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Review Article

Dynamic Modeling COVID-19 for Comparing Containment Strategies in a Pandemic Scenario

Min Lu*

Department of Public Health, University of Miami, USA

***Corresponding author:** Min Lu, Department of Public Health, University of Miami, USA.

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Abstract

Since instances of coronavirus disease 2019 (COVID-19) community spread emerged in the United States, federal and local governments have implemented multiple containment measures. However, in order to satisfy the needs of citizens, the strictest containment measures can be only executed for short period. This article compares two types of containment strategies: a constant containment strategy that could satisfy the needs of citizens for a long period and an adaptive containment strategy whose strict level changes across time. When to implement the strictest measures is also of interest. A prediction model is proposed and a simple tool is developed for policy makers to compare different containment strategies. As an example, a county with 2.8 million populations with initial 200 infected cases is considered, where about 0.2% people dead during the pandemic. Compared with a constant containment strategy, adaptive containment strategies shorten the outbreak length, but executing the strictest measures late, even with stricter overall containment measures, will cause more mortality.

Keywords: Containment measures;; Incubation period; Infectious period; Pandemic; Period of communicability; Survival function.

Introduction

To prevent the spread of a new respiratory disease - coronavirus disease 2019 (COVID-19), policy makers rely on prediction models to foresee the dynamic of infected cases and prepare for adopting containment measures including patient quarantine, active monitoring of contacts, border controls, and community education and precautions [1-4]. There are many prediction models available for the COVID-19 pandemic [5-7,6-11,12,13,14]. To apply them for predicting local COVID-19 spread, there are two major challenges. Firstly, number of actual infected cases is usually unconfirmed and could be far larger than confirmed cases because there is significant number of infected cases in incubation period and test kits may be insufficient. On the other hand, regions that experienced earlier outbreaks can provide valuable information, such as the distribution of cure time, death time, and mortality rate [15], but it is not easy to integrate these dynamic parameters into most of the current models.

This article provides a simple and robust model framework whose parameters are dynamically adjustable and generally interpretable for policy makers. The model allows unconfirmed infected cases and confirmed infected cases have different transmissibility. Survival analysis is integrated in it to borrow information from regions that experienced earlier outbreaks. Moreover, the model enables containment measures to change over time [16] through introducing a novel reproduction number which incorporate containment measures and the basic reproduction number (R_0).

The Model

Assume the disease of interest has an M-day period of communicability so that infected people are either cured or dead within M days. Denote the mortality rate within an infectious period as m_{death} and the cure rate will be $1-m_{death}$. On day t, denote the number of people that have been infected for d days as $p_{t,d}$ and the total number of infected cases is Pt = PM d=1 $p_{t,d}$. $p_{t,d}$ is determined by the following factors:

• Mortality rate for people that have been infected for d days, denoted as m_d ,

• Cure rate for people that have been infected for d days, denoted as c_d ,

• number of people that an infected person can communicate on day t: when an unconfirmed infected case (for the reason of incubation period or insufficient test kits) pass the disease, it is denoted as reproductive number $R_t^{unconfirmed}$; for a confirmed infected case, it is denoted as $R_t^{confirmed}$ and $R_t^{confirmed} < R_t^{unconfirmed}$ because the person will be either hospitalized or quarantined at home with extra care,

• Test rate on day t, denoted as r_t^{test} , which means that among the newly infected cases on day t, $\left(100\% - r_t^{test}\right)$ of them are unconfirmed infected cases and r_t^{test} of them are confirmed infected cases,

• And the number of travelers from other areas who have been infected for d days, denoted as $p_{t,d}^{imp}$.

When moving forward from day t to t + 1, number of people who have been infected for d days (on the d_{th} day in their periods of communicability), $p_{t+1,d}$, is the sum of the number of survived but uncured cases from day t, the number of newly infected cases and the number of imported cases, denoted as $P_t = \sum_{d=1}^{M} P_{t,d}$ [17,18,19]:

$$P_{t+1} = \sum_{d=1}^{M} \rho_{t+1,d} = \sum_{d=1}^{M-1} \rho_{t,d}\left(1 - m_d - c_d\right) + P_t r_t^{test} R_t^{confirmed} + P_t\left(1 - r_t^{test}\right) R_t^{unconfirmed} + P_{t+1}^{imp}$$

Note that people who have been infected for M days $\left(p_{t,M}\right)$ won't affect P_{t+1} since their period of communicability will be over and they will be either dead or cured.

