Epidemiological Analysis of 2019 Wuhan Coronavirus Outbreak

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Using multiple models for an infectious disease spread we present preliminary epidemiological predictions for the novel coronavirus (2019-nCoV) outbreak.

1 Introduction

We present results of two models for epidemic dynamics of the novel coronavirus (2019-nCoV). The simplest exponential model, given in Sec. 2, is valid for short-term predictions, while a more involved SIR model (analogous to the rate equations of chemical kinetics for two consecutive chemical reactions), given in Sec. 3, can be used for mid-term predictions. Expected death toll and model assumptions are discussed in Sec. 4 and 5, respectively.

2 Exponential Model

The novel coronavirus (2019-nCoV) was apparently first confirmed in $N_0 \sim 30$ cases around December 7, 2019 in Wuhan, China. While the variance of recently published epidemiological parameters is significant (*2*), we use an average basic reproduction number $R_0 = 2.5$, and

average incubation time $t_i = 2$ weeks. With $R_0 > 1$ an exponential growth in the number of cases can be expected in the early phases of the epidemic, as evidenced by Fig. 1.

The exponential model yields approx. 30 cases in the 4th generation, indicating that the initial patient likely appeared as early as October 2019. In addition, since not all of the first N_0 cases were linked to the Huanan Seafood Market (suspected ground zero), it is likely that the initial patient (apparently infected via bat-human host switching, based on 2019-nCoV genome sequencing) originated from elsewhere.

We also note that the officially reported incidence rates are about 1-2 orders of magnitude lower than those suggested by our model. Such a discrepancy is expected, however, considering that most cases likely remain unreported due to a combination of factors, primarily the limited capacity of health care providers to admit a new patient, and test it for 2019-nCoV. For comparison, recent literature (*3*) estimates only 5% of 2019-nCoV infections to be officially classified as such.

3 SIR Model

The results of a basic compartment model for an infectious disease spread, SIR model, are depicted in Fig. 2. We employ an explicit Runge-Kutta (4,5) method to solve a coupled system of linear ordinary differential equations, and thus follow the temporal evolution of the Susceptible, Infected and Recovered population compartments. As inputs we use an updated reproduction number $R_0 = 4$ valid for January 2020 (*3*), and assume, based on SARS data, that the mean time to recovery (i.e. mean infectious time) is $T_r = \gamma^{-1} = 3$ weeks, which includes the incubation time t_i. This also implies that an infected person makes, on average,

