{N}$$

or the *Growth rate* $\lambda = \beta - \gamma$.

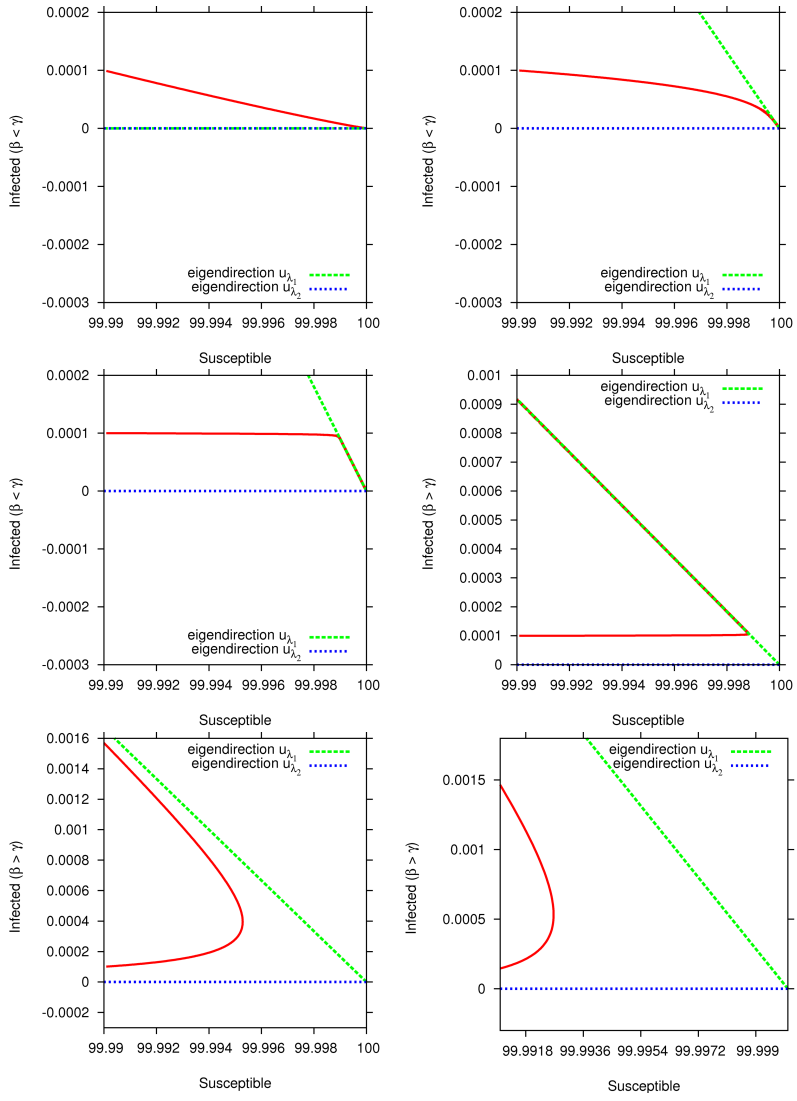

Figure 2.2.3: Eigenvectors for the DFE state in function of β

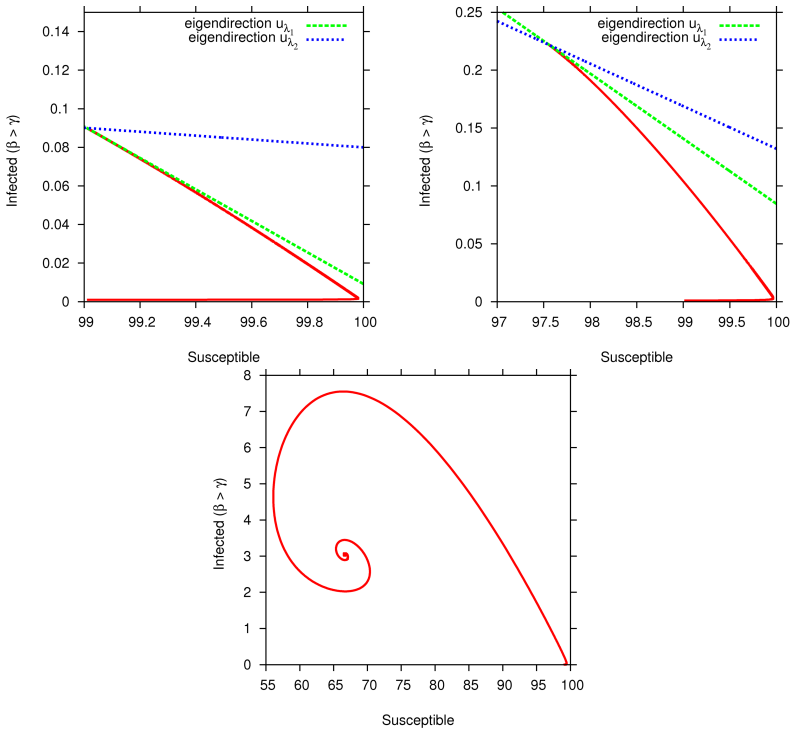

Figure 2.2.4: Eigenvectors for the DEE state in function of β

Chapter 3

The SHAR model

In this chapter, we described and analyzed the SHAR model that is used in our analysis. Then, we used this ODE model to find a numerical solution that can match the data curve of the Hospitalized people detected in the first year of pandemic in Italy.

3.1 The model

To start an analysis of the COVID-19 disease, a more accurate model is necessary than SIS and SIR models.
We considered the SHAR model, that is a modified SIR model in which the infected class is stratified into two subclasses: the hospitalized $H(t)$ and the asymptomatic $A(t)$. Indeed, a COVID-19 infection can be more severe for old people or people with pre-existing comorbidity leading to hospitalization, meanwhile it can be less severe for young people which can be asymptomatic. The dynamic of the SHAR model is the following:

$$\begin{cases} \frac{dS(t)}{dt} = -\beta \frac{S(t)}{N}(H(t) + \phi A(t)) \\ \frac{dH(t)}{dt} = \eta\beta \frac{S(t)}{N}(H(t) + \phi A(t)) - \gamma H(t) \\ \frac{dA(t)}{dt} = (1-\eta)\beta \frac{S(t)}{N}(H(t) + \phi A(t)) - \gamma A(t) \\ \frac{dR(t)}{dt} = \gamma(H(t) + A(t)) \end{cases} \tag{3.1.1}$$

where β is the infection rate, γ is the removal rate, η is the portion of hospitalized people and ϕ is the scaling factor to distinguish infectivity (baseline of severe cases). In the SHAR model, the constant ϕ describes the increase

in the class of infected due to the asymptomatic people. Indeed, thanks to ϕ, the infection rate become $\phi\beta$ for the asymptomatic class.
Notice that in the system (3.1.1) a constant β is considered.

3.1.1 Exponential growth factor

Before imposing control measures, the initial phase of the epidemic exhibits an exponential growth, thank to the fact that the population is considered completely susceptible $S(t) \approx N$ for small time t.
We want to determine the *exponential growth factor* of the system. To do this, we consider at the beginning only the dynamics of $H(t)$ and $A(t)$. Looking at the system (3.1.1), we can write in a compact form:

$$\frac{d}{dt}\begin{bmatrix} H(t) \\ A(t) \end{bmatrix} = \left(\begin{bmatrix} \eta\frac{\beta}{N}S(t) & \phi\eta\frac{\beta}{N}S(t) \\ (1-\eta)\frac{\beta}{N}S(t) & \phi(1-\eta)\frac{\beta}{N}S(t) \end{bmatrix} - \begin{bmatrix} \gamma & 0 \\ 0 & \gamma \end{bmatrix} \right) \begin{bmatrix} H(t) \\ A(t) \end{bmatrix} \tag{3.1.2}$$

Considering $S(t) \approx N$, we have that

$$\frac{d}{dt}\vec{x} = J\vec{x} \tag{3.1.3}$$

where $\vec{x} = [H(t) \quad A(t)]'$, $J = B - G$ with

$$B = \beta \begin{bmatrix} \eta & \phi\eta \\ (1-\eta) & \phi(1-\eta) \end{bmatrix}$$

and

$$G = \begin{bmatrix} \gamma & 0 \\ 0 & \gamma \end{bmatrix}$$

The solution of the equation (3.1.3), via eigenvalue decomposition of J, is given by

$$\vec{x} = Te^{\Lambda(t-t_0)}T^{-1}x(\vec{t_0}) \tag{3.1.4}$$

with $\Lambda = T^{-1}JT$ and T is the matrix that have as column the eigenvectors of J. Let us calculate the eigenvalues of the J matrix:
we consider the matrix

$$J - \lambda\mathbb{I} = \begin{bmatrix} \beta\eta - \gamma - \lambda & \beta\phi\eta \\ \beta(1-\eta) & \beta\phi(1-\eta) - \gamma - \lambda \end{bmatrix}$$

and then we impose $det(J - \lambda\mathbb{I}) = 0$. Then,

$$(\beta\eta - \gamma - \lambda)[\beta\phi(1-\eta) - \gamma - \lambda)] - \beta^2\phi\eta(1-\eta) = 0$$

