# Optimal control strategies to mitigate the COVID-19 outbreak in a multi-region scenario

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## PRESENTATION OUTLINE

- 1 The Decision & Control Laboratory at Politecnico di Bari
- 2 Motivations and Objectives
- 3 Literature Review and Contribution
- 4 Mathematical Models of Infectious Diseases
- 5 SIRCQTHE Model
- 6 Parameters' Identification
- 7 Predictive Control of the COVID-19 Outbreak
- 8 Numerical Experiments

#### 9 Conclusions

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- Supporting courses lab activities
- Performing theoretical/applied research in systems, control optimization, and decision-making

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- smart factories and industry 4.0
- smart manufacturing (decentralized/distributed decision and control algorithms, logistics)
- energy management and energy efficiency (public and private sectors)
- decision-making techniques (supplier selection, re-engineering, ...)
- transport optimization (goods, waste, passengers)
- modeling, estimation and analysis of complex dynamical system.

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#### Collaborations

- Universities: University of Cagliari (Italy), Ecole Centrale de Lille (France), Aix-Marseille Université (France), Hamburg Helmut Schmidt University (Germany), University of Manchester (UK), Chalmers University (Sweden), Universidad Zaragoza (Spain), New Jersey Institute of Technology of Newark (USA), Delft University of Technology (The Netherlands), Politechnika Krakowska (Poland), Université de Lorraine (France), Tsinghua University (China).
- Public companies: Banque Centrale du Luxembourg, Ferrovie del Sud Est, Municipality of Bari, ReteGasBari SpA, AMTAB SpA.
- Private companies in Italy: Centro Ricerche Fiat, IBM, E-Distribuzione, Elettric80 SpA, Masmec SpA, Mermec SpA, General Transport Service SpA, MacNil Srl, Planetek Italia Srl, Divella SpA, Le Gemme, Tera Srl, Cannillo Srl, SimNT Srl, Primadonna SpA, Veronico Srl, Dream Project SpA, Gigant Italia Srl.



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# MOTIVATIONS AND OBJECTIVES



- Since the end of 2019, the SARS-CoV-2 coronavirus has caused more than 2.5 million deaths and 110 million of confirmed cases, thus resulting the most impacting pandemic in the recent decades.
- Currently vaccinations have not yet lead to mass coverage, hence, the main control actions still rely on non-pharmaceutical interventions (NPIs), such as mobility restrictions and social distancing.

The work presented in this talk is motivated by the emerging need for developing effective methods to support policy makers in efficiently mitigating the effects of COVID-19 pandemic contagions.

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## LITERATURE REVIEW

#### Dynamical Modeling of COVID-19 Pandemic

- The recent research trends in the COVID-19 framework have been devoted to disease transmission modeling and control, with the aim of suppressing, or at least mitigating, the spread of infections [Giordano et al., 2020, Lemos-Paião et al., 2020].
- In fact, several different models are available in the literature to describe the COVID-19 dynamics [Zhao and Chen, 2020].
- Some works focus on the analysis of the pandemic at a regional level, thus allowing to take into account the economic and social differences existing within almost any country [Della Rossa et al., 2020, Scharbarg et al., 2020, Brugnano et al., 2020].
- Most papers generally lack an accurate identification of the pandemic's dynamical model parameters.

## LITERATURE REVIEW

#### Control Strategies for COVID-19 Mitigation

- Very few models presented in the related literature are used to investigate the effects of control strategies (simplistic what-if simulations of future scenarios).
- These models do not provide a feedback control method to properly identify the most effective mitigation action(s) and employ them in a real time dynamical framework [Köhler et al., 2020].
- Some works propose open-loop on/off social distancing measures or fast switching policies [Morato et al., 2020, Bin et al., 2020].
- In most of the modeling and control approaches related to COVID-19, a perfect knowledge of parameters is assumed, ignoring uncertainty.
- The optimal control theory has been already successfully applied to identify the best action strategies for other diseases [Zhao and Chen, 2020].

## CONTRIBUTION TO THE LITERATURE

- We present a novel time-varying epidemiological model, that is designed in order to allow a robust parameters' identification.
- This model leverages people's mobility in different categories to represent the time dependency of the infection rate.
- Based on this model, we propose a control approach that allows avoiding the healthcare system to be overloaded.
- Our approach is also able to take into account the economic impacts of the designed control strategies.
- We directly include uncertainty on the parameters in the model by considering the variation of the infection's spreading parameters.
- Our approach is able to simultaneously take into account the specific mitigation strategies undertaken in a diversified multi-region scenario.

The results presented in this talk have been published in the following papers:

- CARLI, R., CAVONE, G., EPICOCO, N., SCARABAGGIO, P., AND DOTOLI, M. (2020).
   MODEL PREDICTIVE CONTROL TO MITIGATE THE COVID-19 OUTBREAK IN A MULTI-REGION SCENARIO.
   Annual Reviews in Control, 50:373 – 393.
- Scarabaggio, P., Carli, R., Cavone, G., Epicoco, N., and Dotoli, M. Modeling, estimation, and analysis of covid-19 secondary waves: the case of the italian country.

In 2021 29th Mediterranean Conference on Control and Automation (under review).

Scarabaggio, P., Carli, R., Cavone, G., Epicoco, N., and Dotoli, M. Stochastic optimal control strategies to mitigate covid-19 secondary waves.

IEEE Transaction on Automation Science and Engineering (under review).

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# Compartmental Models in Epidemic Modeling

The first fundamental mathematical model for epidemic diseases was formulated by Kermack and McKendrick in the early 20th century [Kermack and McKendrick, 1927].

This was the first compartmental model applied to epidemic modeling!



- Today, compartmental models are widely used to model the dynamics of infectious diseases.
- In these models, the population is divided into compartments and people may flow between these with characteristic rates.
- These models are usually defined using ordinary differential equations (ODEs) or finite difference equations.
- Epidemic models may be defined in a deterministic or stochastic framework. The latter class of models is more realistic but more complex.

# SI Model

Susceptible-Infectious (SI) model -> useful for single-wave epidemics where Infectious people cannot be healed (e.g., HIV). In the SI model, people flow from the **Susceptible** to the **Infectious** compartment with a characteristic Infection rate  $\beta$ .



- S: Number of Susceptible individuals
- *I*: Number of Infectious individuals
- $\blacksquare \beta: Infection rate$
- *N*: Total population size

The characteristics of compartmental models is that the dimension of the population is constant N = S(t) + I(t).