$$\beta = R_0 \gamma = \frac{4}{3} \tag{1}$$

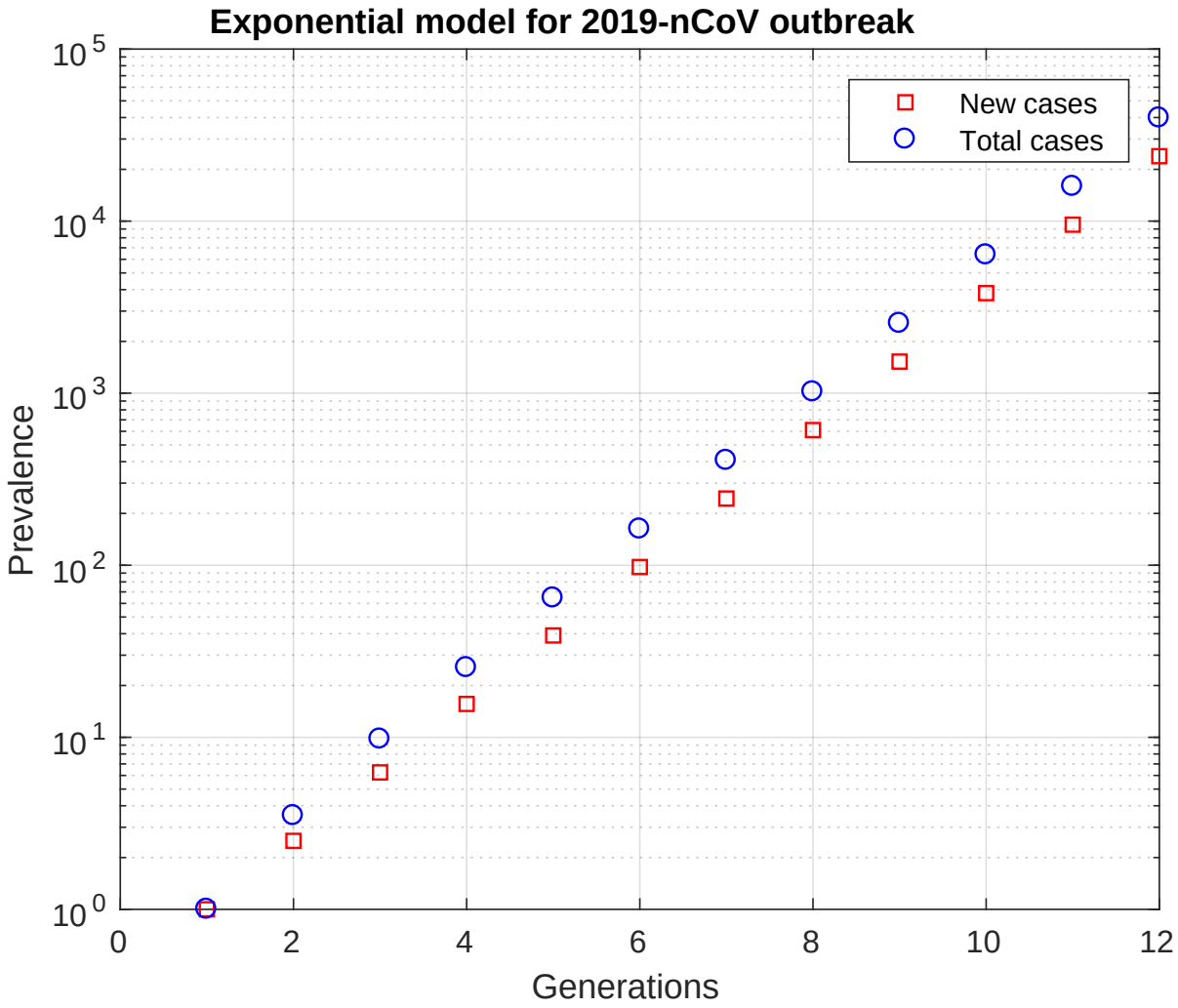

Figure 1: Exponential model for 2019-nCoV outbreak suggests a 4-generation spread potential. $R_0 = 2.5$, incubation time $t_i = 2$ weeks corresponds to the generation spread.

infectious contacts per unit time (week), and suggests that $1 - 1/R_0 = 75\%$ of population would need to be vaccinated to prevent further spread. As the minimum time for influenza vaccine production in ovo is approx. 6 months, the likelihood of the epidemic progressing to pandemic is high.

We see that at the time of this publication there might be approx. 3×10^4 infected, and the infected population size is likely to peak at 40% of world population around the 20th week since the first detection, which corresponds to June 2020. Naturally, these are likely over-estimates, assuming that containment measures are in place (such as a quarantine and/or expedited vaccination, see Sec. 5 for discussion of modeling assumptions), and/or that the virus mutates into a less virulent form.

4 Mortality Prediction

Assuming mortality rate $m = 10\%$, based on recent literature (*1*) and similarities with SARS, we scale the logistic curve for Recovered cases from the SIR model to estimate the temporal evolution of the cumulative deaths in human population, see Fig. 3. As the vaccine would likely be available around week 25, the total number of deaths would remain below 9% of the current world population.

5 Modeling Assumptions and Final Comments

Due to the uncertainty in, and time variability of, the input parameters, and the modeling inaccuracies, the results given above are expected to diverge from reality as the time progresses.

First, the SIR model relies on several simplifying assumptions, most importantly the constancy of population size N and transition rates β and γ, and a well-mixed population, which are all difficult to justify in the long-term. A significant size of the human reservoir and a high mutation rate of RNA viruses such as 2019-nCoV suggests that while R_0 and mortality rate m