Parameter Specification

To specify mortality rate , a cumulative distribution function $F_{death}\left(t\right) = \mathrm{P}\left(T_d \le t\right)$ is defined in interval $\left[0, M\right]$ for death time T_d and $F_{death}\left(M\right) = m_{death}$. A lognormal distribution function is used as $F_{death}\left(t\right) = \frac{1}{2} + \frac{1}{2} erf\left[\frac{\ln t -}{\sqrt{2}}\right.$, where $erf\left(x\right) = \frac{2}{\sqrt{\pi}} \int_0^x e^{-t^2} dt$. Here, parameters are set as $\sigma = 0.8$ and $\mu = \ln\left(M\right) - \sqrt{2}\sigma erf^{-1}\left(2m_{death} - 1\right)$ where $erf^{-1}\left(x\right)$ denotes the inverse function of $erf\left(x\right)$. A patient has the probability of dying from day to $d+1$ as

$$m_d = \mathrm{P}\left(d < T < d+1\right) = F_{death}\left(d+1\right) - F_{death}\left(d\right)$$

Similarly, cure rate is modeled as $c_d = F_{cure}\left(d+1\right) - F_{cure}\left(d\right)$, where $F_{cure}\left(t\right) = \mathrm{P}\left(T_c \le t\right)$ is defined in interval $\left[0, M\right]$ for cure time T_c and $F_{cure}\left(M\right) = 1 - m_{death}$. After specifying $F_{cure}\left(t\right) = \frac{1}{2} + \frac{1}{2} erf\left[\frac{\ln t - \mu_c}{\sqrt{2}\sigma_c}\right]$ we set $\sigma_c = 0.4$ and $\mu_c = \ln\left(M\right) - \sqrt{2}\sigma_c erf^{-1}\left(1 - 2m_{death}\right)$. For initial time, set $F_{death}\left(0\right) = F_{cure}\left(0\right) = 0$.

The reproductive numbers $R_t^{unconfirmed}$ and $R_t^{confirmed}$ are determined by the basic reproduction number R_0 , the containment measures on day and the percentage of uninfected people. It is assumed that cured cases will not get infected again since they are immune to the disease. Since R_0 is a constant, we only need to set

$$R_t^{unconfirmed} = r_t \times \frac{P_{pop} - P_t - \sum_{i=1}^{t}\left(D_i + C_i\right)}{P_{pop}}$$

where $D_i = \sum_{d=2}^{M} \rho_{i-1,d} m_d$ is the number of deaths on day $t = i$, $C_i = \sum_{d=2}^{M} p_{i-1,d} C$ is the number of cured patients on day $t = i$, and P_{pop} denotes the total population. The crucial parameter is which is used to specify the containment scenario. Set $R_t^{confirmed} = k \times R_t^{unconfirmed}$, where $k \in \left(0,1\right)$.

For initialization, infected durations are generated from Poisson distribution to mimic the individual variation [20], where $p_{1,d} = \sum_{i=1}^{P_1} 1_{X_i = d}$ and $p_{t,d}^{imp} = \sum_{j=1}^{p_t^{imp}} 1_{X_j = d}$. $X_i s$ and $X_j s$ are identically and independently distributed from a Poisson distribution with mean λ . When the generated value is zero or larger than M , it is set as 1 or M .

Results and Conclusion

To compare different containment strategies, suppose a county is going to experience a COVID 19 outbreak in the scenario illustrated in Table 1. After monitoring 100 simulation replications, the dynamic of infected cases does not change much from random initialization. (Figure 1) In total, numbers of deaths from strategies A, B and C are 5.34×10^3, 4.99×10^3 and 5.61×10^3; numbers of infected cases are 1.87×10^5, 1.75×10^5 and 1.97×10^5. The number of infected cases, Pt , reaches its peak on the 42th, 36th and 35th day and the number of deaths, D_t , reaches its peak on the 66th, 59th and 60th day from strategies A, B and C. After the peak of P_t , containment strategy does not make much difference on the trend of P_t or D_t .

As a conclusion, compared with a constant containment strategy, adaptive containment strategies shorten the outbreak length. In order to achieve lower death rate, the strictest measures should be implemented two weeks before the peak of infected cases, instead of executing them during the peak. Adaptive strategy is less strict at

the beginning, which results more severe spread. Even that, the following stricter measures effectively shortens the outbreak length [20]. When to choose the strictest measures is critical to achieve minimum total death rate, which is highly affected by the peak of predicted daily infected case under a constant containment strategy. Implementing the strictest measures late even with stricter overall containment measures, will cause more mortality.