By algebraical computation, from the equation above one can find the eigenvalues:

$$\lambda_{1,2} = \frac{1}{2}\beta(\phi(1-\eta)+\eta) - \gamma \pm \frac{1}{2}(\phi(1-\eta)+\eta)$$

The dominating growth factor is given by the largest eigenvalue, that is

$$\lambda_1 = \beta(\phi(1-\eta)+\eta) - \gamma$$

meanwhile the second eigenvalue is given by $\lambda_2 = -\gamma$.
Now, we want to compute the eigenvectors of J, solving $JT = T\lambda$.
One can find that

$$T = \begin{bmatrix} \eta & -\phi \\ 1-\eta & 1 \end{bmatrix}$$

and the inverse matrix is given by, via the computation of the cofactor matrix,

$$T^{-1} = \frac{1}{\eta + \phi(1-\eta)} \begin{bmatrix} 1 & \phi \\ \eta & \eta \end{bmatrix}$$

Therefore, since from equation (3.1.4),

$$\begin{bmatrix} H(t) \\ A(t) \end{bmatrix} = Te^{\Lambda(t-t_0)}T^{-1} \begin{bmatrix} H_0 \\ A_0 \end{bmatrix} \tag{3.1.5}$$

we have that

$$\begin{bmatrix} H(t) \\ A(t) \end{bmatrix} = \begin{bmatrix} K_{H_1} \\ K_{A_1} \end{bmatrix} e^{\lambda_1(t-t_0)} + \begin{bmatrix} K_{H_2} \\ K_{A_2} \end{bmatrix} e^{\lambda_2(t-t_0)} \tag{3.1.6}$$

where the entries K_{H_1}, K_{H_2}, K_{A_1}, K_{A_2} depend on the initial values H_0 and A_0 and on the parameter of the system.
Passing to the limit as $t \longrightarrow \infty$, one can find that

$$\begin{bmatrix} H(t \to \infty) \\ A(t \to \infty) \end{bmatrix} = \begin{bmatrix} K_{H_1} \\ K_{A_1} \end{bmatrix} e^{\lambda_1(t-t_0)} \tag{3.1.7}$$

Indeed, the second part of the equation (3.1.6) tends to zero as $t \longrightarrow \infty$. Therefore, one can see that without control measures the epidemic have an exponential growth with exponential growth rate given by λ_1.

3.1.2 SHAR model with non-constant infection rate: control measures function

As we had explained in Chapter one, after the initial spread of the pandemic in Italy, that coincides with an exponential growth phase of the infected cases, severe controlled measures were adopted which ended with the imposition of a quarantine. The Italian lockdown started on the 9th of March 2020 and ended on the 8th of May 2020.
To describe the effect of the control measures on the infection data curve we have to modify the SHAR model that we presented in the system (3.1.1) with a system in which the infection rate is a function of time $\beta = \beta(t)$. Therefore, we redefine the SHAR model as

$$\begin{cases} \frac{dS(t)}{dt} = -\beta(t)\frac{S(t)}{N}(H(t) + \phi A(t)) \\ \frac{dH(t)}{dt} = \eta\beta(t)\frac{S(t)}{N}(H(t) + \phi A(t)) - \gamma H(t) \\ \frac{dA(t)}{dt} = (1-\eta)\beta(t)\frac{S(t)}{N}(H(t) + \phi A(t)) - \gamma A(t) \\ \frac{dR(t)}{dt} = \gamma(H(t) + A(t)) \end{cases} \tag{3.1.8}$$

We model the effort of the disease control measures introduced the time dependent function

$$\beta(t) = \beta_0\sigma_-(x(t)) + \beta_1\sigma_+(x(t)) \tag{3.1.9}$$

where β_0 and β_1 are constant parameters and the functions

$$\sigma_-(x(t)) = \frac{1}{1 + e^{x(t)}}$$

is called *downward sigmoidal function* and

$$\sigma_+(x(t)) = \frac{1}{1 + e^{-x(t)}}$$

is called *upward sigmoidal function*. Indeed, one can see that thanks to the effort of $\sigma_-(x)$ the numerical solution of the system (3.1.8) is slowed

down, meanwhile the effort of $\sigma_+(x)$ accelerates the numerical solution. This functions are able to describe well the gradual slowing down of the epidemics with β_0 and β_1 that vary.
Notice that the function $x(t)$ is defined as

$$x(t) = a(t - t_c)$$

where t_c is a time that coincides with the start of the Lockdown and a is a constant parameters. We find numerically that $a = 0.38d^{-1}$.

3.1.3 SHAR model with non-constant infection rate: seasonality function

After the relaxation of the control measures, one can consider the effect of seasonality. Indeed, in respiratory diseases such as COVID-19 seasonality can have a great impact in the slow down of the infectious cases.
To model the seasonality effect we substituted in the system (3.1.8) a function for $\beta(t)$ defined as follow:

$$\beta(t) = \beta_0(1 + \beta_1 cos(\omega t)) \tag{3.1.10}$$

where β_0, β_1 and ω are constant parameters. The parameters β_0 and β_1 described respectively the non-seasonality effect and the seasonality effect, while ω represent the frequency of oscillation. In particular,

$$\omega = \frac{2\pi}{365}$$

Notice that the seasonality function for the infection rate is a sinusoidal function. This choice is made to describe the oscillatory nature of the data curve of the COVID-19 infected cases.

3.1.4 Data and parameters

After the definition of the model, we have to determine the parameters of the SHAR model which can describe the data curve.
In this study, we focused on the first year of the pandemic in Italy, before the vaccination plan started.

From Figure 3.1.1, one can see that the first year of COVID-19 pandemic in Italy was characterized by two waves of infections: the first one with peak in March 2020 which was controlled thanks to a hard lockdown, the second one with peak in November 2020, which was controlled thanks to a partial lockdown. The second partial lockdown was characterized by a classification of the regions according to a risk scale, which differentiated them by color, as one can see in Figure 3.1.2.

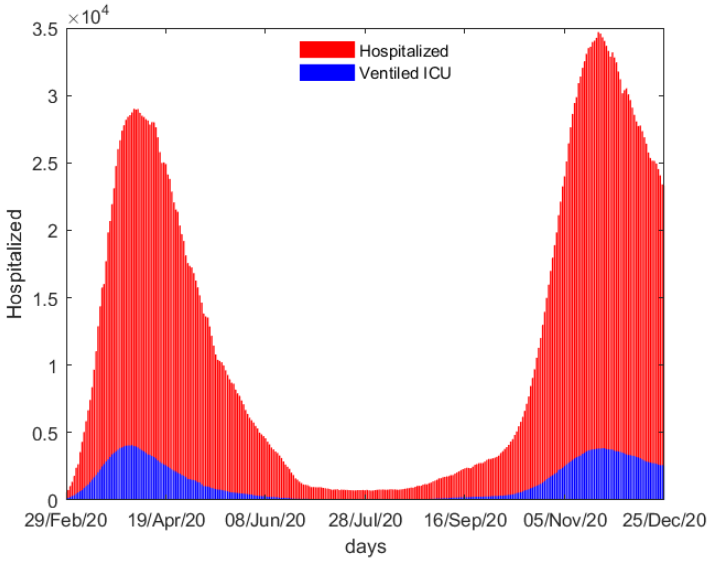

Figure 3.1.1: Data of the total Hospitalized people in the first year of pandemic in Italy

We started to analyze the data dividing the first year of pandemic in phases, according to the trend of the curve in each period, in order to identify the correct parameters for the SHAR model. In the simpler SHAR model, the parameters β (infection rate), γ (removal rate), η (portion of hospitalized people) and ϕ (scaling factor) are constant. This structure is useful to describe the initial exponential phase of the spread of COVID-19, in which no measures had been implemented to avoid contagions. But, since COVID-19 trend change in time due to control measures that the government implemented, we have to define different parameters for different phases of the pandemic.
Notice that the following analysis is made only for the Hospitalized class.

This because in Italy one of the main aspects of the emergency was the saturation of the hospitalized and the difficulty of coping with the number of new hospitalizations.