Since the total population cannot change, we can disregard one differential equation and analyze only the dynamics of:

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

that has the following analytic solution:

$$I(t) = \frac{I(0)N}{(N - I_0)e^{-\beta t} + I(0)}$$

It is easy to prove that this model has two equilibrium points:

$$I = 0$$
 and  $I = N$ 

which correspond to the disease extinction (unstable equilibrium) and to a fully infected population (asymptotically stable equilibrium), respectively.

Example with  $\beta = 0.3$ , N = 1000 and I(0) = 1.



Example with  $\beta = 0.6$ , N = 1000 and I(0) = 1.



Susceptible-Infectious-Susceptible (SIS) model -> useful for endemics where a healed individual can be infected again (e.g., a common cold). In the SIS model, people flow back to the **Susceptible** compartment from the **Infectious** one after recovering.

$$\frac{dS}{dt} = -\frac{\beta IS}{N} + \gamma t$$
$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I$$



- S: Number of Susceptible individuals
- *I*: Number of Infectious individuals
- $\blacksquare \beta: Infection rate$
- $\gamma$ : Recovery rate
- *N*: Total population size: N = S(t) + I(t).

Also in this case, since the total population cannot change, we can remove one differential equation and analyze only the dynamics of:

$$\frac{dI}{dt} = \frac{\beta(N-I)I}{N} - \gamma I$$

that has the following analytic solution:

$$I(t) = \frac{\frac{N}{\beta}(\beta - \gamma)}{1 + \left(\frac{N}{\beta}\frac{(\beta - \gamma)}{I(0)} - 1\right)e^{-(\beta - \gamma)t}}$$

It is easy to prove that this model has two equilibrium points:

$$I = 0$$
 and  $I = \frac{(\beta - \gamma)N}{\beta}$ 

which correspond to the disease extinction (unstable equilibrium) and to the maximum infection capacity (asymptotically stable equilibrium), respectively.

Example with  $\beta = 0.3$ ,  $\gamma = 0.1$ , N = 1000 and I(0) = 1.



Example with  $\beta = 0.6$ ,  $\gamma = 0.1$ , N = 1000 and I(0) = 1.



Susceptible-Infectious-Removed (SIR) model -> useful for single-wave epidemics with natural immunity (e.g., measles, mumps, rubella).

$$\frac{dS}{dt} = -\frac{\beta IS}{N}$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I$$

$$S \xrightarrow{\beta I/N} I \xrightarrow{\gamma} R$$

$$\frac{dR}{dt} = \gamma I$$

- *S*: Number of Susceptible individuals
- *I*: Number of Infectious individuals
- R: Number of Removed/Recovered individuals (immune or dead)
- $\blacksquare \beta: Infection rate$
- $\gamma$ : Removing rate
- *N*: Total population size: N = S(t) + I(t) + R(t).

# SIR MODEL

Since the total population cannot change, we can remove one equation and study only two of the three variables.

However, we cannot solve these equations analytically in closed form! The equation may be solved numerically using an engineering computation software.

- Infinite equilibrium points with I = 0,  $R = R^*$  and  $S = N - R^*$
- For fixed parameters (β and γ) we can solve numerically the system equations and determine the final epidemic size, i.e., the values S(+∞) and R(+∞).
- In the figure different possible dynamics are presented considering an initial condition (*R* = 0)



# SIR MODEL

Example with  $\beta = 0.3$ ,  $\gamma = 0.1$ , N = 1000, I(0) = 1 and R(0) = 0.



# SIR MODEL

Example with  $\beta = 0.6$ ,  $\gamma = 0.1$ , N = 1000, I(0) = 1 and R(0) = 0.



How we can simply evaluate epidemics? -> basic reproduction number

### Definition

The basic reproduction number  $R_0$  is the number of secondary infections that a single infected person (I(0) = 1) would produce in a fully susceptible (S = N - 1) population through the entire duration of the infectious period.

For basics compartmental models,  $R_0$  provides a threshold condition for the system dynamical behavior.

It can be demonstrated that:

- If *R*<sup>0</sup> < 1, we are not in the case of an epidemic (number of infectious individuals decreases monotonically to 0).
- If *R*<sub>0</sub> > 1, we are in the case of an epidemic (we have a peak in the number of infectious individuals before a reduction to 0).

## **BASIC REPRODUCTION NUMBER**

- Note that this definition is valid for simple homogeneous autonomous models!
- For a given model and fixed parameters, *R*<sup>0</sup> is constant.

For the SIR model,  $R_0$  is defined by the following ratio:

$$R_0 = \frac{\beta}{\gamma}$$

For COVID-19, the basic reproduction number  $R_0$  is estimated between 2 and 6 (when no restrictions are applied).



## **BASIC REPRODUCTION NUMBER**



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## **BASIC REPRODUCTION NUMBER**



So how can an epidemic be controlled?

- 1. Reduce S: vaccination (heard immunity).
- 2. Reduce  $\beta$ : wash hands, isolate sick persons, shut down public events, close schools (enforce the decrease of  $R_0$  over time, such that  $R_0 < 1$ ).
- 3. Increase  $\gamma$ : better and faster clinical treatments, antivirals (enforce the decrease of  $R_0$  over time, such that  $R_0 < 1$ ).



Variation of the COVID-19  $R_0$  parameter in different countries for the first two months of the pandemic during the lockdown.

#### The SIR model can be modified for different purposes:

- Model the dynamics of births and deaths (this is often neglected).
- Include time-varying parameters to take into account the effects of seasonality and control policies.
- Divide the population into different groups based on infection status (Exposed = infected but not yet infectious, Asymptomatic and Symptomatic individuals).
- Include additional compartments for vaccinated, dead, healed and hospitalized individuals.
- Model heterogeneity in age, regions or host species.

#### Other classical SIR-based models

Single epidemic wave: SIRD, SEIR, SITR and MSEIR.

**Endemic equilibrium** (the disease cannot be totally eradicated but remains in the population): SISD, SEIS, SIRS and SIR (births/deaths).

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We propose a novel time-varying discrete-time epidemiological model for the COVID-19 spread, named *SIRCQTHE*.

The overall population is divided into the following compartments:

- Susceptible;
- Infected (infected by someone and not yet contagious);
- Removed (undetected and completely recovered);
- Contagious (infected and undetected, contagious);
- Quarantined (infected and detected)
- Threatened (either in a life-threatening or noncritical situation);
- Healed (detected and completely recovered);
- Extinct (detected dead).

We reasonably assume that the probability of becoming susceptible after being healed is neglectable, since such a dynamics is much slower than the actual main time constant of the model.

