Model Predictive Control

MPC application for COVID-19 epidemic control

Practical session

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Abstract

The main purpose of this lab is to apply a non-linear MPC control to a multi-age model of COVID-19 pandemic. The control objective is to design a vaccination protocol for reducing the number of overall deceased people at the end of the pandemic spread and to prove that, depending on the model parameters value, the standard strategy of vaccinating the older populations first, affected by higher lethality rates, might be not the optimal one.

1 Logistics and evaluation

The following aspects will concur to the **final grade** of the lab work:

- the final report, to be submitted **one week after the end of the last lab session**;
- the python code, to be submitted **at the end of the last session**;
- the **teacher's personal evaluation** of the student attitude during the lab sessions.

2 Introduction

The model used in this practical session takes into account the age of the individuals in the implementation of the vaccination strategy. This is motivated by the fact that several studies (such as [1] for instance) have shown that the COVID-19 transmission is age-dependent. Moreover, as it was the case in several countries, the vaccination policies adopted by the government were age-based. Furthermore, since COVID-19 is a deadly disease, the model used contained an additional compartment, compared to the classical SIR model introduced by Kermack and McKendrick [2]. This compartment is denoted by D, for the deceased individuals in the population. The model used is given by

$$\begin{cases} \dfrac{dS_k(t)}{dt} &= -\lambda_k S_k(t) \displaystyle\sum_{j=1}^{n_a} C_{kj} I_j(t) - U_k(t) \\ \dfrac{dI_k(t)}{dt} &= \lambda_k S_k(t) \displaystyle\sum_{j=1}^{n_a} C_{kj} I_j(t) - (\gamma_{R_k} + \gamma_{D_k}) I_k(t) \\ \dfrac{dR_k(t)}{dt} &= \gamma_{R_k} I_k(t) + U_k(t) \\ \dfrac{dD_k(t)}{dt} &= \gamma_{D_k} I_k(t), \end{cases} \tag{1}$$

with $k = 1, \ldots, n_a$, where n_a is the number of class of age considered.

The parameters of this model have been calibrated using COVID-19 data for Belgium, considering $n_a = 6$ classes of age and whose parameters are given in a csv and python files. For every age range indexed by k with $k = 1, \ldots, n_a$, the model considers four populations, namely:

- $S_k(t)$: the set of susceptible individuals at time t, that are people that have never been infected by the virus and are then potentially affected by infection;
- $I_k(t)$: the set of infected individuals, people belonging to the k-th age range class that are currently infected by COVID-19;
- $R_k(t)$: the set of recovered people, that have already been infected and are current healed. The members of this class are supposed to be immune to the virus and then they cannot be infected any more;
- $D_k(t)$: the set of deceased people of age range class k, individuals that passed away due to the COVID-19 infection.

The different terms in the system dynamics have the aim of representing the different phenomena involved in the pandemic diffusion, namely:

- terms $\lambda_k S_k(t) C_{kj} I_j(t)$ represent the rate of the k-th susceptible population that are infected at time t by infected individuals of class j. Indeed, this rate depends on the product of S_k and I_j, that denotes the number of susceptible individuals of class k that meet infected ones of class j at time t. The parameter $\lambda_k C_{kj}$ models the probability of infection due to the meeting occurrence. These terms appear with negative sign in the susceptible population and with positive one for the infected, since they reduce the number of susceptible and increase those of infected ones, to model the infection process.
- the term U_k is the rate of vaccination of population S_k at time t. These individuals are then removed from susceptibles and added to the set of recovered, becoming immune from now on.
- terms $\lambda_{R_k} I_k(t)$ and $\lambda_{D_k} I_k(t)$ are the rate of infected people that are healed, becoming recovered, and that die, adding their number to the set of deceased ones. Parameter λ_{R_k} and λ_{D_k} model the recovery and lethality probability associated to the k-th age range, respectively.