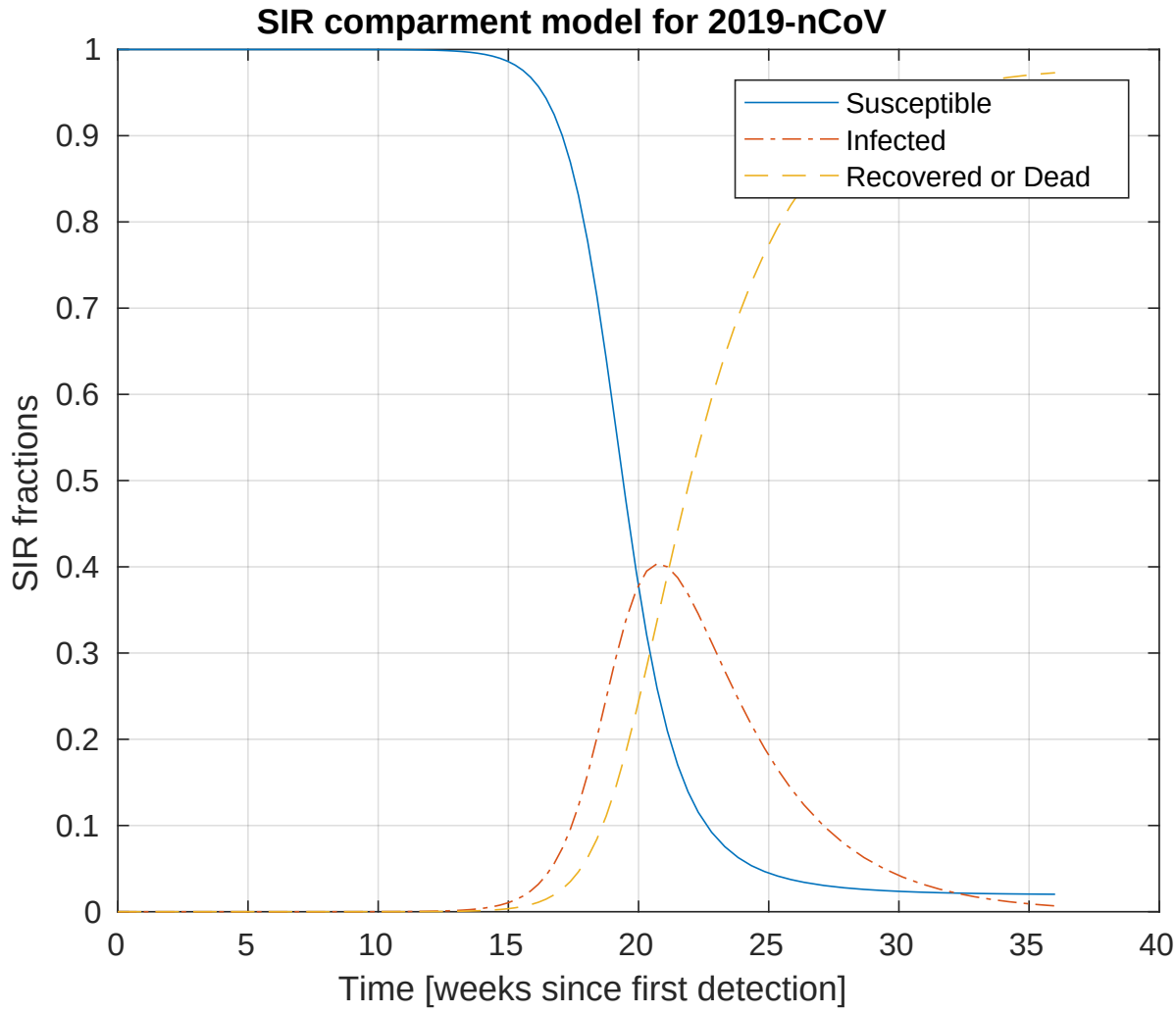

Figure 2: SIR compartment model (without vital dynamics) for 2019-nCoV outbreak. $R_0 = 4$, $\gamma^{-1} = 3$ weeks, $N_0 = 30$ cases. The 0th week corresponds to first detection (49th week of 2019, or, equivalently, -4th week of 2020). SIR fractions scaled by world population, $N = 7.7 \times 10^9$.