# SINGLE-REGION SIRCQTHE MODEL



Scheme of the SIRCQTHE model: the compartments whose state is directly observable are indicated by filled rectangles.
The model is composed of eight time-varying difference equations, representing the dynamics of people's flows between compartments.

$$\begin{split} \tilde{S}(k+1) &= \tilde{S}(k) - \beta(k)\tilde{C}(k)\tilde{S}(k)/N \\ \tilde{I}(k+1) &= \tilde{I}(k) + \beta(k)\tilde{C}(k)\tilde{S}(k)/N - \rho\tilde{I}(k) \\ \tilde{R}(k+1) &= \tilde{R}(k) + \gamma\tilde{C}(k) \\ \tilde{C}(k+1) &= \tilde{C}(k) + \rho\tilde{I}(k) - (\gamma + \theta(k) + \lambda)\tilde{C}(k) \\ Q(k+1) &= Q(k) + \theta(k)\tilde{C}(k) + \pi T(k) - (\delta + \mu)Q(k) \\ T(k+1) &= T(k) + \mu Q(k) + \lambda\tilde{C}(k) - (\pi + \varepsilon(T(k)))T(k) \\ H(k+1) &= H(k) + \delta Q(k) \\ E(k+1) &= E(k) + \varepsilon(T(k))T(k) \end{split}$$



The symbol tilde identifies the state variables that cannot be directly observed with a reasonable confidence, since no official data is available.

## MULTI-REGION SIRCQTHE MODEL

In order to correctly represent the COVID-19 spread in a multi-region scenario, we can generalize our *SIRCQTHE* model to a case with *M* regions with index  $i \in M$  as follows.

Susceptible: individuals that can be infected but cannot infect others.

$$\tilde{S}_i(k+1) = \tilde{S}_i(k) - \beta_i(k) \tilde{C}_i(k)\tilde{S}_i(k)/N + \sum_{j=1}^M \xi_{i,j}(k)\tilde{S}_j(k)$$

Susceptible: individuals that can infect others.

 $\tilde{C}_i(k+1) = \tilde{C}_i(k) + \rho_i \tilde{I}_i(k) - (\gamma_i + \theta_i(k) + \lambda_i) \tilde{C}_i(k) + \sum_{j=1}^M \xi_{i,j}(k) \tilde{C}_j(k)$ 

- We add a further term in the right-hand side of the difference equations to take into account the **migration** of individuals between regions.
- In particular, we use the time-varying coefficients  $\xi_{i,j}(k)$ ,  $\forall i, j$  to represent the inter-region mobility that affects the first and the fourth equation of the model.

We impose the balance of the migrations flows between all regions:

$$\sum_{j\in\mathcal{M}}\xi_{i,j}(k)=0,\quad orall i\in\mathcal{M}$$

hence, we assume that all parameters  $\xi_{i,j}(k) \; (\forall j \neq i)$  assume non-negative values, thus:

$$\xi_{i,i}(k) = -\sum_{j \in \mathcal{M} \setminus \{i\}} \xi_{j,i}(k), \quad orall i \in \mathcal{M}$$



Scheme of the multi-region SIRCQTHE model.

### Advantages of the SIRCQTHE Model

With respect to other models, the SIRCQTHE has several advantages.

- We compress or eliminate some classes, and we disregard some connections between the compartments. In this way we define a simpler model to ensure a good accuracy in the fitting phase. Nevertheless, the model is still able to represent all facets of the pandemic diffusion.
- The model employs two terminal compartments (*H* and *E*) whose characteristic parameters ( $\delta$  and  $\epsilon$ ) are **easy to calculate** given the observed variables.
- The model only requires a minimal set of epidemiological data, which are typically available in most occidental countries.
- The infection rate  $(\beta(k))$  is assumed time-varying since it depends on the population behavior.
- The death rate (*ε*(*T*(*k*))) is modeled as a function that depends on the number of Threatened people.
- The model has a **broad applicability** when it is considered in its multi-region version.

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# Italian Scenario

After the exponential growth of cases, from November 6 2020, the 20 Italian regions have been grouped into different epidemiological categories based on the monitoring of 21 contagion indicator.

The local restrictive measures are indicated by different colors.

- White (minimal contagion, no control actions)
- Yellow (low contagion, reduced control actions)
- *Orange* (intermediate contagion, significant control actions)



*Red* (serious contagion, maximal control actions)

The **different colors** correspond to **different control actions** (with increasing enforcement in accordance with the density of the color) that must be taken into account in the model since they affect the infection rate  $\beta(k)$  (fitting phase)!

We employ the Italian Civil Protection Department epidemiological data, including:

- hospitalized people in a non-critical situation and hospitalized people in a critical situation (*T*(*k*));
- quarantined people (Q(k));
- healed people (H(k));
- deceased people (E(k));
- swabs number (w(k)).

The main issue related to these data, as well as to almost all the data similarly available worldwide, is that they **represent a screenshot of the epidemiological situation** every day.

In other words, for each compartments, the available data only represent the number of people in that compartment for each day, without any indication about the flows within the different categories.

Therefore some assumptions must be made to compute each parameter!

# Infection Rate $\beta(k)$

- The value of the infection rate  $\beta(k)$  for the COVID-19 pandemic is usually assumed between 0.25 and 0.8 in the **absence of any social distancing policies** and people awareness.
- Lockdown periods can significantly reduce this parameter!
- To achieve a continuous fitting of the COVID-19 dynamics, we assume that the variation of β(k) is related to the evolution of people's mobility in different socio-economic categories.

After preliminary experiments, we assume a linear relation between mobility in *G* socio-economic categories and the infection rate:

$$\beta(k) = \beta_0 + \boldsymbol{\beta}^\top \mathbf{m}(k), \quad \forall k \in \mathcal{K}(h)$$



where  $\beta = (\beta_1, ..., \beta_G)^{\top}$  collects the infection rates corresponding to *G* categories and  $\mathbf{m}(k) = (m_1(k), ..., m_G(k))^{\top}$  collects the mobility levels in the [0,1] range (where 0 indicated no mobility and 1 indicated the nominal mobility).

# Infection Rate $\beta(k)$

We estimate the mobility levels through the **Google Mobility Reports**. Data are obtained through Android smartphones.

We select the following G = 3 mobility categories:

- Workplaces
- Retail & recreation
- Public transport

These reports show how visits and length of stay at different places change compared to a baseline in the different categories.

Note the local minima appearing in the various region after the DPCM of november 6 and the corresponding changes in color.



Google Mobility Reports for all the italian regions in the last quadrimester of 2020: Workplaces (red), Retail & recreation (blue) and Public transport (orange).