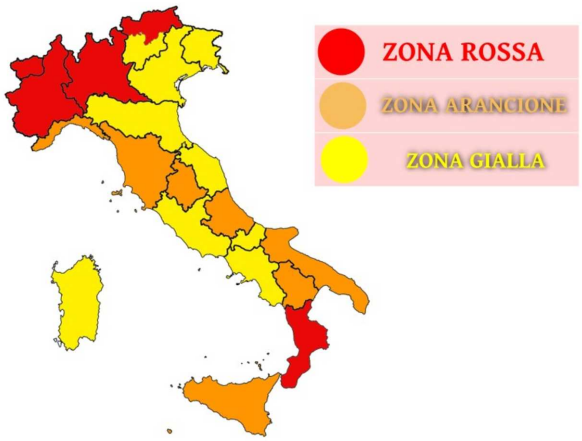

Figure 3.1.2: Scale of risk from November 2020

3.1.5 Phase One: Exponential phase

We start describing the first phase on the pandemic in which there were no control measures. For Italy this phase goes from the 24th of February (when the first case was recognized) to the 9th of March (when lockdown started). Because of the quick spread of the disease and the limitation in testing capacity, at the beginning of the pandemic in Italy the total number of infected people corresponded more or less to the number of hospitalized people. For this reason, for the first 15 days of the pandemic in Italy we plot the data and the numerical solution for the hospitalized to find the correct parameters.
Implementing the model on MATLAB (see Appendix A), we tuned the parameters in order to match the epidemiological data curve as much as we can. We started using the parameters for the exponential phase of COVID-19 in the Basque Country [15].
The best parameters for which the curve match the data are:

- $\gamma = 0.125$
- $\beta = 3.2\gamma$
- $\eta = 0.65$

- $\phi = 1.3$

with initial condition $H_0 = 80$ and $A_0 = 110$.
From [15], we can see that the parameters for the Basque Country are significantly different. In particular, the recovery rate γ is significantly smaller ($\gamma = 0.05d^{-1}$) and it is the same for the portion of hospitalized ($\eta = 0.45$). Meanwhile, the scaling factor ϕ is slightly higher for the Basque country ($\phi = 1.6$) and β is the same for both of them. This reflects the fact that the COVID-19 crisis in Italy was more severe, in terms of number of infections and saturation of the hospitals and the ICU facilities.

3.1.6 Phase two: Lockdown phase

For the second phase, we considered the SHAR model in which a control measure function is implemented (look at the model (3.1.8) with the equation (3.1.9) for $\beta(t)$).
In this case, we found that

- $\gamma = 0.125$
- $\eta = 0.9$
- $\phi = 1.21$
- $\beta_0 = 0.2$
- $\beta_1 = 0.095$

Compering to the previous phase, the values of some parameters changed. In particular, notice that we have a bigger η. This is reasonable because, as one can see from Figure 3.1.4, in this phase we have a peak of the infectious and consequently of the hospitalized people.
Moreover, in this phase we have a slightly smaller ϕ. Remember that ϕ describes the increase in the infected class due to the asymptomatic people. Therefore, in this phase it is reasonable to assume that this parameter is smaller, because the people were forced to stay at home because of the quarantine.
For what concern the parameters β_0 and β_1, they describe the contribution of the control measures function. In particular, β_0 is the contribution given by the downward sigmoidal function and β_1 is the contribution given by

the upward sigmoidal function. In this phase assuming $\beta_0 > \beta_1$ is correct, because we want to describe the change of trend of the epidemiological data curve and, consequently, the presence of a peak.
From Figure 3.1.4, notice that there are two weeks of delay before the control measures started producing effects. Indeed, one can observe a change of the trend after this period. This is due to the large number of the infections in the phase one.

3.1.7 Phase three: The end of the lockdown and release of the control measures

For the third phase, we changed the time-dependent function for $\beta(t)$. Here, we started to assume the seasonality effect. For this reason, $\beta(t)$ have the form described in the equation (3.1.10).
For this phase, we found that:

- $\gamma = 0.125$
- $\eta = 0.65$
- $\phi = 1.3$
- $\beta_0 = 0.15$
- $\beta_1 = 0.095$

Notice that the portion of hospitalized people η is less than the previous phase. This reflects the seasonality effect and the decrease in the hospitalized class, because of the increase of the temperature.
Meanwhile, ϕ assumed the same value that it has in phase one and this reflect the end of the Lockdown and the new possibility of the people to meet again.

3.1.8 Phase four: Coexistence with the virus

In this phase we continued to use the seasonality function for $\beta(t)$. As compared to the previous case, in this phase changed only the parameters β_0 and β_1, that becomes:

- $\beta_0 = 0.1$

- $\beta_1 = 0.03$

Therefore, the seasonality effect is decreases. This is in agreement with the epidemiological curve that started to change its trend, as we can see from Figure 3.1.4.

3.1.9 Phase five: New Restrictions

At the end of the summer 2021 the number of new infections in Italy started to increase again. The Italian Government introduced some new restriction, but their was so mild that did not stop the speed of the epidemiological curve. For this reason we continued to use for $\beta(t)$ the seasonality function. The parameters that we found are:

- $\gamma = 0.125$
- $\eta = 0.85$
- $\phi = 1.3$
- $\beta_0 = 0.1$
- $\beta_1 = 0.003$

As one can see, the parameter β_1 that described the seasonality effort is very low. This describes the effect of seasonality in this phase can not delay the increase of the epidemiological curve. Moreover, in this period winter was coming and the temperature became low.
Moreover, we can see that the parameter η is greater than the previous phase and this reflects the increment in the hospitalized class.

3.1.10 Phase six: Partial Lockdown

In November 2021 the increase of the infectious cases was so significant such that it was necessary to implement more severe control measures. For this reason, a partial lockdown started. As we saw at the the beginning of this chapter, this second lockdown was characterized by a classification of the regions according to a risk scale and the control measures adopted for all regions depended on this classification. Anyway, in the whole Country a curfew was established from 10 pm to 5 am of the next day. Because of this background, for this phase we considered again $\beta(t)$ described by the control

measures function of the second phase.
We found the following parameters for the description of this phase:

- $\gamma = 0.127$
- $\eta = 0.65$
- $\phi = 1.2$
- $\beta_0 = 0.25$
- $\beta_1 = 0.15$

In this following table there is a summary of the whole parameters that we used for each phase.

Phase	gamma	eta	phi	beta	Beta0	Beta1	a	omega
1: Initial spread (exponential phase) 24/02/2020-09/03/2020	0.125	0.65	1.3	3.2*gamma				
2: Lockdown phase 09/03/2020-03/05/2020 (Control Measers)	0.125	0.9	1.21		0.2	0.095	0.38	
3: Lockdown's end 03/05/2020-18/07/2020 (seasonality)	0.125	0.65	1.3		0.15	0.095		2*pi/365
4: Coexistence with the virus 18/07/2020-07/10/2020 (seasonality)	0.125	0.65	1.3		0.1	0.03		2*pi/365
5: New control measures 07/10/2020-06/11/2020 (seasonality)	0.125	0.85	1.3		0.1	0.003		2*pi/365
6: Partial Lockdown 06/11/2020-01/01/2021 (Control Measures)	0.127	0.65	1.2		0.25	0.15	0.38	

Figure 3.1.3: Parameters table

The figure below shows the match between the epidemiological curve of the first year of pandemic in Italy and the numerical solution of the SHAR model that we found. Despite the simplicity of the chosen model, one can observe that we reached a good approximation.
Notice that in the first phase the two curves does not match well. We supposed that this happened because at the beginning of the pandemic the data detected are not completely reliable. Indeed, due to the large spread of the disease, in the first phase of the pandemic there was a low testing capacity of the infected people.