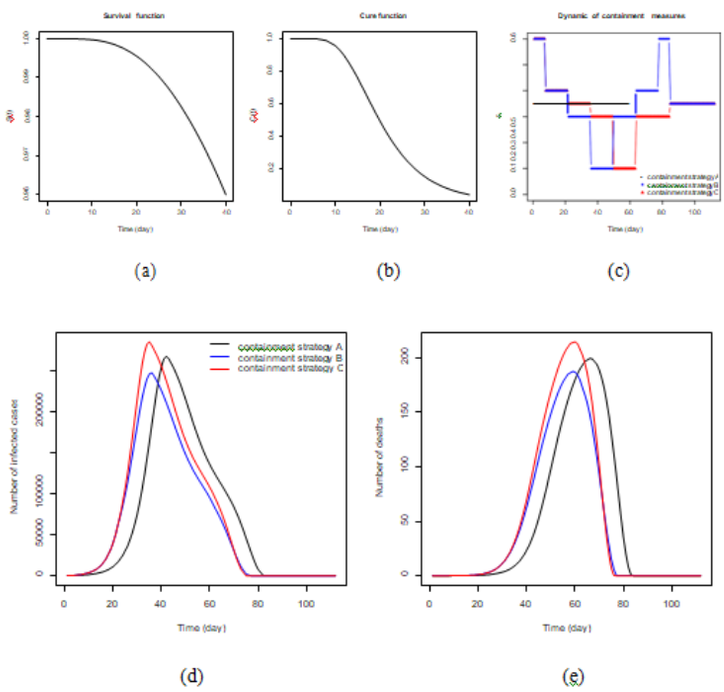

Figure 1: Containment strategy comparison from inputs illustrated in Table 1. Survival and cure functions with 4% mortality rate within 40 days are plotted in sub-figures (a) and (b). Sub-figure (c) demonstrates the strict level of containment strategies across time. Strategy A (black) has constant strict level while level of strictness can change weekly from strategies B (blue) and C (red). Strategy C implements the strictest measures two weeks earlier than strategy B. The averages of rt for strategies A and B are both 0.35, and the average of rt for strategy C is 0.325, which means that strategy C is overall stricter. From sub-figure (d) and (e), we can see that strategy C results in the largest number of infected patients and deaths, followed by A and B. More adaptive containment strategies, B and C, ends the outbreak faster.

Table 1: Necessary inputs for policy makers to compare different containment strategies.

Domain	Value	Description
Disease	$M = 40$	Infected cases will be either cured or dead within M days.
	$m_{death} = 4\%$	Within M days, m_{death} of infected cases will be dead.
	$r_t^{test} = (30 + 0.3t)\%$	On day t, r_t^{test} of newly infected cases are tested for virus.
	$\sigma_c = 0.8$	Parameter to shape the distribution function of death time.
	$\sigma_c = 0.8$	Parameter to shape the distribution function of cure time.
People	$P_{pop} = 2.8 \times 10^6$	On day 1, P_{pop} individuals are not infected within the region.
	$P_1 = 200$	On day 1, P_1 individuals are infectious.
	$P_{15}^{imp} = P_{48}^{imp} = 2$ $P_{29}^{imp} = P_{63}^{imp} = 4$	On day 15, 29, 48 and 63, there are two, four, two and four infectious people who travel into the region.
	$\lambda = 10$	Initial infectious cases, counted in P_1 and P_t^{imp}, have been infected for λ days on average.

Policy	r_t described in Figure 1(c)	Smaller value represents stricter containment measures*.
	$k = 0.1$	$k = R \leq_t^{unconfirmed} / R_t^{confirmed}$

* r_t can be interpreted as the average number of newly infected case communicated *per infectious person per day* on day , if nearly all the population are uninfected. For example $r_t = 0.35$ from strategy A, implies every 100 infectious cases will communicate to 35 individuals per day on average. The model will adjust these inputs with percentage of infected cases across time, which produces $R_t^{unconfirmed}$ and $R_t^{confirmed}$.

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Conflict of Interest

No conflict of interest.

Supplement

An online prediction tool is provided at https://minlu.shinyapps.io/killCOVID19/, where $R_t = r_t^{test} R_t^{confirmed} + \left(1 - r_t^{test}\right) R_t^{unconfirmed}$ and R_t across time is available for every state and county in the United States at https://minlu.shinyapps.io/killCOVID19map/.

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