# Parameters $ho,\lambda$ and $\mu$

#### Incubation rate $\rho$

- The incubation rate ρ is the rate of infected people that become contagious and can infect other people.
- The incubation time is estimated between 2 and 7 days, i.e.,  $\rho \in [1/7, 1/2]$  and is selected with the fitting algorithm described in the sequel.



#### Hospitalization rates $\lambda$ and $\mu$

These parameters are the constant hospitalization rates. They correspond to people recognized when severe symptomatic conditions appears and to Quarantined people that have to be hospitalized, respectively.

# Healing Rate $\gamma$

### Healing Rate $\gamma$

The healing rate of Contagious people γ can be well represented by a constant and in the literature is typically approximately in 14 days.



Note that, in our model, we do not remove people from the Contagious compartment when they are completely healed, but already when they are not contagious or have a really low viral load. In the literature, this period is estimated between 3 and 10 days, i.e.,  $\gamma \in [1/10, 1/3]$  and is selected with the fitting algorithm described in the sequel.

## Removing Rate of Quarantined People $\delta$

- The removing rate of Quarantined people (not needing hospitalization) δ can also be approximated by a constant value.
- Note that in some related works δ is substituted with γ, assuming that an individual is removed from the Quarantined compartment immediately after he/she becomes not contagious.



- However, in most countries, people are forced to be in quarantine even after being clinically healed because the procedure requires two negative tests.
- In Italy the quarantine period cannot be shorter than 10-14 days, depending on the swabs' tests results.

Thanks to the structure of the SIRCQTHE model, the healing rate  $\delta$  can be expressed as follows:

$$\delta(k) = (H(k) - H(k - 1)) / Q(k).$$

In other words,  $\delta$  may be obtained by simply observing data of Quarantined and Healed people.

Our experiments show that this parameter is on average constant!

# Detection Rate $\theta(k)$

The detection rate  $\theta(k)$  models the rate of Contagious people recognized and Quarantined. It is mainly related to the tracking and testing policies.

- Numerous researches point out that the ratio r(k) = p(k)/w(k) between **new daily discovered cases** p(k) and **daily swabs** w(k) is crucial to understand how the tracking system is operating.
- When *r*(*k*) increases, it means that the tracking system is not working well and the pandemic is out of control.
- Conversely, when r(k) is low, then few cases have been recognized compared to the amount of swabs an the pandemic is under control.
- These remarks hold when the tests are made stochastically, i.e., in a non selective way.

Some experiments lead to the selection of the simplest possible relation:

$$\theta(k) = \theta_0 \ (1 - r(k))$$

Parameter  $\theta$  is one of the most critical (**and hard to estimate**) in COVID-19 modeling due to the high number of asymptomatic people.



Note that, to the best of authors knowledge, no other approach in the related literature assumes  $\theta$  to be time-varying ( $\theta$  is simplistically chosen to be constant).

### First stage of the COVID-19 pandemic

The recovery rate  $\pi(k)$  was far from being constant during the first spread of COVID-19. The national healthcare system was not prepared and did not have therapeutic procedures for patients with symptoms never been seen before.

Therefore, to model this parameter in the first outbreak we employ the following formulation (selected to best fit data among different relation):

$$\pi(k) = a_1 + a_2 k^{a_3}$$

Second stage of the COVID-19 pandemic After the implementation of new standardized clinical approaches, we can reasonably assume that this parameter is constant.



# Recovery Rate $\pi(k)$

#### Recovery rate $\pi(k)$ for the first stage of the COVID-19 pandemic



The healing rate  $\pi(k)$  for all the Italian regions from March to June 2020: real data (red stars) and Single-region SIRQTHE model output (blue line).

# Death Rate $\varepsilon(k)$

Thanks to the structure of the *SIRCQTHE* model the death rate  $\varepsilon(k)$  can be expressed as:

$$\varepsilon(k) = \left(E(k) - E(k-1)\right)/T(k).$$

However, we can also foresee the death rate as follows.

#### First stage of the COVID-19 pandemic

This rate is not constant at the beginning of an epidemic and hopefully decreases with time, due to the availability of new clinical treatments. For the first outbreak we employ the following formulation (selected to best fit data among different relation):

$$\varepsilon(k) = a_4 + \exp\left(-a_5\left(k + a_6\right)\right)$$

#### Second stage of the COVID-19 pandemic

With the pandemic's development, this parameter becomes easily identifiable, and it can be shown that it depends on how much the healthcare system is under pressure and is perfectly described by a linear relation:

 $\varepsilon(T(k)) = \varepsilon_0 + \varepsilon_1 T(k)$ 



# Death Rate $\varepsilon(k)$

#### Death rate $\varepsilon(k)$ for the first stage of the COVID-19 pandemic



The death rate  $\varepsilon(k)$  for all the Italian regions from March to June 2020: real data (red stars) and Single-region SIRQTHE model output (blue line).

# Death Rate $\varepsilon(k)$

#### Death rate $\varepsilon(k)$ for the second stage of the COVID-19 pandemic



The death rate with respect to the number of Threatened cases in all Italian regions: Real data (red asterisks) and fitting result (blue line).

- To estimate the described parameters we adopt an approach based on a least-squares optimization technique.
- Due to the high nonlinearity of the model and nonconvexity of the resulting least-squares optimization technique, the fitting is nontrivial.
- Therefore, we introduce a multi-step fitting procedure that considers at each step a sub-model of the system.

# During the identification we employ bounds on parameters to enforce the scientific knowledge on the COVID-19 pandemic resulting on the related literature.

	Description		Bound	Reference
$\beta_0$	Base infection rate	$S \rightarrow I$	0.01 - 0.1	[Della Rossa et al., 2020, Lemos-Paião et al., 2020, Gatto et al., 2020, Wei et al., 2020]
$\beta_g$	Mobility coefficients	$S \rightarrow I$	0.1 - 0.5	[Della Rossa et al., 2020, Lemos-Paião et al., 2020, Gatto et al., 2020, Wei et al., 2020]
ρ	Incubation rate	$I \rightarrow C$	0.15 - 0.5	[Guan et al., 2020b, Lauer et al., 2020, Li et al., 2020, Pedersen and Meneghini, 2020]
$\theta_0$	Detection rate	$C \rightarrow Q$	0.001 - 0.5	[Gatto et al., 2020, Della Rossa et al., 2020]
$\gamma$	Healing rate	$C \rightarrow R$	0.1 - 0.3	[Della Rossa et al., 2020, Ehmann et al., 2020, Bai et al., 2020, Liu et al., 2020]
δ	Healing rate	$Q \rightarrow H$	0.01 - 0.1	[Wei et al., 2020, Gatto et al., 2020, Della Rossa et al., 2020, Romano et al., 2020]
λ	Threatening rate	$C \rightarrow T$	0.001 - 0,02	[Giordano et al., 2020, Gatto et al., 2020, Della Rossa et al., 2020]
$\mu$	Threatening rate	$Q \rightarrow T$	0.001 - 0,08	[Giordano et al., 2020, Della Rossa et al., 2020]
$\pi$	Healing rate	$T \to H$	0.01 - 0, 2	[Giordano et al., 2020, Gatto et al., 2020, Della Rossa et al., 2020, Zhou et al., 2020]