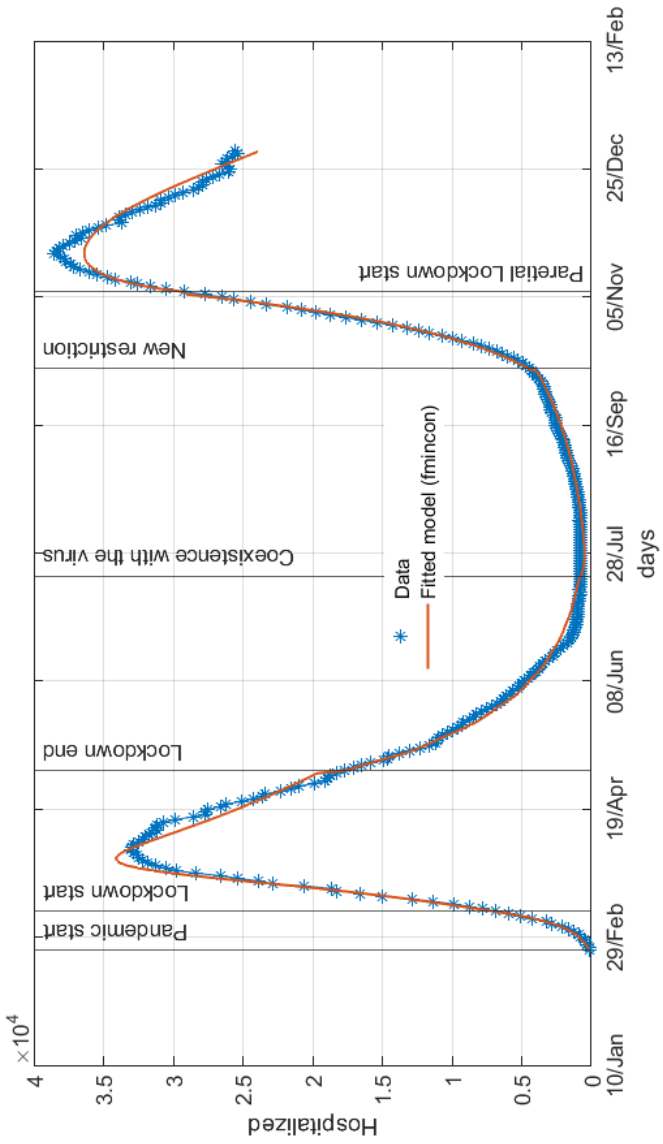

Figure 3.1.4: Final match of data curve and numerical solution

Chapter 4

Future projects and applications

In this Chapter we describe future projects and possible applications of our study. Firstly, we modify the SHAR model to continue the analysis for the whole emergency period. Then, we describe the stochastic formulation of the SHAR model and an optimization problem that can be used to determine a balance between economic cost and health cost. Finally, we describe the spatial formulation of the SHAR model.

4.1 Modification of the SHAR model: the SHARD model

Since we reached a good approximation with the SHAR model for the first year of the spread of COVID-19 disease in Italy, we would continue the description extending it to the whole emergency period.
At the beginning of 2021 we had a new scenario of the epidemic because vaccination campaign started. Therefore, it is necessary that the solution of the model interpretes the decrease in the infected class due to the effect of vaccination. This can be easily implemented in the model considering a new parameter α, that can describes the immunity reached by an individual that received the vaccine. This parameter describes a waning immunity, because we know that with the current vaccine an individual cannot reach a complete immunity from the coronavirus.
Another useful aspect to taking into account is the import factor ρ, that can

describe the import to the total population given by the immigration, births and deaths. This can be implemented in the model by multiply the total population N by ρ.
In the previous model we supposed the total population N constant in order to simplify the model and because, during the first year of pandemic, the travels between different country was severely forbidden.
Moreover, in the new model it can be useful to describe the dynamics of deaths. For this reason we could define the class of the deceased individuals D, that depends on the mortality rate μ. During the emergency period in Italy the mortality rate reached the value of $\mu = 12.5$. One can calculate this number finding the number of deaths during the specify period, then dividing it by the population size.
The definition of the SHARD is the following:

$$\begin{cases} \frac{dS(t)}{dt} = -\beta\frac{S(t)}{N}(H(t) + \phi A(t) + \rho N(t)) + \alpha R(t) \\ \frac{dH(t)}{dt} = \eta\beta\frac{S(t)}{N}(H(t) + \phi A(t) + \rho N(t)) - \gamma H(t) \\ \frac{dA(t)}{dt} = (1-\eta)\beta\frac{S(t)}{N}(H(t) + \phi A(t) + \rho N(t)) - \gamma A(t) \\ \frac{dR(t)}{dt} = \gamma(H(t) + A(t)) - \alpha R(t) \\ \frac{dD(t)}{dt} = \mu H(t) \end{cases} \tag{4.1.1}$$

In this formulation the parameters α, ρ and μ are assumed constant. Moreover, the removed class consists in this new formulation with the population class of the healed individuals.
An interesting results could be given by analyzing how the dynamics of the hospitalized class changes due to the vaccination. It could be taken that the parameter η, which gives us the portion of the hospitalized class, is describes by a time-dependent function, as we did for the infection rate β, that depends on the waning immunity α.

4.2 The stochastic formulation

Once a good model has been determined for the whole emergency period, from February 2020 to March 2022, our idea is to move to a stochastic formulation of the system. Define the stochastic model can be useful to determine the future trend of the epidemic.
The stochastic SHAR model is modeled as a continuous-time Markov process

to capture population noise [13]. The model could be reformulated using a *Master Equation* for the dynamics of probability, that consists of a set of differential equations of the first order that describe the temporal evolution of the probability of a system to occupy each of the possible states at a certain time t. The basic formulation of the Master Equation is given by:

$$\frac{d\vec{P}}{dt} = A\vec{P}$$

in which $\vec{P}$ is the vector of all the possible states and A is the infinitesimal generator of the Markov process matrix [20].
The explicit formulation for the SHAR model is given by:

$$\begin{aligned}
\frac{d}{dt}p(S,H,A,t) &= \eta\frac{\beta}{N}(S+1)Ap(S+1,H-1,A,t) \\
&+ (1-\eta)\frac{\beta}{N}(S+1)(A-1)p(S+1,H,A-1,t) \\
&+ \eta\frac{\beta}{N}(S+1)\phi(H-1)p(S+1,H-1,A,t) \\
&+ (1-\eta)\frac{\beta}{N}(S+1)\phi Hp(S+1,H,A-1,t) \\
&+ \gamma(A+1)p(S,H,A+1,t) \\
&+ \gamma(H+1)p(S,H,A,t) \\
&+ \alpha(N-(S-1)-H-A)p(S-1,H,A,t) \\
&- \Big(\frac{\beta}{N}S(A+\phi H)+\gamma(A+H)+\alpha(N-S-H-A)\Big)p(S,H,A,t) \qquad (4.2.1)
\end{aligned}$$

From this formulation of the system one can produce simulations of the realizations of a stochastic process, through the Gillespie algorithm [7]. In this way a "toy" data set is built, useful to determine the parameters of the stochastic model through numerical methods (as we did for the deterministic model). Once the stochastic model has been determined, we can predict the future trend of the epidemic and this could be useful in order to determine the condition for the implementation of any containment measures and to guarantee a right response from health facilities.
Understanding the dynamics of stochastic populations and how they interact with the deterministic components of epidemiological models have maximum benefit on the practical predictability of the dynamical system by analyzing the available epidemiological data via mathematical methods, since the clas-

sical parameters estimation and its application are generally restricted to fairly simple dynamical scenarios [14].

4.3 Optimization problem

The diffusion of COVID-19 caused a public health crisis but the measures necessary to control the spread of the virus led to serious economic and social crisis.
We want to present a technique to optimally control the infectious rate $\beta(t)$ so as to minimize the number of individuals that get infected from the disease, in order to avoid the collapse of the health system. The idea is to define a control function for $\beta(t)$ in order to take the Basic Reproduction number $R_0(t)$ (3.1.10) below a given threshold. In particular, we need that $R_0(t) < 1$ to have an extinction of the disease.
Using a mathematical structure, the optimal problem for $\beta(t)$ is given by:

$$\begin{cases} \dot{\beta(t)} = \mathbf{f}(\beta(t), g(t)) \quad for \quad t > 0 \\ \beta(0) = \bar{\beta} \end{cases} \tag{4.3.1}$$

where $\bar{\beta}$ is a given constant value and $g : [0, \infty) \longrightarrow A$ is the control function, with $A \in \mathbb{R}$. Notice that $\beta(t) : [0, \infty) \longrightarrow \mathbb{R}$.
Our task will be to determine what is the "best" definition for the control function $g(t)$ for our system. For this we need to specify a specific *payoff* criterion.
Let us define the *payoff functional* as

$$P[g(\cdot)] := \int_o^T r(\beta(t), g(t))\, dt + h(\beta(T))$$

where $r : \mathbb{R} \times A \longrightarrow$ and $h : \mathbb{R} \longrightarrow \mathbb{R}$ are given function called respectively *running payoff* and *terminal payoff*. Moreover, $T > 0$ is called terminal time.
Our aim is to find a control $\hat{g}(\cdot)$ which maximizes the payoff. In other words, we want that

$$P[\hat{g}(\cdot)] \geq P[g(\cdot)]$$

for all controls $g(\cdot) \in A$. Such a control $\hat{g}(\cdot)$ is called *optimal*.
Obviously, this goal presents us with various mathematical issues:

- Does an optimal control exist?
- How can we characterize an optimal control mathematically?
- How can we construct an optimal control?

