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Flattening the Curve

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ABSTRACT: We quantify flattening the curve under the assumption of a soft quarantine in the spread of a contagious viral disease in a society. In particular, the maximum daily infection rate is expected to drop by twice the percentage drop in the virus reproduction number. The same percentage drop is expected for the maximum daily hospitalization or fatality rate. A formula for the expected maximum daily fatality rate is given.

Keywords: Infectious disease modelling, Reproduction number, SIR models, Flattening the curve, Maximum daily fatality rate.

Introduction

In the middle of March 2020 the Canadian government reacted to the spread of the virus Covid-19 by implementing social interaction restrictions in the society. This was in line with other world government actions. It was not known how many people were infected at the time nor was it known how contagious the virus was. However, it was expected, based on reports from experts, the virus had a high contagious value, a high reproduction number. It was also unclear as to what the mortality rate was since the overall number of infected people was unknown. There was an overall fear the virus would cause high rates of hospitalization and thus put an unsustainable pressure on the medical system. The slogan of the day was to flatten the curve. What is flattening the curve?

Flattening the curve is a popular expression where the society is implementing social physical distancing, a certain level of a soft quarantine, in an attempt to reduce the maximum daily infection rate due to COVID-19. The aim is to reduce the maximum daily hospitalization and fatality rate. As a result the duration of the pandemic is extended and the time till the arrival of the maximum daily infection rate is delayed. Flattening the curve is not about reducing the total number of infected in the long run, albeit for larger flattening it would reduce the total number of infected to a certain degree.

The curves that are being flattened are the graphs of daily infection rates from the virus that initially pick up fast (exponential growth) reach a peak and then dissipate due to the fact that the virus is infecting people that have been already infected. The shapes of these curves resemble the bell shape graph with its peak being the maximum daily infection rate and the width being the bulk of the duration of the pandemic in days. The area under the curve is the total number of people that will be infected over the course of the pandemic.

The value R is a quantity that indicates how contagious an infectious disease is, called the reproduction number. It indicates the number of people one person will infect on average during their contagious period. If the reproduction R value is below one then the pandemic does not take off as the number of infected decreases immediately. However, for higher reproduction values the pandemic does occur.

If for instance, $R = 2$ then the number of infected doubles every time the length of the contagious period passes. Note that the reproduction number can be a decimal value, for example $R = 1.8$ would indicate that on average one person will infect 1.8 people over the duration of their contagious period. To put it differently, on average ten people will infect 18 people over their contagious period.

One can use basic yet revealing so called SIR models to predict the reduction in the maximum daily rate of infection (how much you flatten the curve) in terms of the reduction in the R value. In the acronym SIR the letter S stands for susceptible, I for infected and R for recovered.

We give the following rule of thumb under the assumption of a soft quarantine. If you manage to decrease the reproduction number by a certain percentage (apply stricter restriction measures) then the maximum daily infection rate is expected drop by twice the percentage. The same percentage drop is expected for the maximum daily hospitalization or fatality rate. This estimate is valid for reproduction R values that are significantly bigger than one that result from implementing soft quarantines. Under this soft quarantine scenario we would have at least half of the population infected by the virus in the long run.

We also assume the pandemic lasts significantly longer than the duration of the disease, in particular, the R values are not too high. This latter assumption is met in the case COVID-19. For example, if the reproduction number is reduced from $R = 2$ to $R = 1.9$ (a drop of 5 %) due to a certain implemented societal restriction, then we would expect a 10 % drop in the maximum daily infection rate and thus expect a 10 % drop in the maximum daily hospitalization or fatality rate.

In reality the implementations of societal restrictions are time dependent and therefore the corresponding reproduction R value is also time dependent. Moreover, the societal restrictions, and hence the resulting quarantine, can become strict enough to bring down the reproduction R value below one and hence stop the pandemic altogether for the time being. However, the above rule of thumb is of value in order to understand the sensitivity of the maximum daily rate of infection to the changes in the R value, albeit for R values well above one. We provide an example later on based on data from the province of Alberta, Canada.

Assuming the implementation of a soft quarantine, with at least half of the population infected by the virus in the long run, we propose a formula for the expected maximum daily fatality rate to be given by

$$\frac{R^2 K m}{4T}$$

where m is the mortality rate (proportion of infected that die), K is the population count of the society, and T is the duration of the disease. For example, if $m = 0.0001$, one in ten thousand, $K = 40$ million and $T = 14$ days, we get the expected maximum daily fatality rate to be about 231 per day if we have $R = 1.8$.