#### First step

In the first step, we analyze the following sub-model for each region:

$$\tilde{S}(k+1) = \tilde{S}(k) - (\beta_0 + \boldsymbol{\beta}^\top \mathbf{m}(k))\tilde{C}(k)\tilde{S}(k)/N$$
$$\tilde{I}(k+1) = \tilde{I}(k) - \rho\tilde{I}(k) + (\beta_0 + \boldsymbol{\beta}^\top \mathbf{m}(k))\tilde{C}(k)\tilde{S}(k)/N$$
$$\tilde{R}(k+1) = \tilde{R}(k) + \gamma\tilde{C}(k)$$
$$\tilde{C}(k+1) = \tilde{C}(k) + \rho\tilde{I}(k) - (\gamma + \lambda + \theta_0 (1 - r(k)))\tilde{C}(k)$$
$$Z(k+1) = Z(k) + (\lambda + \theta_0 (1 - r(k)))\tilde{C}(k)$$

where Z(k) = Q(k) + T(k) + H(k) + E(k) is the cumulative number of Infected people. The estimation of the unknown parameters consists in minimizing the mean squared error (MSE) of the model with respect to real data, as follows:

$$MSE(\Xi_1) = \frac{1}{K} \sum_{k=1}^{K} \left( \frac{\hat{Z}(\Xi_1, k) - Z(k)}{Z(k)} \right)^2$$

where  $\Xi_1 = (\beta_0, \beta, \rho, \gamma, \theta_0, \lambda, \tilde{I}(0), \tilde{C}(0))$  collects the unknown parameters and *K* is the number of samples defining the fitting horizon.

#### Second step

In the second step, we estimate the constant **healing rate** for each region by simply averaging the available data:

$$\delta = \frac{1}{K} \sum_{k=1}^{K} \left( \frac{H(k) - H(k-1)}{Q(k)} \right)$$

This parameter resulted to be different in the north of Italy and southern regions. In the latter regions, this parameter is significantly lower. This can be explained with poorer and less organized healthcare systems.

Moreover, we estimate the **death rate** linear relation for each region by minimizing the mean squared error (MSE) of the linear approximation with respect to real data, that is by minimizing the following index:

$$MSE(\varepsilon_0, \varepsilon_1) = \frac{1}{K} \sum_{k=1}^{K} \left( \frac{(\varepsilon_0 + \varepsilon_1 T(k)) - \varepsilon(k)}{\varepsilon(k)} \right)^2$$

#### Third step

Lastly, we analyze the following sub-model:

$$\begin{aligned} &Q(k+1) = Q(k) + (\theta_0 (1 - r(K))) \tilde{C}(k) + \pi T(k) - (\delta + \mu)Q(k) \\ &T(k+1) = T(k) + \mu Q(k) + \lambda \tilde{C}(k) - (\pi + \varepsilon(T(k)))T(k) \\ &H(k+1) = H(k) + \delta Q(k) \end{aligned}$$

and we minimize the following MSE for each region:

$$MSE(\Xi_2) = \frac{1}{K} \sum_{k=1}^{K} \left( \frac{\hat{Q}(\Xi_2, k) - Q(k)}{Q(k)} \right)^2 + \left( \frac{\hat{T}(\Xi_2, k) - T(k)}{T(k)} \right)^2 + \left( \frac{\hat{H}(\Xi_2, k) - H(k)}{H(k)} \right)^2$$

to compute  $\Xi_2 = (\mu, \pi, \theta_0, \lambda)$  that collects the remaining parameters for each region.



Quarantined cases for all the Italian regions: real data (red asterisks) and SIRCQTHE model output (blue line) over the evolution of restriction measures (different background colors).



Threatened cases for all the Italian regions: real data (red asterisks) and SIRCQTHE model output (blue line) over the evolution of restriction measures (different background colors).



Healed cases for all the Italian regions: real data (red asterisks) and SIRCQTHE model output (blue line) over the evolution of restriction measures (different background colors).



Deaths for all the Italian regions: real data (red asterisks) and SIRCQTHE model output (blue line) over the evolution of restriction measures (different background colors)

# Dynamical Identification of the Model Parameters

To foresee the evolution of the pandemic in the future, we additionally implement the multi-step fitting procedure in a *Dynamical Identification* (DI) algorithm that computes the model parameters observing them over a **fitting window** (e.g., 3 weeks) and generates a forecast of system variables over a **forecasting period** (e.g., one month).

The algorithm employs:

- the parameters computed employing the most recent data;
- the mobility trends of different categories extrapolated from the Google mobility data;
- the future control actions in term of mobility reduction;
- the model equations to determine the eight state variables.

Algorithm 1 Dynamical Identification Algorithm Input:  $\tau_1, \tau_2, O(d - \tau_1 ; d), T(d - \tau_1 ; d), H(d - \tau_1 ; d)$  $E(d - \tau_1 : d), \mathbf{m}(d - \tau_1 : d), r(d - \tau_1 : d)$ 1: Data pre-processing and filtering Computation of β<sub>0</sub>, β<sub>1</sub>, β<sub>2</sub>, β<sub>3</sub>, ρ, γ, θ<sub>0</sub>, λ, I(0), C(0) with (25) based on fixed bounds Computation of δ with (26) 4: Computation of  $\varepsilon(k)$ ,  $\forall k \in \{d - \tau_1, ..., d\}$  with (19) 5: Computation of so and s1 with (27) 6: Computation of  $\delta, \mu, \pi$  with (31) based on fixed bounds 7: Extrapolation of a trend from  $r(d - \tau_1 : d)$ 8: Extrapolation of a trend from  $m(d - \tau_1 : d)$ 9: Prevision of  $\tau(k)$ ,  $\forall k \in \{d, ..., d + \tau_2\}$ 10: Prevision of  $m_i(d - \tau_1 : d)$ ,  $\forall k \in \{d, ..., d + \tau_2\}$  based also on expected mobility restrictions 11: Simulation of the SIRCQTHE model with (1)-(8) over 72 time step **Output:**  $S(d : d + \tau_2)$ ,  $I(d : d + \tau_2)$ ,  $R(d : d + \tau_2)$ ,  $C(d : d + \tau_3)$ ,  $C(d : t_3)$ ,  $C(d : t_3)$ ,  $C(d : t_3)$ ,  $C(d : t_3)$ ,  $d + \tau_2$ ),  $Q(d : d + \tau_2)$ ,  $T(d : d + \tau_2)$ ,  $H(d : d + \tau_2)$ .