In order to numerically implement the algorithm, a discrete version of model (1) is introduced. It is obtained by using the Euler discretization of the previous model with a time step of one day. The discrete-time age structured SIRD epidemic model is given by

$$\begin{cases} S_k\left(n+1\right) & = S_k\left(n\right) - \lambda_k S_k(n) \displaystyle\sum_{j=1}^{n_a} C_{kj} I_j(n) - U_k\left(n\right) \\ I_k\left(n+1\right) & = I_k\left(n\right) + \lambda_k S_k(n) \displaystyle\sum_{j=1}^{n_a} C_{kj} I_j(n) - \left(\gamma_{R_k} + \gamma_{D_k}\right) I_k\left(n\right) \\ R_k\left(n+1\right) & = R_k\left(n\right) + \gamma_{R_k} I_k\left(n\right) + U_k\left(n\right) \\ D_k\left(n+1\right) & = D_k\left(n\right) + \gamma_{D_k} I_k\left(n\right), \end{cases} \tag{2}$$

with $k = 1, \ldots, n_a$. Notice that a new control law $u_k(n)$ has been introduced. It represents the number of susceptible individuals of class k that are vaccinated at time n. This can be equivalently rewritten as

$$x^+ = f(x, u)$$

where $x = (S_1 \ldots S_{n_a} I_1 \ldots I_{n_a} R_1 \ldots R_{n_a} D_1 \ldots D_{n_a}) \in \mathbb{X}$ is the state, x^+ denotes the successor state, $u = (U_1 \ldots U_{n_a}) \in \mathbb{U}$ is the input and $f : \mathbb{X} \times \mathbb{U} \to \mathbb{X}$ is locally bounded, with state and input constraints given by

$$\mathbb{X} =: \left\{x \in \mathbb{R}^{4n_a} : 0 \leq S_k, I_k, R_k, D_k \leq P_k,\ k = 1, \ldots, n_a\right\} \tag{3}$$

$$\mathbb{U} =: \left\{u \in \mathbb{R}^{n_a} : u \geq 0,\ \sum_{k=1}^{n_a} u_k \leq U_{max}\right\} \tag{4}$$

where $P \in \mathbb{R}^{n_a}$ is the vector with the overall populations, per age, and U_{max} is the maximal number of vaccinations that can be administered.

3 Simulation and implementation of the standard protocol

The first session of the laboratory project, would consist in implementing the continuous-time dynamical system (1) and in the design and implementation of the standard vaccination protocol often applied by several national health institutions. The next step will be to design an alternative strategy for vaccination based on nonlinear MPC and then compare the two approaches.

1) Given the system parameters of model (1), present in the python file, implement the continuous-time COVID-19 pandemic system. The control input is the vaccinations rate in terms of number of suitable vaccinations per day, the state is the populations of susceptible, infected, recovered and deceased individuals.

2) Implement the standard vaccination protocol that consists in proceeding vaccinating from the older population to the younger ones. There are indeed two approaches to simulate such strategy:

   (i) supposing that the vaccination takes place in continuous time, along the whole day. This would mean to determine $U(t)$ for $t \in \mathbb{R}$ and apply it to (1), that is then a function of the time. The continuous-time model is then simulated day by day.

(ii) suppose that the whole admissible amount of daily vaccinations U_{max} is administered instantaneously at the beginning of every day. An appropriate value of $U_k(n)$ is computed for all k-th age range with $k = 1, \ldots, n_a$ such that their summation is equal to U_{max} and the older susceptible individuals are vaccinated first. After the instantaneous update of the number of susceptibles and recovered, the system (1) is simulated in open loop till the following day.

Simulate and compare the two implementations.

3) **Optional**: implement the discrete-time model (2), with the vaccination input determined as in point (ii) and compare the trajectory with those of the point 2).

References

[1] G. C. Calafiore and G. Fracastoro. Age structure in sird models for the covid-19 pandemic - a case study on italy data and effects on mortality. *PLOS ONE*, 17(2), 2022.

[2] W. Kermack and A. Mckendrick. Contributions to the mathematical theory of epidemics - ii. the problem of endemicity. *Bulletin of Mathematical Biology*, 53(1-2):57–87, 1991.