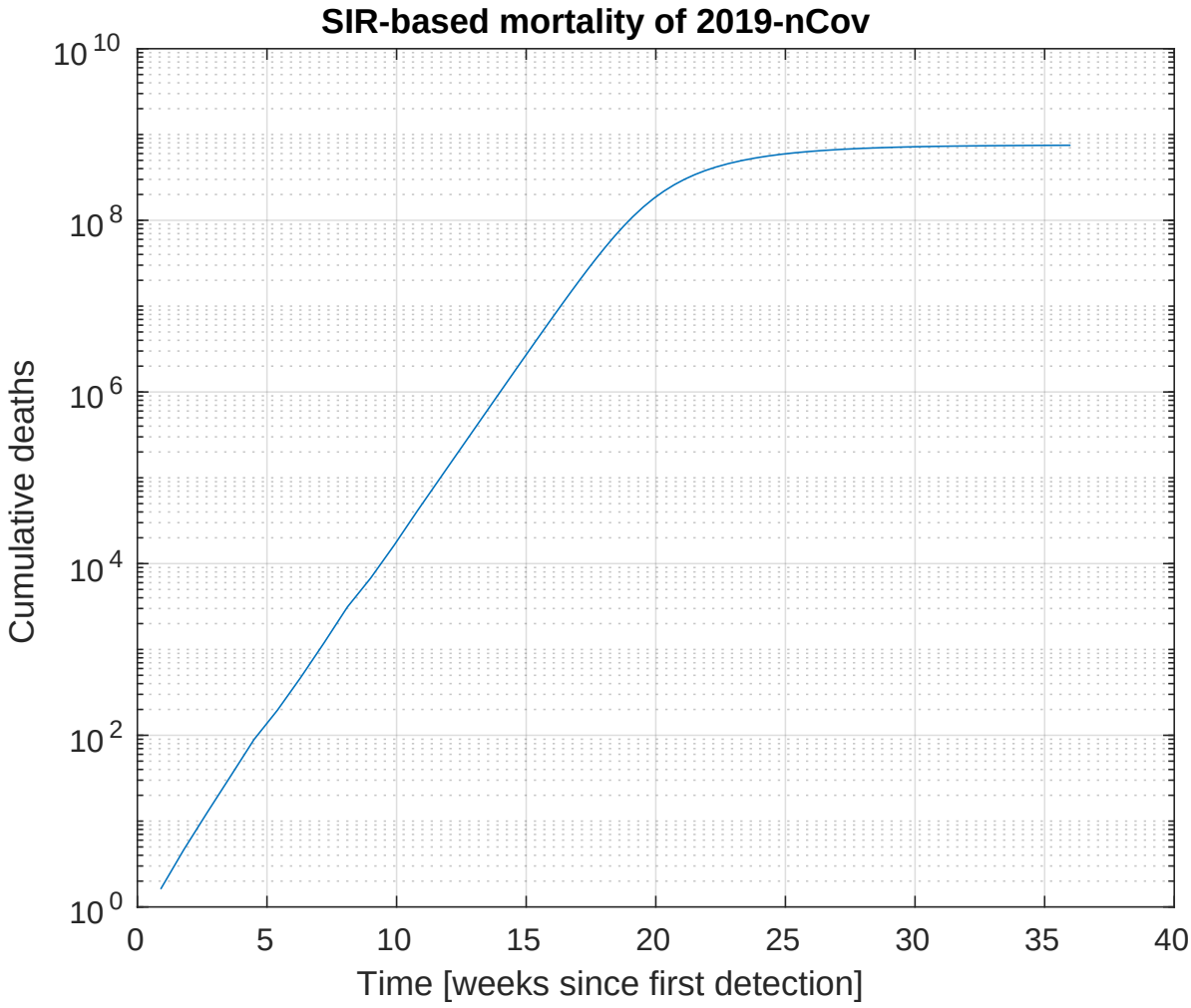

Figure 3: SIR-based mortality of 2019-nCov, assuming mortality rate 10%.

may initially increase due to increased virulence, a long-term differential reproductive success will be conferred upon the virus only by mutations that lower the mortality of the host.

Containment protocols often include various types of quarantine, which also violates the assumption of a well-mixed population and modifies the input parameters.

About the author

Petr Hotmar received Master of Science in Cybernetics from The Institute of Chemical Technology, Prague, Czech Republic, Master of Science and Ph.D. in Chemical and Biomedical Engineering from Florida State University, Tallahassee, USA, and a post-doctoral fellowship in Plasma Physics from LAPLACE Laboratory in Toulouse, France. He specializes in computational physics, applied mathematics and biology.

References and Notes

1. Huang C. et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China.

2. Imai N et al. Report 3: Transmissibility of 2019-nCoV.

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