The algorithm cannot take into account unexpected changes in governmental policies unless manually specified!

## DởC Lab First Dashboard(7 магсн - 11 мау)

# From march to may 2020, the Decision and Control Laboratory made available a first dashboard based on a simple model.

### ITALIA 07-MAG-2020

Aggiornamento

- numero totale di infetti: 89624
- numero di nuovi casi oggi: 1904
- numero di guariti: 96276
- numero di decessi: 29958

#### Previsioni

- numero totale previsto di contagiati: 111396
- superamento previsto del picco: 23-Mar-2020
- inizio previsto fase di stabilizzazione: 07-Apr-2020
- inizio previsto fase finale: 04-Mag-2020





# DởC Lab First Dashboard (7 маrch - 11 мау)

#### Provincia di Bari



#### Provincia di BAT



#### Provincia di Brindisi



#### Provincia di Foggia



#### Provincia di Lecce



#### Provincia di Taranto



# Dở℃ Lab Current Dashboard (24 august - present)

Since august 2020 a new dashboard, including a running version of the *SIRCQTHE* model for the Puglia region, is available at:

http://dclab.poliba.it/covid-19

- The model is updated regularly, and it employs the real data for the fitting horizon (e.g, 3 weeks) to predict the evolution in the forecasting horizon (e.g, next 4 weeks) for the quarantined, threatened, healed, and dead people.
- The model is based on the Department of Civil Protection data and on the Google Mobility Reports.
- The old predictions are also shown to assess the model's accuracy.



# Dở℃ Lab Current Dashboard (24 august - present)

#### Interactive charts for the SIRCQTHE model



**Quarantined - Puglia** 

Home People Research Collaborations Projects Consultancies Covid-19 Industry 4.0 PhD Program

#### SIRCQTHE model – Puglia



#### **Threatened - Puglia**



Chart: Paolo6540 · Created with Datawrapper

#### Healed - Puglia



#### Deaths - Puglia



66

- Real value = 1 week forecasting = 2 weeks forecasting = 3 weeks forecasting

Chart: Paolo6540 - Created with Datawrapper

Chart: Paolo6540 - Created with Datawrapper

## DởC Lab Current Dashboard (25 august - present)

#### **Threatened - Puglia**



Chart: Paolo6540 · Created with Datawrapper

# DởC Lab Current Dashboard (25 august - present)

#### **Threatened - Puglia**



The dash lines represented expected Threatened cases with the estimated mobility trends if no restriction were applied (DPCM november 6)!

# DởC Lab Current Dashboard (24 august - present)

#### Other resources

→D&C→ Lab

Home People Research Collaborations Projects Consultancies Industria 4.0 🚺 Q

#### **COVID-19 DASHBOARD**

#### Growth trajectories in cases and deaths



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- We assume that the mitigation strategies are focused on reducing the parameter β(k) (infection rate), such that on the long-term, even in the absence of vaccinations, heard immunity can be reached.
- We assume that the infection rate is strongly influenced by people's mobility in different socio-economic categories.
- Our assumptions are confirmed by the works in [Santamaria et al., 2020, Guan et al., 2020a, lacus et al., 2020].
- The mitigation strategy should ensure that the hospitalization capacity is not violated and economic losses are minimized.

We define an optimal control problem, where the optimal control policy  $\mathbf{u} := (\mathbf{u}(h)^{\top}, ..., \mathbf{u}(h + K - 1)^{\top})^{\top}$  is assigned over a control horizon  $\mathcal{K}(h) = \{h, ..., h + K - 1\}$  of *K* time steps, where *h* is the current time step.
# Model of Control Actions

At each time step, we collect the *G* control actions (mitigation strategies) in vector  $\mathbf{u}(k) = (u_1(k), ..., u_G(k))^\top$ . Hence, this vector collects the interventions on mobility for all *G* socio-economic categories.

We recall that the open-loop relation between mobility in different categories  $\mathbf{m}(k)$  and the infection rate is:

$$\beta(k) = \beta_0 + \boldsymbol{\beta}^\top \mathbf{m}(k), \quad \forall k \in \mathcal{K}(h)$$

hence, the above relation is modified as follows:

$$\beta(k) = \beta_0 + \boldsymbol{\beta}^\top (1 - \mathbf{u}(k)), \quad \forall k \in \mathcal{K}(h).$$

where each control action  $u_g(k)$  is selected in the interval [0-1].

- We assume that an intervention on mobility in one category  $u_g(k)$  cannot be chosen independently from the others  $u_f(k) \forall f \neq g$ . For instance, a restrictive measure that aims at reducing mobility in the retail category will also affect mobility in the transport category.
- In order to avoid too frequent and impractical changes in the strategies, the control actions are kept constant over a week (i.e., for seven subsequent samples if the time period equals one day).

## THE OPTIMAL CONTROL PROBLEM

We employ the MPC approach to optimizes the impact of the restrictive measures on the economic framework of the overall system.

To this aim, we minimize an objective function composed of three cost terms:

$$J(\bar{\mathbf{u}},\mathbf{u}) = \boldsymbol{\phi}_{K}^{\top} \mathbf{u} + \alpha_{1} \boldsymbol{\phi}_{K}^{\top} \Delta \mathbf{u} + \alpha_{2} \boldsymbol{\phi}_{K}^{\top} \Delta \bar{\mathbf{u}}.$$

- The first term takes into account the economic impact of restrictive measures.
- The second term is a regularization term that smooths the restrictive measures over the control horizon (avoiding a bang-bang control), where  $\Delta \mathbf{u} := (\mathbf{0}_{G}^{\top}, (\mathbf{u}(h+1) - \mathbf{u}(h))^{\top}, ..., (\mathbf{u}(h+K-1) - \mathbf{u}(h+K-2))^{\top})^{\top}.$
- The last term is a memory term to avoid the variation of decisions taken in a previous time step, where  $\Delta \bar{\mathbf{u}} := (\mathbf{0}_{G}^{\top}, (\mathbf{u}(h) - \bar{\mathbf{u}}(h))^{\top}, ..., (\mathbf{u}(h + K - 2) - \bar{\mathbf{u}}(h + K - 2))^{\top})^{\top}.$
- α<sub>1</sub> and α<sub>2</sub> are weights selected by the decision maker in order to tune the importance of the different terms in the objective function.
- vector  $\phi_K$  collects the cost coefficients and allows giving a different importance to different categories.