The Analysis

We set the time of the beginning of the pandemic, $t = 0$, when the society implemented the social restrictions. Time t is measured in days. We will assume people are contagious for the time period close to that of the duration of the disease and then they leave the contagious pool. While they are infected they can be either asymptomatic or have symptoms and self isolate or not.

We assume the disease will last for T days and then people will recover from the disease and obtain immunity. Statistically vast majority get cured, albeit, unfortunately, a certain limited small proportion will have a fatality.

We have $P(t)$, the number of people infected or past infected at time t, with the initial number of infected being $P(0)$. Note that the amount $P(t)$ contains all the people that had recovered from the disease. The value T is the number of days after which an infection ability ends, people no longer infect others.

We define a contagious value $r = R/T$. For example, the value of $r = 0.15$ (per day), would indicate that on average two people infect three people over the span of ten days. The corresponding R value is then $R = Tr = 14(0.15) = 2.1$, if $T = 14$ days. Note that the r value inherently contains the contagiousness of the virus along with the implemented quarantine.

We set forth the following model.

$$\frac{dP}{dt} = \begin{cases} rP(t)\left(1 - \frac{P(t)}{K}\right) & t \leq T \\ r\left(P(t) - P(t-T)\right)\left(1 - \frac{P(t)}{K}\right) & T < t. \end{cases}$$

With the onset of the pandemic the (daily) rate of change of infected people is proportional to the r value as well as the amount of infected people $P(t)$. For time $t \leq T$ every member of $P(t)$ is contagious. However, a person might be, by chance, infecting a person that has been infected already. The probability that, at time t, an infected person infects a non-infected person is $1 - \frac{P(t)}{K}$. After T days only the amount of people $(P(t) - P(t-T))$ is contagious. In this model we assume people are free to mix, albeit in restrictive way, understanding some are unaware of their infection status, some are, and they are self isolating or not. The effect of fatality on the value K is assumed to be negligible, thus the term $1 - \frac{P(t)}{K}$ remains unchanged.

The (daily) rate of infection $\frac{dP}{dt}$ initially picks up exponentially as the dominant driver is the term rP, as the multiplier $\left(1 - \frac{P(t)}{K}\right)$ is close to one due to small values of P. However, after a while the bracket $\left(1 - \frac{P(t)}{K}\right)$ will be dropping to zero as P increases and thus mitigating and slowing down the exponential growth of the infection spread. Eventually, the (daily) rate of infection will approach zero.

The above model is a variant of the many SIR models. For a reference on SIR models, logistic and exponential growth models, we refer the reader to [Ba], [Be], [H], [HLM], [KM], [V].

For those who have died from the disease the mean time to death in days since infected is denoted by Q. Therefore, the expected daily fatality rate function is given by

$$m\frac{dP}{dt}(t - Q)$$

people dying per day. For a typical seasonal influenza virus the mortality rate is about one in ten thousand, $m = 0.0001$. The Q value is tougher to estimate, somewhere between 3 to 10 days. A typical seasonal influenza virus has a higher mortality rate among older population or among people with pre-existing conditions. This phenomenon is even more pronounced in the case of COVID-19. The case of

hard hit nursing homes, which are to a certain degree islands in themselves, needs to be treated separately from our model here.

Let us now study the maximum daily rate of infection and hence the maximum daily fatality rate. The associated function for this maximum is the function $\frac{dP}{dt}$. At the time of the daily maximum rate in infection we have the following estimate

$$(P(t) - P(t - T)) \approx rPT$$

due to the observation that the rate of change of P is maximal then. It is the time when the graph of $P = P(t)$ has the highest slope and thus the secant line slope and the tangent line slope are close to each other. It is here that we assume the pandemic has to extend well past the time T. Therefore, we have

$$
\begin{aligned}
\max \frac{dP}{dt} &= \max \left\{ r\left(P(t) - P(t-T)\right)\left(1 - \frac{P(t)}{K}\right) \right\} \\
&\approx r\left(rPT\right)\left(1 - \frac{P(t)}{K}\right) \\
&= r^2 PT\left(1 - \frac{P(t)}{K}\right).
\end{aligned}
$$

The maximum for the expression $P\left(1 - \frac{P(t)}{K}\right)$ occurs when $P = K/2$ which we assume will happen under our scenario. In particular, we have

$$\max P\left(1 - \frac{P(t)}{K}\right) = \frac{K}{4}.$$

Therefore we obtain

$$\max \frac{dP}{dt} \approx \frac{r^2 TK}{4}.$$

If we set mortality at m then we obtain the desired formula.

$$\max \text{daily fatality rate} \approx \frac{r^2 TKm}{4} = \frac{R^2 Km}{4T}.$$

To obtain the double the percentage rule mentioned in the introduction we denote

$$M(R) = \frac{R^2 Km}{4T}$$

and observe

$$dM = \frac{2RKm}{4T} dR.$$

The desired rule

$$\frac{dM}{M} = 2\frac{dR}{R}$$

then follows.

