Limits of Predicting Epidemic Outbreaks

Bastian Prasse, Massimo A. Achterberg and Piet Van Mieghem

During the outbreak of a virus, perhaps the greatest concern is the future evolution of the epidemic: *How many people will be infected and which regions will be affected the most?* For many epidemic models, the cumulative number of infections $\mathcal{I}_c(t)$ at time t follows, at least approximately, a logistic function

$$\mathcal{I}_c(t) = \frac{y_\infty}{1 + e^{-K(t-t_0)}}, \tag{1}$$

where the *steady-state* $y_\infty > 0$ is the eventual, total number of infections, and $K > 0$ denotes the *growth rate*. The *inflection point* t_0 specifies the time of the largest increase of new infections called the peak of the epidemic. By fitting (1) to the reported infections until some observation time t_{obs}, the logistic function can predict the infections at times $t > t_{\text{obs}}$. Figure 1 shows that the prediction of a logistic function is ill-conditioned. More specifically, a good fit to the epidemic data until the observation time t_{obs} does *not* imply accurate predictions at times $t > t_{\text{obs}}$. *Hence, even under idealised conditions, the long-term prediction of an epidemic is inherently difficult, regardless of the particular prediction algorithm.*

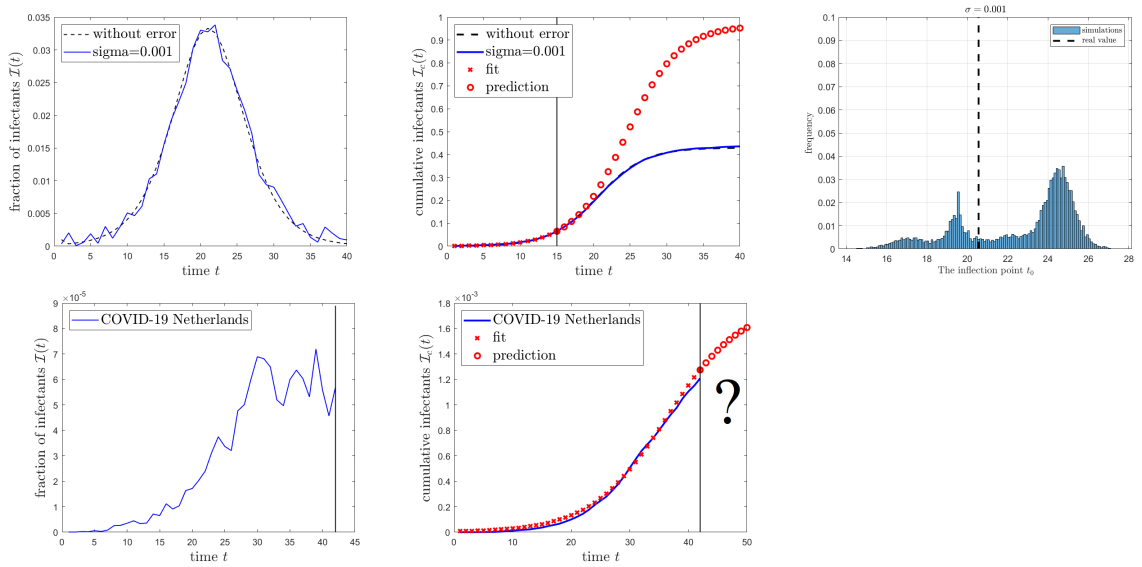

Figure 1: ***Sensitivity of predicting an epidemic outbreak.*** *The first row corresponds to the logistic function (1) with and without additive Gaussian model errors $w(t) \sim \mathcal{N}(0, 10^{-6})$. The COVID-19 infections in the Netherlands (up to April 9) are shown in the second row. The first column shows the new number of infections $\mathcal{I}(t) = d\mathcal{I}_c(t)/dt$, and the vertical line indicates the observation time t_{obs}. The cumulative number of infections $\mathcal{I}_c(t)$ is shown in the second column. Repeating the simulations in the top row for 10,000 times yields the histogram of inflection-point estimate $\hat{t}_0$ of the fitted logistic function in the top right subfigure.*

References

[1] B. Prasse, M. A. Achterberg, and P. Van Mieghem, "Fundamental limits of predicting epidemic outbreaks," *TU Delft report2020410*, 2020. [Online]. Available: `www.nas.ewi.tudelft.nl/people/Piet/TUDelftReports.html`