Why do we consider regularization/memory terms? A continuous switch of decisions would be unpractical in a real application -> we model a social system!

The optimal control problem is defined as follows:

```
\begin{array}{ll} \underset{\mathbf{u}}{\text{minimize}} & J(\bar{\mathbf{u}}, \mathbf{u}) \\ \text{subject to} & SIRCQTHE \text{ model }, \ \forall k \in \mathcal{K}(h) \\ & \text{Constraints on the decision variables vector } \mathbf{u}, \ \forall k \in \mathcal{K}(h) \\ & \mathbf{T} - T^{\max} \mathbf{1}_{K} \leq \mathbf{0}_{K} \end{array}
```

where constrains on **u** impose that its valued are selected in a set of predefined mobility levels and  $\mathbf{T} - T^{\max} \mathbf{1}_K \leq \mathbf{0}_K$  is a non-linear constraint that ensures the containment of Threatened cases under a **safety threshold**  $T^{\max}$ . This models a percentage of the regional healthcare system capacity (e.g., 30% of the total hospital beds).

Solving the above optimization problem allows to select the best control actions (i.e., mobility restrictions in the *G* mobility categories) that lead to reducing the infection rate  $\beta(k)$ , i.e., contain the pandemic, and at the same time minimize the impact of the restrictive measures on economy, while respecting the given threshold on the number of hospitalized people.

# **MULTI-REGION CONTROL ACTIONS**

We now consider the defined control approach in a multi-region framework. In such a framework, we can additionally control the mobility between two regions *i* and *j* by reducing the parameter  $\xi_{i,j}(k)$  that influence the dynamics of the two state variables S(k) and C(k), i.e., Susceptible and Contagious individuals.

We assume an on/off control action  $c_i(k)$  that implements the inter-region travel restriction of the *i*-th region, included in  $C_i = \{0, 1\}$ , defined as:

 $\xi_{i,j}(k) = (1 - c_i(k))\xi_{i,j}^0, \quad \forall i, j \in \mathcal{M}, \quad \forall k \in \mathcal{K}(h)$ 

where  $\xi_{i,j}^0$  denotes the coefficient of migration from region *j* into the considered *i*-th region when no mobility restrictions are applied.

- The objective function in thus redefined as the summation of the single-region objective functions.
- We remark that in the multi-region case the cost coefficients  $\phi_{K,i}$  become region-dependent ( $i \in \mathcal{M}$ ): policy makers can adjust these coefficients in accordance with their importance and priority (also in terms of regional GDPs).

In case of a multi-region scenario, a political question arises: how can we select the control actions  $c_i$  (inter-region travel restrictions) and  $\mathbf{u}_i$  (intra-region mobility restrictions)?

1) Uniform intra-region activity and inter-region travel restrictions. This policy was implemented by the Italian government during the so-called COVID-19 Phase 1: the lockdown and the closure of regional boundaries was simultaneously imposed to each Italian region.

# 2) Differentiated intra-region activity restrictions and uniform inter-region travel restrictions.

This policy is currently implemented by the Italian government: all the regional boundaries are closed, while each region determines independently its restricting strategy locally.

3) Differentiated intra-region activity and inter-region travel restrictions. This is the policy currently applied at the global level between different countries, e.g., between Italy and the United States.

# THE STOCHASTIC OPTIMAL CONTROL PROBLEM

To take into account the variability and uncertainty in the characteristic model parameters, we can modify the control approach employing stochastic techniques.

Hence, we rewrite the MPC problem: instead of satisfying the safety threshold exactly we ensure that the probability of keeping the number of Threatened people below the safety threshold is above a certain level (e.g., 80%).

 $\begin{array}{ll} \underset{\mathbf{u}}{\text{minimize}} & J(\bar{\mathbf{u}}, \mathbf{u}) \\ \text{subject to} & SIRCQTHE \text{ model}, \ \forall k \in \mathcal{K}(h) \\ & \text{Constraints on the decision variables vector } \mathbf{u}, \ \forall k \in \mathcal{K}(h) \\ & \mathbb{P}\left\{\mathbf{T}(\boldsymbol{\xi}) - T^{\max} \mathbf{1}_{K} \leq \mathbf{0}_{K}\right\} \geq 1 - \epsilon \end{array}$ 

- $\mathbb{P} \{ \mathbf{T}(\boldsymbol{\xi}) T^{\max} \mathbf{1}_K \leq \mathbf{0}_K \}$  is the probability of satisfying the constraint .
- $\epsilon \in [0, 1]$  is the risk level that the decision-maker is willing to accept.

## THE MODEL PREDICTIVE CONTROL FORMULATION

- According to the Model Predictive Control approach, the optimal control problem is solved at each time step in an rolling horizon manner (the problem is defined and solved iteratively, e.g, weekly).
- More precisely, the computed control actions for the first time step are then applied to the system to steer its behavior to the desired one, while the horizon is shifted forward of one step. Hence, the next control action is computed iteratively.
- The resulting closed-loop feedback control technique depends on quantities that cannot be measured (the four state variables *S*, *I*, *R* and *C*).
- Therefore, the previously described identification procedure is performed at each time step to estimate the *SIRCQTHE* parameters.



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- The approach is tested on the Italian scenario over a simulation period of 10 weeks using a prediction horizon of six weeks.
- The cost coefficients are based on the percentage of the Italian GDP correlated with the different G = 3 mobility categories and the M = 20 different regions.
- The maximum number of Threatened people T<sup>max</sup> is defined for each region based on the Italian Ministry of Health's official data.
- We assume that the finite set of mobility restriction combinations  $\mathcal{U}$  corresponds to the different strategies applied by the Italian government to tackle the COVID-19 outbreak indicated with different colors.

Set of the estimated control actions related to the scenario considered in the numerical experiments.