To answer to this question, we refer to [11].

4.4 The SHARUCD model

A further generalization that can be applied to the case of COVID-19 is given by the SHARUCD model [17]. It consists in a SHAR model in which new population classes are added: the class U of the hospitalized individuals in intensive care unit (ICU) and the class D of the deceased individuals. Moreover, we could considered classes that take into account the cumulative cases: C_H is the class of the cumulative hospitalized, C_A is the class of the cumulative asymptomatic, C_U is the class of the cumulative ICU and C_R is the class of the cumulative removed. Considering these classes can make the description more complete and can be useful for determining the conditions of saturation of hospitals.
The SHARUCD model is the following:

$$\begin{cases} \frac{dS}{dt} = -\beta \frac{S}{N}(H + \phi A + \rho N) \\ \frac{dH}{dt} = \eta\beta \frac{S}{N}(H + \phi A(t) + \rho N) - (\gamma + \mu + \nu)H \\ \frac{dA}{dt} = (1-\eta)\beta \frac{S}{N}(H + \phi A(t) + \rho N) - \gamma A \\ \frac{dR}{dt} = \gamma(H + A + U) \\ \frac{dU}{dt} = \nu H - (\gamma + \mu)U \\ \frac{dC_H}{dt} = \eta\beta \frac{S}{N}(H + \phi A + \rho N) \\ \frac{dC_A}{dt} = \psi(1-\eta)\beta \frac{S}{N}(H + \phi A + \rho N) \\ \frac{dC_R}{dt} = \gamma(H + U + \psi A) \\ \frac{dC_U}{dt} = \nu H \\ \frac{dD}{dt} = \mu(H + U) \end{cases} \tag{4.4.1}$$

In this model new parameters are considered:

- ν represents the portion of hospitalized individuals that develop a serious form of illness and enter in intensive care units (ICU);

- μ is the mortality rate;
- ψ describes the portion of the asymptomatic individuals recorded by the testing operation in comparison with all the cases registered.

4.5 Spatially extended SHAR model

The inclusion of a spatial component in epidemiological models is important to understand and address many relevant ecological and public health questions. For example, when wanting to differentiate transmission patterns across geographical regions or when considering spatially heterogeneous intervention measures.
In this section, we present the formulation spatial version of the stochastic SHAR model.
Let us consider a lattice consisting of N sites, each of which is occupied by an individual and labeled by the indicators S_i, H_i, $A_i \in \{0, 1\}$, according to its state. Each site i can either have a susceptible
($S_i = 1$, $H_i = A_i = 0$), hospitalized ($H_i = 1$, $S_i = A_i = 0$), asymptomatic ($A_i = 1$, $S_i = H_i = 0$), or recovered ($S_i = H_i = A_i = 0$). Notice that there is no need to explicitly introduce the indicator R_i, since in the present settings $R_i = 1 - S_i - H_i - A_i$. The state vector for the system is thus given by $(S_1, H_1, A_1, \ldots, S_i, H_i, A_i, \ldots, S_N, H_N, A_N)$. Let J be the lattice adjacency matrix with entries

$$\begin{cases} J_{ij} = 1 \quad if \quad sites \quad i \quad and \quad j \quad are \quad connected \\ J_{ij} = 0 \quad otherwise \end{cases} \tag{4.5.1}$$

From the matrix J and any given configuration, the following quantities of interest can be computed:

- the number of neighbors to site i

$$Q_i = \sum_{j=1}^{N} J_{ij}$$

- the number of the infected neighbors to site i

$$\sum_{j=1}^{N} J_{ij}(H_j + A_j)$$

- the force of infection to site i

$$\beta \sum_{j=1}^{N} J_{ij}(H_j + \phi A_j)$$

Notice that we assume that the process involving contagion between individuals within the considered population may only occur when sites i and j are connected.
Considering the deterministic formulation of the SHAR model given by (4.1.1), the master equation for the stochastic spatial SHAR model is given by:

$$\begin{aligned}
&\frac{d}{dt}p(t, S_1, H_1, A_1, \ldots, S_i, H_i, A_i, \ldots, S_N, H_N, A_N) = \\
&\quad = \sum_{i=1}^{N} \Big[\beta\eta\Big(\rho + \sum_{j=1}^{N} J_{ij}(H_j + \phi A_j)\Big) H_i p(t, S_1, H_1, A_1, \ldots \\
&\qquad \ldots, 1 - S_i, 1 - H_i, A_i, \ldots, S_N, H_N, A_N) + \beta(1-\eta) \\
&\qquad \times \Big(\rho + \sum_{j=1}^{N} J_{ij}(H_j + \phi A_j)\Big) A_i p(t, S_1, H_1, A_1, \ldots \\
&\qquad\quad \ldots, 1 - S_i, H_i, 1 - A_i, \ldots, S_N, H_N, A_N) \\
&+ \gamma(1 - S_i - H_i - A_i) p(t, S_1, H_1, A_1, \ldots, S_i, 1 - H_i, A_i, \ldots, S_N, H_N, A_N) \\
&+ \gamma(1 - S_i - H_i - A_i) p(t, S_1, H_1, A_1, \ldots, S_i, H_i, 1 - A_i, \ldots, S_N, H_N, A_N) \\
&\qquad + \alpha S_i p(t, S_1, H_1, A_1, \ldots, 1 - S_i, H_i, A_i, \ldots, S_N, H_N, A_N)\Big] \\
&- \sum_{i=1}^{N} \Big[\beta\Big(\rho + \sum_{j=1}^{N} J_{ij}(H_j + \phi A_j)\Big) S_i + \gamma(H_i + A_i) + \alpha(1 - S_i - H_i - A_i)\Big] \\
&\qquad\qquad \times p(t, S_1, H_1, A_1, \ldots, S_i, H_i, A_i, \ldots, S_N, H_N, A_N) \quad (4.5.2)
\end{aligned}$$

For a deeper analysis, we refer to [5].

Appendices

Appendix A

Matlab code

In this section we reported the MATLAB code that we used to find the numerical solution of the SHAR model and the fitting parameters.

