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Learning Epidemic Trajectories Through Kernel Operator Learning: From Modelling to Optimal Control

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Abstract. Since infectious pathogens start spreading into a susceptible population, mathematical models can provide policy makers with reliable forecasts and scenario analyses, which can be concretely implemented or solely consulted. In these complex epidemiological scenarios, machine learning architectures can play an important role, since they directly reconstruct data-driven models circumventing the specific modelling choices and the parameter calibration, typical of classical compartmental models. In this work, we discuss the efficacy of kernel operator learning (KOL) to reconstruct population dynamics during epidemic outbreaks, where the transmission rate is ruled by an input strategy. In particular, we introduce two surrogate models, named KOL-m and KOL-∂, which reconstruct in two different ways the evolution of the epidemics. Moreover, we evaluate the generalization performances of the two approaches with different kernels, including the neural tangent kernels, and compare them with a classical neural network model learning method. Employing synthetic but semi-realistic data, we show how the two introduced approaches are suitable for realizing fast and robust forecasts and scenario analyses, and how these approaches are competitive for determining optimal intervention strategies with respect to specific performance measures.

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1. Introduction

The recent global SARS-CoV-2 pandemic has underlined the paramount importance of developing mathematical models and numerical schemes for predictions and forecasts of epidemic illnesses: from the perspective of policy-makers, it is often useful to

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dispose of qualitative and quantitative results for making scenario analyses and forecasts; from the social point of view sharing information about possible outcomes can be beneficial in order to increase social awareness and public knowledge on the illness current spreading and its future evolutions. A typical approach relies on traditional compartmental mathematical frameworks, where specific modelling choices and parameters embody the different features that characterize the epidemic spreading, the virological effects of the illness and the impact of different pharmaceutical interventions. However, in presence of new epidemic outbreaks many key-features could still be unknown or difficult to isolate in clinical trials, and consequently the illness itself could be difficult to be completely described by the classical compartmental models. Indeed, clinical symptoms of different illnesses are multifaceted and strictly depend on the origin of the pathogenic microbial agent responsible of the disease, which can be bacterial, parasitic, fungal, viral or originated by prions, i.e. other kinds of toxic proteins, and on the pathway through which the illness naturally diffuses [7,26]. Moreover, in order to accurately describe the disease through compartmental models, it is fundamental to account for possible DNA or RNA mutations from the wildtype strain in long-term outbreaks, as well as for possible preventive measures and control, including vaccination, treatments, prophylaxis, quarantine, isolation or other measures minimizing social activities (like the use of face-masks, compulsory home-schooling, different levels of lockdowns). In these highly complex and rapidly changing scenarios, the efficacy of compartmental models for making fast scenario-analyses may be severely limited by the delicate and sometimes ad-hoc parameter calibration process that becomes even harder if one aims at embodying age-dependency or other geographical features, see, e.g., [5,15,33].

Alongside with scenario analysis, recent upcoming epidemic events have shown the importance of disposing of computational tools measuring the impact of pharmaceutical resources [17] and other non-pharmaceutical interventions (NPIs) [19] so to guide policy-makers in choosing how to intervene limiting the social and economic burden. From the mathematical perspective, we can leverage on the versatility of optimal control theory in order to derive useful quantitative and qualitative guidelines for minimizing the amount of infectious or deceased individuals [23,43], the total incidence of the spreading disease [8], or the amount of contacts and, consequently, of cases [11]. Other problems which have been further investigated, analytically and numerically, are more delicate from the mathematical viewpoint such as the minimization of epidemic peaks [29] or the minimization of the eradication time [6].

In view of the above discussion, it is of paramount importance to provide the society with mathematical tools able to output computationally cheap and reliable scenario analyses, so to compare different prevention measures and solve optimal control problems (OCPs). Among recently developed mathematical frameworks, a prominent position is covered by operator learning, which, roughly speaking, deal with the development and application of algorithms designed to build approximations of operators starting from a given set of input/output pairs. In the family of operator learning tools, an increasing attention has been devoted to the so called deep operator networks