		White			Green			Yellow			Orange		1	Red	
Name	Retail	Workplaces	Transport												
Piedmont	0.11	0.20	0.18	0.22	0.19	0.25	-	-	-	-	-	-	0.55	0.34	0.54
Aosta	-	-	-	0.40	0.22	0.40	-	-	-	-	-	-	0.69	0.39	0.63
Lombardy	0.15	0.24	0.25	0.25	0.23	0.33	-	-	-	-	-	-	0.57	0.36	0.59
Trentino - S. Tyrol	0.07	0.15	0.00	0.28	0.15	0.14	0.54	0.32	0.40	-	-	-	-	-	
Veneto	0.06	0.17	0.13	0.17	0.14	0.21	0.30	0.22	0.42	-	-	-	-	-	
Friuli-Ven. Giulia	0.07	0.17	0.05	0.17	0.15	0.10	0.29	0.21	0.27	0.49	0.26	0.36	-	-	
Liguria	0.06	0.13	0.07	0.22	0.18	0.22	0.31	0.24	0.32	0.41	0.29	0.37	-	-	
Emilia-Romagna	0.07	0.16	0.15	0.17	0.14	0.20	0.29	0.21	0.40	0.45	0.24	0.47	-	-	
Tuscany	0.07	0.15	0.10	0.21	0.16	0.22	0.32	0.23	0.35	0.43	0.28	0.43	0.54	0.31	0.52
Umbria	0.07	0.15	0.00	0.21	0.15	0.11	0.34	0.23	0.25	0.44	0.26	0.35	-	-	
Marche	0.03	0.12	0.01	0.18	0.13	0.12	0.28	0.20	0.27	0.43	0.23	0.38	-	-	
Lazio	0.15	0.25	0.31	0.24	0.24	0.36	0.32	0.29	0.47	-	-	-	-	-	
Abruzzo	0.01	0.12	0.00	0.16	0.15	0.10	0.28	0.22	0.29	0.41	0.27	0.42	0.53	0.34	0.55
Molise	-	-	-	0.15	0.11	0.06	0.31	0.24	0.34	-	-	-	-	-	
Campania	0.07	0.22	0.14	0.26	0.26	0.31	0.37	0.33	0.45	-	-	-	0.55	0.40	0.59
Apulia	0.00	0.16	0.04	0.15	0.16	0.20	-	-	-	0.39	0.29	0.49	-	-	
Basilicata	0.00	0.13	-	0.13	0.12	0.29	0.29	0.22	0.47	0.41	0.29	0.56	-	-	
Calabria	0.00	0.12	0.00	0.17	0.16	0.10	-	-	-	-	-	-	0.52	0.38	0.51
Sicily	0.04	0.16	0.05	0.19	0.17	0.19	-	-	-	0.43	0.30	0.49	-	-	
Sardinia	0.00	0.14	0.00	0.15	0.15	0.12	0.25	0.23	0.33	-	-	-	-	-	
Mean	0.06	0.16	0.09	0.20	0.17	0.20	0.32	0.24	0.36	0.43	0.27	0.43	0.56	0.36	0.56

We estimate the value of the control action employing the Google Mobility Reports (absent data correspond to the fact that the corresponding region have never been to in the selected color category).

- Based on the estimated parameters for the SIRCQTHE model, the control system selects the most suitable strategy to apply by solving the optimal control problem.
- We solve the stochastic optimal control problem assuming that the **level of risk** that the decision-maker is willing to accept is *e* = 0.2.
- Having defined the control actions for the control horizon, a Monte Carlo simulation with 1,000 iterations is performed by randomly changing the model parameters at each time.
- The results obtained for different regularization coefficients α<sub>1</sub> and α<sub>2</sub> show that, by employing higher values of α<sub>1</sub> and α<sub>2</sub>, it is possible to smooth the control action, while keeping the number of hospitalized cases lower, albeit with an increased socio-economic cost.

- Solution of an instance of the stochastic optimal control problem with no information of future trends with prediction and control horizon of six weeks starting from (5 december).
- The safety level T<sup>max</sup> is defined as 100% of the total beds.
- To validate the approach a Monte Carlo simulation with 1,000 iterations is performed by randomly changing the model parameters at each time.
- Only the first step of the optimal control result is applied!



Results of the Monte Carlo simulation in terms of Threatened cases: expected Threatened (blue line), confidence interval for the Threatened cases (cyan area), maximum number of Threatened cases (black dotted line), and the evolution of the control action in the control horizon (different background colors).

#### Simulation start: 5 december.



Results of the Monte Carlo simulation in terms of Threatened cases over the 6 weeks control/prediction horizon: expected Threatened (blue line), confidence interval for the Threatened cases (cyan area), maximum number of Threatened cases (black dotted line), and the evolution of the control action in the control horizon (different background colors).

- Solution of the MPC approach over a simulation period of 10 weeks starting from (5 december).
- We include noise and disturbances to model uncertainty.
- The safety level T<sup>max</sup> is defined as 50% of the total beds.
- Each step of the simulation period is the result of an instance of the optimal control result!



Results obtained by the stochastic MPC when  $\alpha_1 = \alpha_2 = 0.1$  and  $\alpha_1 = \alpha_2 = 1$ : Threatened cases (blue line), maximum number of Threatened cases that can be treated by each region (black line), and evolution of the control action in the control horizon (different background colors).

#### Simulation start: 5 december.



Results obtained by the stochastic MPC for each region when  $\alpha_1 = \alpha_2 = 0.1$ : Threatened cases (blue line), maximum number of Threatened cases that can be treated by each region (black line), and evolution of the control action in the control horizon (different background colors).

#### Simulation start: 5 december.



Results obtained by the stochastic MPC for each region when  $\alpha_1 = \alpha_2 = 1$ : Threatened cases (blue line), maximum number of Threatened cases that can be treated by each region (black line), and evolution of the control action in the control horizon (different background colors).

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## Conclusions

- Over the last months, the COVID-19 pandemic has affected the whole world. Since vaccinations require a long time to obtain herd immunity, the main mitigation actions of the pandemic rely on the use of non-pharmaceutical interventions.
- Such control measures have proven to be effective, albeit at the cost of a significant socio-economic impact on the population.
- It is therefore essential to develop methods to support policy-makers in taking decision to mitigate the effects of COVID-19 pandemic.
- To this aim, our works present a feedback control approach which makes joint use of a novel compartmental epidemiological model and a novel Model Predictive Control technique.
- We employ a multi-region framework, to properly represent the regional differences in healthcare systems.
- The proposed approach is tested on real data of the Italian case study showing its effectiveness in controlling the pandemic, i.e., keeping the number of Threatened cases below a fixed maximum limit, while simultaneously minimizing the socio-economic impact of the required restriction periods.
- As a further development of the approach, age-differentiated control actions can also be addressed, and, with the ongoing vaccination for the COVID-19 disease, we also plan to investigate the most effective way for distribution of the vaccine.

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