A.1 The main code

```
clear all
close all
clc

%% Data retrieval
csv_file_Italy = 'COVID19LastData'; % collection of data
Italy_sheet=readtable(csv_file_Italy);
data_raw=cell2mat(table2cell(Italy_sheet(:,3:15)));
num_days_data=length(data_raw);
fit_window=1:num_days_data-1;
H_data=data_raw(fit_window,1); % Hospitalized
M_data=data_raw(fit_window,4); % hoMe
V_data=data_raw(fit_window,2); % Ventilated in ICU
I_data=data_raw(fit_window,5); % Infected (I=H+V+M)
L_data=data_raw(fit_window,8); % heaLed
D_data=data_raw(fit_window,9); % Dead
W_data=data_raw(fit_window,13); % Swab tests
R_data=L_data+D_data; %Removed
day_start_pandemic=datenum(2020,02,24,0,0,0);
```

```
day_end=datenum(2021,01,01,0,0,0);

%% Phase 1: exponential phase
day_start1=day_start_pandemic;
day_end1=datenum(2020,03,09,0,0,0);
T0=day_start1-day_start_pandemic+1;
day_vec1=day_start1:day_end1;
num_days=length(day_vec1);
N = 60*10^6; % total population
% init condition
H0 = H_data(T0+1)+V_data(T0+1);
A0 = M_data(T0+1);
R0 = R_data(T0+1);
S0 = N - H0 - A0 - R0;
% parameters
gamma = 0.125;
fi = 1.3;
eta = 0.65;
beta = 3.2*gamma;
T_vec=0:num_days-1;
param_SHAR_init1=[beta fi eta gamma]';
param_SHAR_fixed1=[H0 A0 R0 N]';
% data to track
H_data_vec1=H_data(T0+1:T0+num_days)'+....
...V_data(T0+1:T0+num_days)';
% ErrorModel used in lsqnonlin
ErrorModel1=@(param_SHAR) ...
...SHAR_ex_modelfun(T_vec,param_SHAR,param_SHAR_fixed1)-...
...H_data_vec1;
% CostModel used in fmincon
CostModel1=@(param_SHAR)norm(ErrorModel1(param_SHAR));
% Optimization
param_SHAR_fit_fmin1=fmincon(CostModel1,param_SHAR_init1,...
...[],[],[],[],zeros(length(param_SHAR_init1),1),[]);
% Run fitted model
H_vec_fmin1=SHAR_ex_modelfun(T_vec,param_SHAR_fit_fmin1,...
```

```
...param_SHAR_fixed1);

%% Phase 2: Start Lockdown (control measures)
day_start2=datenum(2020,03,10,0,0,0);
day_end2=datenum(2020,05,03,0,0,0);
T0=day_start2-day_start_pandemic+1; % pre-lockdown phase
day_vec2=day_start2:day_end2;
num_days=length(day_vec2);
N = 60*10^6;
% init condition
H0 = H_data(T0+1)+V_data(T0+1);
A0 = M_data(T0+1);
R0 = R_data(T0+1);
S0 = N - H0 - A0 - R0;
% parameters
tc=T0;
gamma = 0.125;
fi = 1.3;
eta = 0.65;
beta_0 = 0.25;
beta_1 = 0.095;
a = 0.38;
T_vec=0:num_days-1;
param_SHAR_init2=[beta_0 beta_1 a tc fi eta gamma]';
param_SHAR_fixed6=[H0 A0 R0 N]';
% data to track
H_data_vec2=H_data(T0+1:T0+num_days)'+...
...V_data(T0+1:T0+num_days)';
% ErrorModel used in lsqnonlin
ErrorModel2=@(param_SHAR)...
...SHAR_modelfun(T_vec,param_SHAR,param_SHAR_fixed6)-...
...H_data_vec2;
% CostModel used in fmincon
CostModel2=@(param_SHAR)norm(ErrorModel2(param_SHAR));
% Optimization
param_SHAR_fit_fmin2=fmincon(CostModel2,param_SHAR_init2,...
```

```
...[],[],[],[],zeros(length(param_SHAR_init2),1),[]);
% Run fitted model
H_vec_fmin2=SHAR_modelfun(T_vec,param_SHAR_fit_fmin2,...
...param_SHAR_fixed6);

%% Phase 3: end lockdown (seasonality)
day_start3=datenum(2020,05,04,0,0,0);
day_end3=datenum(2020,07,18,0,0,0);
T0=day_start3-day_start_pandemic+1;
day_vec3=day_start3:day_end3;
num_days=length(day_vec3);
N = 60*10^6;
% init condition
H0 = H_data(T0+1)+V_data(T0+1);
A0 = M_data(T0+1);
R0 = R_data(T0+1);
S0 = N - H0 - A0 - R0;
% parameters
gamma = 0.125;
fi = 1.3;
eta = 0.65;
omega = 2*pi/365;
beta_0 = 0.15;
beta_1 = 0.095;
T_vec=0:num_days-1;
param_SHAR_init3=[beta_0 beta_1 omega fi eta gamma]';
param_SHAR_fixed3=[H0 A0 R0 N]';
% data to track
H_data_vec3=H_data(T0+1:T0+num_days)'+...
...V_data(T0+1:T0+num_days)';
% ErrorModel used in lsqnonlin
ErrorModel3=@(param_SHAR)...
...SHAR_solfun(T_vec,param_SHAR,param_SHAR_fixed3)-...
...H_data_vec3;
% CostModel used in fmincon
CostModel3=@(param_SHAR)norm(ErrorModel3(param_SHAR));
```

```
% Optimization
param_SHAR_fit_fmin3=fmincon(CostModel3,param_SHAR_init3,...
...[],[],[],[],zeros(length(param_SHAR_init3),1),[]);
% Run fitted model
H_vec_fmin3=SHAR_solfun(T_vec,param_SHAR_fit_fmin3,...
...param_SHAR_fixed3);

%% Phase 4: Coexistance with virus (seasonality)
day_start4=datenum(2020,07,19,0,0,0);
day_end4=datenum(2020,10,07,0,0,0);
T0=day_start4-day_start_pandemic+1;
day_vec4=day_start4:day_end4;
num_days=length(day_vec4);
N = 60*10^6;
% init condition
H0 = H_data(T0+1)+V_data(T0+1);
A0 = M_data(T0+1);
R0 = R_data(T0+1);
S0 = N - H0 - A0 - R0;
% parameters
gamma = 0.125;
fi = 1.3;
eta = 0.65;
omega = 2*pi/365;
beta_0 = 0.1;
beta_1 = 0.03;
T_vec=0:num_days-1;
param_SHAR_init4=[beta_0 beta_1 omega fi eta gamma]';
param_SHAR_fixed4=[H0 A0 R0 N]';
% data to track
H_data_vec4=H_data(T0+1:T0+num_days)'+...
...V_data(T0+1:T0+num_days)';
% ErrorModel used in lsqnonlin
ErrorModel4=@(param_SHAR)...
...SHAR_solfun(T_vec,param_SHAR,param_SHAR_fixed4)-...
...H_data_vec4;
```

```
% CostModel used in fmincon
CostModel4=@(param_SHAR)norm(ErrorModel4(param_SHAR));
% Optimization
param_SHAR_fit_fmin4=fmincon(CostModel4,param_SHAR_init4,...
...[],[],[],[],zeros(length(param_SHAR_init4),1),[]);
% Run fitted model
H_vec_fmin4=SHAR_solfun(T_vec,param_SHAR_fit_fmin4,...
...param_SHAR_fixed4);

%% Phase 5: new restriction (seasonality)
day_start5=datenum(2020,10,08,0,0,0);
day_end5=datenum(2020,11,06,0,0,0);
T0=day_start5-day_start_pandemic+1;
day_vec5=day_start5:day_end5;
num_days=length(day_vec5);
N = 60*10^6;
% init condition
H0 = H_data(T0+1)+V_data(T0+1);
A0 = M_data(T0+1);
R0 = R_data(T0+1);
S0 = N - H0 - A0 - R0;
% parameters
gamma = 0.125;
fi = 1.3;
eta = 0.65;
omega = 2*pi/365;
beta_0 = 0.1;
beta_1 = 0.027;
T_vec=0:num_days-1;
param_SHAR_init5=[beta_0 beta_1 omega fi eta gamma]';
param_SHAR_fixed5=[H0 A0 R0 N]';
% data to track
H_data_vec5=H_data(T0+1:T0+num_days)'+...
...V_data(T0+1:T0+num_days)';
% ErrorModel used in lsqnonlin
ErrorModel5=@(param_SHAR)...
```

```
...SHAR_solfun(T_vec,param_SHAR,param_SHAR_fixed5)-...
...H_data_vec5;
% CostModel used in fmincon
CostModel5=@(param_SHAR)norm(ErrorModel5(param_SHAR));
% Optimization
param_SHAR_fit_fmin5=fmincon(CostModel5,param_SHAR_init5,...
...[],[],[],[],zeros(length(param_SHAR_init5),1),[]);
% Run fitted model
H_vec_fmin5=SHAR_solfun(T_vec,param_SHAR_fit_fmin5,...
...param_SHAR_fixed5);

%% Phase 6: partial lockdown (control measures)
day_start6=datenum(2020,11,07,0,0,0);
day_end6=day_end;
T0=day_start6-day_start_pandemic+1; % pre-lockdown phase
day_vec6=day_start6:day_end6;
num_days=length(day_vec1);
N = 60*10^6;
% init condition
H0 = H_data(T0+1)+V_data(T0+1);
A0 = M_data(T0+1);
R0 = R_data(T0+1);
S0 = N - H0 - A0 - R0;
% parameters
tc=T0;
gamma = 0.127;
fi = 1.3;
eta = 0.65;
beta_0 = 0.25;
beta_1 = 0.095;
a = 0.28;
T_vec=0:num_days-1;
param_SHAR_init6=[beta_0 beta_1 a tc fi eta gamma]';
param_SHAR_fixed6=[H0 A0 R0 N]';
% data to track
H_data_vec6=H_data(T0+1:T0+num_days)'+...
```

```
...V_data(T0+1:T0+num_days)';
% ErrorModel used in lsqnonlin
ErrorModel6=@(param_SHAR)...
...SHAR_modelfun(T_vec,param_SHAR,param_SHAR_fixed6)-...
...H_data_vec6;
% CostModel used in fmincon
CostModel6=@(param_SHAR)norm(ErrorModel6(param_SHAR));
% Optimization
param_SHAR_fit_fmin6=fmincon(CostModel6,param_SHAR_init6,...
...[],[],[],[],zeros(length(param_SHAR_init6),1),[]);
% Run fitted model
H_vec_fmin6=SHAR_modelfun(T_vec,param_SHAR_fit_fmin6,...
...param_SHAR_fixed6);

%% Plots
day_vec=day_vec1+day_vec2+day_vec3+day_vec4+...
...day_vec5+day_vec6;
H_data_vec=[H_data_vec1 H_data_vec2 H_data_vec3 ...
...H_data_vec4 H_data_vec5 H_data_vec6];
H_vec_fmin=[H_vec_fmin1 H_vec_fmin2 H_vec_fmin3 ...
...H_vec_fmin4 H_vec_fmin5 H_vec_fmin6];
figure
plot(day_vec,log(H_data_vec)', '-*')
hold on
plot(day_vec,log(H_vec_fmin),'Linewidth',1.2)
grid on
xlabel('days')
ylabel('log(Hospitalized)')
datetick('x', 'dd/mmm', 'keepticks')
legend('Data','Fitted model (fmincon)',...
...'location','southeast')
```

