

Analytical and numerical study of infection progression under social distancing measures

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Motivation and Aim: The unprecedented worldwide social distancing measures are introduced to respond to the COVID-19 pandemic outburst. While epidemiological compartmental models have conveyed extensive studies on interventions such as quarantine or vaccination, the effects of social distancing on infection outbursts are poorly understood, and even when considered, they have been addressed only numerically. To this end, we develop an analytically tractable model, which considers the gradual introduction of social distancing and optimally utilizes the vast of publicly available data.

Methods and Algorithms: Building upon standard SEIR epidemiological compartmental models, we develop a realistic and analytically solvable SPEIRD (Susceptible-Protected-Exposed-Infected-Recovered-Detected) model [1, 2] that accounts for the effect of social measures by introducing a new compartment – Protected. In particular, the model implies solving highly nontrivial inhomogeneous differential equations. Moreover, an approach well known to theoretical physics (and more recently to quantitative biology) is applied, where one searches for common dynamical features, regardless of other differences.

Results: The model delivers closed-form mathematical expressions for the time dependence of infected (I) [2], detected cases (D) [3], and fatalities (F) [3]. These main infection progression data (I(t), D(t), F(t)) are well reproduced (for a majority of COVID-19 hotspots) through joint analytical and numerical analysis, capturing empirically observed COVID-19 growth signatures of detected cases, that is its three distinct growth signatures (exponential, superlinear, and sublinear regime). The growth signatures and associated scaling laws are utilized [2] to pinpoint regions where analytical derivations are most effective for i) assessing the nearly constant value of the scaling exponent in the superlinear regime; ii) understanding the relationship between the duration of this regime and strength of social distancing (α); iii) recognizing changes in the reproduction number from infection outburst to its extinguishing; vi) constraining the main parameter quantifying the effect of social distancing (α), by analyzing the time duration of the sublinear regime. The combination of α and the time of social measures introduction [3] defines a new parameter – protection time, essential for public policy decision making. For instance, our study not only suggests that rigorous measures can be often substituted by more relaxed ones imposed at earlier times, but provides a direct analytical expression to quantify this balance. We also provide simple analytical expressions [3] to estimate the peak's timing, the epidemic wave's tipping points, and the maximum of detected cases per day. Additionally, our model is applied to infer key infection parameters [2], such as case fatality, infected fatality, and attack rates.

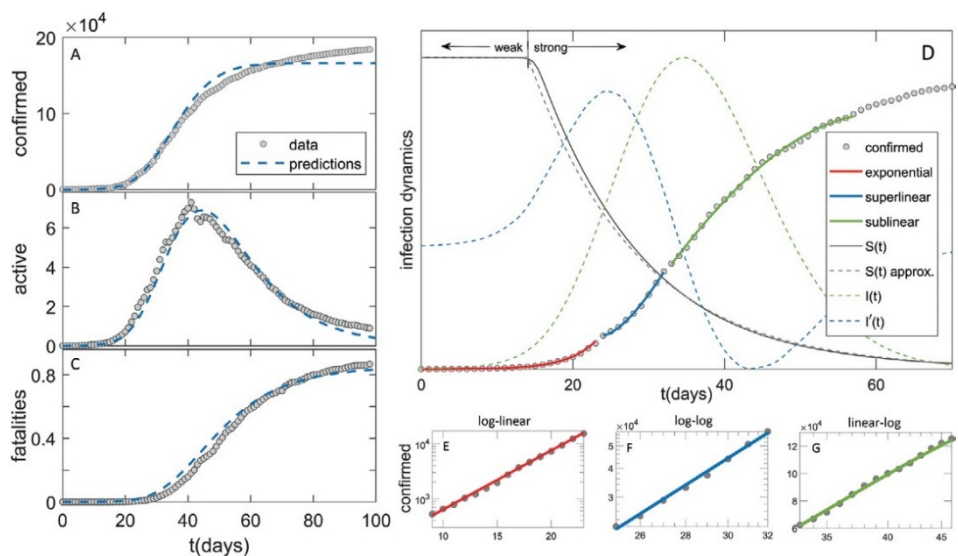


Fig. 1. Comparison between the model (dashed blue curves) and the data (grey circles) in the case of Germany, during the first pandemic wave, for A) detected, B) active cases, and C) fatalities. D) exponential, superlinear, and sublinear fit to detected case data is presented. Arrows indicate the regions with a small and large magnitude of social distancing. The dashed green and blue curve corresponds to the number of infected and its first derivative (whose maxima is $I(t)$ inflection points) respectively. The detected case counts in the three regimes are displayed on E) log-linear, F) log-log, and G) linear-log scale. Figure adapted from [2]

Conclusion: The strength of our analytically tractable model is its ability to qualitatively and quantitatively explain universal growth signatures of infection progression; to provide simple quantitative relations between the model variables and epidemiological observables; to ensure highly constrained infection parameters inference; and to shed light on cause-effect connections that underlie the epidemiological dynamics under social distancing measures, which are obscured in more standard, i.e., purely numerical, approaches. Due to its general relevance, it is applicable to the early stages of any new pandemics when pharmaceutical treatments and vaccines are unavailable and well-timed and appropriately chosen social distancing measures are of the utmost importance. The model does not consider loosening the measures, as was the case during the first COVID-19 wave in many countries. As an outlook, it can be done in our model through a reversible transition from the protected back to the susceptible compartment. Thus, the analytical expressions would be much more cumbersome (or unachievable), though exploring the model numerically in such a case would be highly relevant, which is our future goal.

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