A Cooperative Epidemiological Model of Infectious Disease Dynamics:
A COVID-19 Case Study

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Abstract. A cooperative epidemiological mathematical model that can be used to describe the transmission dynamics of several infectious diseases is presented in this study. The analysis is general, however the study of COVID-19 pandemic prioritized. For instance, the model is used to estimate the cumulative number of infected cases and deaths in many countries due to COVID-19 outbreak. The model assumes a homogeneous population mix, where parameters and uncertainty in the model are inferred using various available data sets. The proposed model is compared to the classical SIRD compartmental modelling type of infectious diseases.
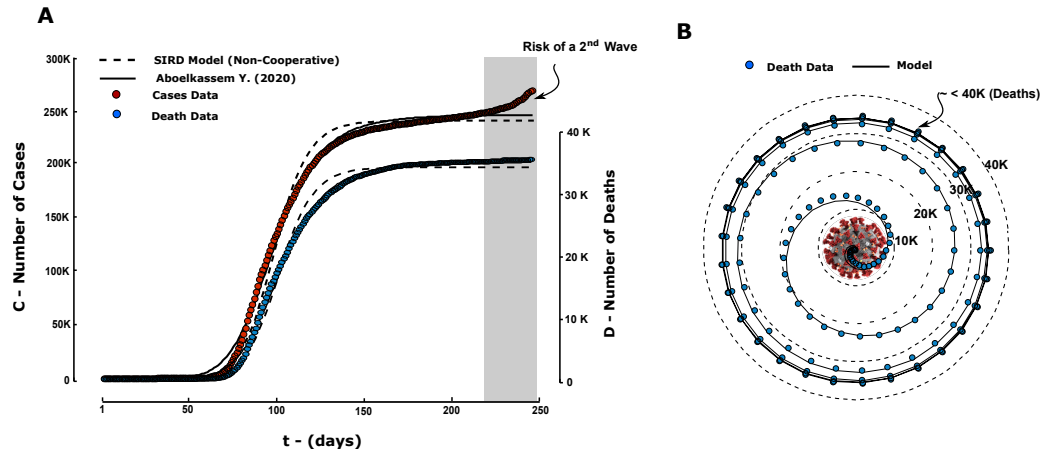
Introduction

Figure 1: Model prediction of the COVID-19 pandemic in Italy. **A:** The number of infected cases (C) and deaths (D) over days is calculated using the optimized model parameters.**B:** Prediction of the total number of deaths in Italy represented by polar plots. The virus illustration is created by the Centers for Disease Control and Prevention (CDC).

The coronavirus disease 2019 (COVID-19) is part of the ongoing worldwide pandemic caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [1]. Epidemiological mathematical models can be useful tools to describe how infectious diseases progress and spread in a given population [2, 3]. Many of these models have proven successful in predicting the outcome growth patterns of an epidemic and help inform public health interventions. Although our current mechanistic understanding of COVID-19 infection dynamics is still very limited. Yet, simplified probabilistic models, uncertainty quantification tools, and computational data analysis can be used to forecast an accurate measure of disease spread.

Results and Discussion

In Figure 1, we show the results that describe the dynamic spread of COVID-19 transmission in a given population (Italy). A comparison between the proposed cooperative mathematical model with essential dynamics and the classical SIRD model is given. More specifically, the total number of infected cases (C) and deaths (D) as a function of the pandemic spread time are calculated using the optimized model parameters. The results are validated using the reported data which show that the cooperative model has performed better than the SIRD model and agreed well with the data during most of the spread time span, Fig.1A. The model prediction suggests that, a total number of cases $C_{ss} = \sim < 300K$ is expected. Similarly, the number of deaths as a function of time is also calculated and is shown on the same plot i.e., on the other y-axis of Fig. 1A. The time distribution of the number of deaths clearly exhibits a sigomidal behavior. The steady-state value of the death curve suggest that, a total number of deaths $D_{ss} \sim < 40K$ is expected, unless there will be a second wave of the virus spread. It should be noted that both models failed to predict the observed second rise in the number of cases. In Fig. 1B, the predicted total number of deaths is represented by a polar plot. In conclusion, the proposed epidemiological model provides a better mechanistic understanding of the virus transmission dynamics.

References

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