A.2 Matlab function for the definition of the SHAR model

A.2.1 Model for the exponential phase

```
function y_dot=SHAR_ex_fun(t,x,param)
% parameters
beta=param(1);
fi=param(2);
eta=param(3);
gamma=param(4);
% state variables
S=x(1);
H=x(2);
A=x(3);
R=x(4);
N=S+H+A+R;
% model dynamics
S_dot=-beta*S/N*(H+fi*A);
H_dot=eta*beta*S/N*(H+fi*A)-gamma*H;
A_dot=(1-eta)*beta*S/N*(H+fi*A)-gamma*A;
R_dot=gamma*(H+A);
y_dot=[S_dot H_dot A_dot R_dot]';
```

A.2.2 Model with control measure function $\beta(t)$

```
function x_dot=SHAR_odefun(t,x,param)
% parameters
beta0=param(1);
beta1=param(2);
a=param(3);
tc=param(4);
fi=param(5);
eta=param(6);
gamma=param(7);
% state variables
```

```
S=x(1);
H=x(2);
A=x(3);
R=x(4);
N=S+H+A+R;
% time-varyibg infection rate
beta_t=...
...beta0*1/(1+exp(a*(t-tc)))+beta1*1/(1+exp(-a*(t-tc)));
% model dynamics
S_dot=-beta_t*S/N*(H+fi*A);
H_dot=eta*beta_t*S/N*(H+fi*A)-gamma*H;
A_dot=(1-eta)*beta_t*S/N*(H+fi*A)-gamma*A;
R_dot=gamma*(H+A);
x_dot=[S_dot H_dot A_dot R_dot]';
```

A.2.3 Model with seasonality function $\beta(t)$

```
function y_dot=SHAR_seasfun(t,x,param)
% parameters
beta0=param(1);
beta1=param(2);
omega=param(3);
fi=param(4);
eta=param(5);
gamma=param(6);
% state variables
S=x(1);
H=x(2);
A=x(3);
R=x(4);
N=S+H+A+R;
% time-varyibg infection rate
beta_t=beta0*(1+beta1*cos(omega*t));
% model dynamics
S_dot=-beta_t*S/N*(H+fi*A);
H_dot=eta*beta_t*S/N*(H+fi*A)-gamma*H;
```

```
A_dot=(1-eta)*beta_t*S/N*(H+fi*A)-gamma*A;
R_dot=gamma*(H+A);
y_dot=[S_dot H_dot A_dot R_dot]';
```

A.3 Matlab function for the solution of the model

```
function ...
... Y_vec=SHAR_ex_modelfun(T_vec,param_SHAR,param_fixed)
N=param_fixed(4);
S0=N-sum(param_fixed(1:3));
x_init=[S0; param_fixed(1:3)];
[~,X_vec]=...
... ode45(@(t,x)SHAR_ex_fun(t,x,param_SHAR),T_vec,x_init);
Y_vec=(X_vec(:,2)); % select the output(s) you want to fit
```

Notice that the Matlab function above solve the model for the exponential phase. In the cases in which $\beta(t)$ is given by control measure function or seasonality function we have to replace "SHAR_ex_fun" with "SHAR_odefun" or "Shar_seasfun" respectively.

Appendix B

From ODE to Markov chains via SDE

Let us introduce a methodology to connect an ordinary differential equation (ODE) model to a Markov chain model via a stochastic differential equation (SDE).

Definition 1. *A Stochastic process is a sequence*

$$\{X(t,\omega)\}, \quad t \geq t_0$$

*such that, for any fixed $t \geq t_0$, $X(\cdot,\omega)$ is a **random variable** [23] and for fixed ω, $X(t,\cdot)$ is a function of time called **realization** of the process.*

Definition 2. *A **Brownian motion** is a stochastic process $W(t), t \in [t_0, T]$ such that $W(t)$ is a continuous function of t and*

- *$W(0) = 0$ with probability 1;*
- *for any $t_0 \leq s < t \leq T$, $W(t) - W(s) \sim N(0, t-s)$, with N normal random variable [23];*
- *for any $t_0 \leq s < t < u < v \leq T$, $W(t) - W(s)$ and $W(v) - W(u)$ are independent.*

Definition 3. *We call **Stochastic Ito integral** the quantity*

$$\int_{t_0}^{T} f(t)\, dW(t) \approx \sum_{i=0}^{N-1} f(t_i)(W_{t_i+1} - W_{t_i}) \tag{B.0.1}$$

where N is a discretization of the interval $[t_0, T]$, such that

$$\lim_{\Delta t \to 0} \mathbb{E}\left[\left| \int_{t_0}^{T} f(t)\, dW(t) - \sum_{i=0}^{N-1} f(t_i)(W_{t_i+1} - W_{t_i})\right|^2\right] = 0$$

where $\mathbb{E}$ denote the mean value. This limit is called ***mean-square limit****.*

Let us suppose that we have a model given by the Cauchy-Lipschitz ordinary differential equation [12], satisfying some regularity assumptions and an initial condition:

$$\begin{cases} \frac{d}{dt}x(t) = f(t, x(t)) \quad t \in [t_0, T] \\ x(t_0) = x_0 \end{cases} \tag{B.0.2}$$

with exact solution

$$x(t) = x_0 + \int_{t_0}^{t} f(s, x(s))\, ds \quad t \in [t_0, T] \tag{B.0.3}$$

Suppose that we add a noise, given by an Ito integral with respect to a Brownian motion $W(t), t \in [t_0, T]$, defined on a probability space $(\Omega, F, \mathbb{P})$ [23], to the equation (B.0.3). In this way, we get a stochastic differential equation (SDE), given by, for $\omega \in \Omega$,

$$X(t, \omega) = X_0(\omega) + \int_{t_0}^{t} f(s, X(s, \omega))\, ds + \int_{t_0}^{t} g(t, X(t, \omega))\, dW(t, \omega) \tag{B.0.4}$$

where $X_0(\omega) = X(t_0, \omega)$ and $g(t, X(t, \omega))$ is the function give us the noise, or in the differential form,

$$\begin{cases} dX(t) = f(t, X(t))dt + g(t, X(t))dW(t) \\ X(t_0) = X_0 \end{cases} \tag{B.0.5}$$

Let us observe that, under sufficient hypotheses, the Ito stochastic integral part of equation (B.0.4) is a martingale with constant null mean value. Therefore, we have

$$\mathbb{E}[X(t, \omega] = \mathbb{E}[X_0(\omega)] + \int_{t_0}^{t} \mathbb{E}[f(s, X(s, \omega))]\, ds$$

which, upon comparing with equation (B.0.3), allows the interpretation that

the solution of equation (B.0.3) is the mean value with respect to the probability $\mathbb{P}$ (or the average) of the solution of equation (B.0.4). From this point, we will not distinguish $X(t)$ from $x(t)$.
Now, suppose that we discretize equation (B.0.4) with the Euler-Maruyama discretization [6] scheme to get:

$$X_{n+1} = X_n + f(t_n, X_n)(t_{n+1} - t_n) + g(t_n, X_n)(W(t_{n+1} - W(t_n))$$

for $0 \leq t_0 < t_1 < \ldots < t_N = T$ a subdivision of $[t_0, T]$. In the unidimensional case it is known that $W(t_{n+1}) - W(t_n) \sim N(0, t_{n+1} - t_n)$, with $N(0, t_{n+1} - t_n)$ normal standard distribution, and we have that the sequence $U_n, n = 0, \ldots, N-1$ defined by

$$U_n := F_n^{-1}(W(t_{n+1} - W(t_n)$$

with F_n^{-1} the inverse of the distribution function of a random variable distributed with the law $N(0, t_{n+1} - t_n)$, is a sequence of independent uniformly distributed random variables. In this way, calling $, t_{n+1} - t_n = h$, $f(t, x) = f(x)$ and $g(t, x) = g(x)$ such that

$$G(x, t) := x + f(x)h + g(x)y$$

we may write that

$$X_{n+1} = G(X_n, U_n), n = 0, \ldots, N-1$$

which is the functional definition of a Markov chain [18] [24].
To each pair of states a and b of the Markov chain is associated a transition probabilities $p_{a,b}(t)$. In order to determine the possible paths from a state to another we can study the dynamics of the transition probabilities via a differential equation, that we called Master equation (or Kolmogorov differential equation). The general form for the Master equation is given by

$$\frac{dp_{a,b}(t)}{dt} = \sum_{k \neq a} p_{a,k}(t) q_{k,b} - q_{a,a} p_{a,b}(t) \tag{B.0.6}$$

where the values of $q_{k,b}$ and $q_{a,a}$ are defined from the transition rates [13].