Example with Data.

We will estimate the number of people infected by COVID-19 in the province of Alberta, Canada, by the end of April 2020. Our findings will be based on the work in [SH] that indicates that mortality rate due to COVID-19 is around one in ten thousand, similar to that of seasonal influenza virus. The authors pivot around few studies done on random testing, one in particular, a recent random testing of $3,200$ inhabitants of Santa Clara County, California, population around 2 million, showed the death rate was similar to the annual flu rate, and that a large number of residents probably carry the virus antibodies.

Let us apply the results of this study to the Alberta case. It is estimated, see [AHS], that about three quarters of deaths occur in long term care homes, which we treat as islands in themselves and thus remove from our model. By April 28, 2020 Alberta government reported 80 deaths. However, we keep only 20 deaths, one quarter, for our model. Assuming a mortality $m = 0.0001$ we estimate Alberta had about $200,000$ people infected or past infected by COVID-19 by April 28, 2020. By April 8, 2020 the death count was at 50, keeping a quarter, therefore we estimate 125000 people infected or past infected by April 8. Note that during this time period international travel was extremely limited and inter-provincial movements as well. The assumption of a closed society with only only natural increases in infected or past infected is a viable one for this time.

The average rate of change of infections during the time between April 8 and April 28, 2020 is given by

$$\frac{dP}{dt}_{\text{ave}} = \frac{200000 - 125000}{20} = 3750$$

people infected per day. By the Mean Value Theorem there was a time instant, in Alberta, between April 8 and April 28, 2020, when the instantaneous infection rate was 3750 people per day.

We would like to expose a common approach, yet hugely erroneous, how to calculate the mortality rate due to COVID-19. We are referring to a calculation that takes the number of deceased due to COVID-19 in a society divided by the number of people that tested positive for COVID-19. This, however, presents a huge error as the number of deaths is drawn from the whole population, whereas the number that tested positive for COVID-19 is drawn from a very small, albeit biased sample from the society. This ratio massively overestimates the mortality rate from COVID-19. Hypothetically, if we test no-one then we would divide by zero. We definitely need a random testing to answer the question of the mortality rate due to COVID-19.

Conclusion and Remark

Many countries have implemented soft quarantines during the COVID-19 pandemic. There was a frenzy of media attention to the concept of flattening the curve. The idea was to introduce social distancing in order to reduce the maximum daily hospitalization rate in the future. Our paper provides a quantitative formula as how the maximum daily hospitalization rate is going to be reduced as the reproduction number of the virus drops due to the implemented societal restrictions. We also provide a closed form formula for the expected daily maximum fatality rate.

References

[AHS]   *Alberta Health Services.* https://www.alberta.ca/covid-19-alberta-data.aspxtoc-1

[Ba]   Bailey, Norman T. J. (1975). *The mathematical theory of infectious diseases and its applications (2nd ed.).* London: Griffin. ISBN 0-85264-231-8.

[Be]   Bernstein, Ruth (2003). *Population Ecology: An Introduction to Computer Simulations.* John Wiley Sons. p. 37. ISBN 978-0-470-85148-7.

[HLM]   Harko, Tiberiu; Lobo, Francisco S. N.; Mak, M. K. (2014). Exact analytical solutions of the Susceptible-Infected-Recovered (SIR) epidemic model and of the SIR model with equal death and birth rates. *Applied Mathematics and Computation.*, 236, 184–194.

[H]   Hethcote, H. (2000). The Mathematics of Infectious Diseases. *SIAM Review*, 42(4), 599–653.

[KM]   Kyurkchiev, Nikolay; Markov S. (2015). *Sigmoid functions: some approximation and modelling aspects.* LAP LAMBERT Academic Publishing, Saarbrucken.

[SH]   Simpson, E.; Harris, T. (2020) A National Random Testing is Essential to Determine the True Infection and Mortality Rate of Coronavirus *Frontier Center for Public Policy* Commentary, COVID-19, Government, April 25, 2020 https://fcpp.org/2020/04/25/a-national-random-testing-is-essential-to-determine-the-true-infection-and-mortality-rate-of-coronavirus/

[V]   Vynnycky, E.; White, R. G., eds. (2010). *An Introduction to Infectious Disease Modelling..* Oxford: Oxford University Press. ISBN 978-0-19-856576-5.

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