Appendix C

An introduction about optimization problems

Let us introduce the basic concepts of Mathematical Optimal Control Theory.

Consider an ODE having the form

$$\begin{cases} \frac{d}{dt}x(t) = f(x(t)) & t > 0 \\ x(t_0) = x_0 \end{cases} \tag{C.0.1}$$

where $x_0 \in \mathbb{R}^n$ is the initial condition and $f : \mathbb{R}^n \to \mathbb{R}^n$. The solution of the system $x : [0, \infty) \to \mathbb{R}^n$ corresponds to the dynamical evolution of the system.
Suppose now that f depends also apon some "control" parameters belonging to a set $A \in \mathbb{R}^m$. So that $f : \mathbb{R}^n \times A \to \mathbb{R}^n$. Then if we select some value $a \in A$ and consider the corresponding dynamics

$$\begin{cases} \frac{d}{dt}x(t) = f(x(t), a) & t > 0 \\ x(t_0) = x_0 \end{cases} \tag{C.0.2}$$

we obtain the evolution of our system when the parameter is constantly set to the value a. Another possibility is that we change the value of the parameter as the system evolves. For instance, suppose we define the function

$\alpha : [0, \infty) \to A$ in this way:

$$\alpha(t) = \begin{cases} a_1 & 0 \leq t \leq t_1 \\ a2 & t_1 < t \leq t_2 \\ a_3 & t_2 < t \leq t_3 \quad etc. \end{cases} \tag{C.0.3}$$

for times $0 < t_1 < t_2 < t_3 ...$ and parameter values $a_1, a_2, a_3, ... \in A$. Then we solve the dynamical system

$$\begin{cases} \frac{d}{dt} x(t) = f(x(t), \alpha(t)) & t > 0 \\ x(t_0) = x_0 \end{cases} \tag{C.0.4}$$

Notice that the system may behave quite differently as we change the control parameters. We call the function $\alpha : [0, \infty) \to A$ a *control* and the corresponding ODE and its trajectory $x(t)$ as the *response* of the system.
The task will be to determine what is the "best" control for our system. For this we need to specify a specific payoff criterion. Let us define the payoff functional

$$P[\alpha(\cdot)] := \int_o^T r(x(t), \alpha(t))\, dt + g(x(T)) \tag{C.0.5}$$

where $x(\cdot)$ solves the ODE for the control $\alpha(\cdot)$ and $r : \mathbb{R} \times A \longrightarrow$ and $h : \mathbb{R} \longrightarrow \mathbb{R}$ are given function called respectively *running payoff* and *terminal payoff*. Moreover, $T > 0$ is called terminal time.
Our aim is to find a control $\hat{\alpha}(\cdot)$ which maximizes the payoff. In other words, we want

$$P[\hat{\alpha}(\cdot)] \geq P[\alpha(\cdot)]$$

for all controls $\alpha(\cdot) \in A$. Such a control $\hat{\alpha}(\cdot)$ is called *optimal*.

C.1 Example: control of production and consumption

Suppose we own a factory whose output we can control. Let us begin to construct a mathematical model by setting

$$x(t) = \text{amount of output produced at at time } t \geq 0$$

We suppose that we consume some fraction of our output at each time and likewise can reinvest the remaining fraction. Let us denote

$$\alpha(t) = \text{fraction of output reinvested at time } t \geq 0$$

This will be our control and is subject to the obvious constraint

$$0 \leq \alpha(t) \leq 1 \text{ for each time } t \geq 0$$

Given such a control, the corresponding dynamics are provided by the ODE

$$\begin{cases} \frac{dx(t)}{dt} = k\alpha(t)x(t) \\ x(0) = x_0 \end{cases} \tag{C.1.1}$$

where the constant $k > 0$ modelling the growth rate of our reinvestment. Let us take as a payoff functional

$$P[\alpha(\cdot)] = \int_0^T (1 - \alpha(t))x(t)\, dt$$

The meaning is that we want to maximize our total consumption of the output. This model fits into our general framework for $n = m = 1$ once we put

$$A = [0, 1], \quad f(x, a) = kax, \quad r(x, a) = (1 - a)x, \quad g = 0$$

One can prove that an optimal control $\hat{\alpha(\cdot)}$ is given by

$$\hat{\alpha(t)} = \begin{cases} 1 & 0 \leq t \leq \hat{t} \\ 0 & \hat{t} < t \leq T \end{cases} \tag{C.1.2}$$

for an appropriate switching time $0 \leq \hat{t} \leq T$. In other words, we should reinvest all the output (and therefore consume nothing) up until time $\hat{t}$ and afterwards, we should consume everything (and therefore reinvest nothing). The switchover time $\hat{t}$ will have to be determined. We call $\hat{\alpha(\cdot)}$ a *bang-bang* control [11].

Appendix D

An introduction about network theory

Let us give an introduction about the network theory for the spatial formulation of the model.

A *graph* is a mathematical structure used to model pairwise relations between objects. A graph in this context is made up of *vertices* (also called nodes or points) which are connected by *edges* (also called links or lines). A distinction is made between *indirect graphs*, where edges link two vertices symmetrically, and *directed graphs*, where edges link two vertices asymmetrically.

Definition 1. *A* ***graph*** *is an ordered pair* $G = (V, E)$ *where*

- V *is a set of vertices;*
- $E \subseteq \{\{x, y\} | x, y \in V \text{ and } x \neq y\}$ *is a set of edges which are unordered pairs of vertices.*

To avoid ambiguity, this type of object may be called precisely an *indirect simple graph*. In a more general sense, we have the following definition.

Definition 2. *A* ***graph*** *is an ordered triple* $G = (V, E, \phi)$ *where*

- V *is a set of vertices;*
- E *is a set of edges;*

- $\phi : E \to \{\{x, y\} | x, y \in V \text{ and } x \neq y\}$ *is an incidence function mapping every edges to an unordered pair of vertices (that is, an edges is associated with two distinct vertices).*

This type of object may be called precisely an *indirect multigraph*.
A *loop* is an edge that joins a vertex to itself. Graphs as defined in the two definitions above cannot have loops.
V and E are usually taken to be finite and many of the well-known results are not true (or are rather different) for infinite graphs. Moreover, V is often assumed to be non-empty, but E is allowed to be an empty set.
The *order* of a graph is $|V|$ and it is the number of vertices. The *size* of a graph is $|E|$ and it is the number of edges. The *degree* of a vertex is the number of edges that are incident to it, where a loop is counted twice.
The degree of a graph is the maximum of the degrees of its vertices.

Definition 3. *A **directed graph** or digraph is a graph in which edges have orientations. We indicate it with the pair $G = (V, E)$ where*

- *V is the set of vertices;*
- *$E \subseteq \{(x, y) | (x, y) \in V^2 \text{ and } x \neq y\}$ is the set of edges which are ordered pairs of vertices.*

To avoid ambiguity, this type of object may be called precisely a *directed simple graph* [10].
Two nodes connected by an edge are called adjacent. A *path* on a graph G is a sequence of distinct nodes such that every node is adjacent to the previous or the next node. A graph G is called *connected* if for every pair of vertices exist a path that connects them.

Definition 4. *Given a graph $G = (V, E)$, $V' \subset V$ and $E' \subset E$, we call $G' = (V', E')$ **subgraph** of G.*

Definition 5. *Given a connected graph $G = (V, E)$ a **spanning tree** is a connected subgraph of G such that it has all the vertices of V, some edges of E and do not have loops.*

Definition 6. *The **adjacency matrix** of a graph G is a symmetric square matrix $A(G)$ that gives a representation of G, i.e. represents the adjacent*

relationship between the nodes.

$$A_{i,j} = \begin{cases} 1 \text{ if } (v_i, v_j) \in E, \text{ with } v_i, v_j \in V \\ 0 \text{ otherwise} \end{cases} \tag{D.0.1}$$

Definition 7. *We call* ***degree matrix*** $\Delta(G)$ *of a graph* G *a square diagonal matrix such that the diagonal element* i *is the degree of the vertex* i*.*

Definition 8. *We call* ***Laplacian matrix*** *of a unoriented graph* G *the matrix given by* $L(G) := \Delta(G) - A(G)$*.* $L(G)$ *is a symmetric matrix.*

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